

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:50:31 ; Search time 28.0159 Seconds
(without alignments)
1678.958 Million cell updates/sec

Title: US-09-885-478-28
Perfect score: 1824
Sequence: 1 MDLEASLLPTGPNASNTSDG.....LRVSNQAQTADERTESKGT 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

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19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1824	100.0	353	19	AAW61370	Human 11CB splice
2	1824	100.0	353	20	AAV16570	Amino acid sequenc
3	1824	100.0	353	21	AAB13442	Truncated human MC
4	1824	100.0	353	21	AAV90258	Human 11cby protel
5	1824	100.0	353	22	AAE07328	Human melanin-conc
6	1824	100.0	353	22	AAE04747	Human 11CBY protel
7	1824	100.0	353	22	AAV97668	Human MCH-R1 prote
8	1824	100.0	353	22	AAB85895	Human short form M
9	1824	100.0	353	23	AAU76893	Human melanin-conc
10	1824	100.0	353	23	AAU75859	Human melanin conc

11	1824	100.0	417	22	AAE07329	Human melanin-conc
12	1824	100.0	417	22	AAV97669	Human MCH-R2 prote
13	1824	100.0	422	21	AAB12779	Human SLC-1 protei
14	1824	100.0	422	21	AAB13436	Human MCH1 recepto
15	1824	100.0	422	22	AAE07330	Human melanin-conc
16	1824	100.0	422	22	AAB81123	Human melanin conc
17	1824	100.0	422	22	AAB96871	Human SLC-1, Homo
18	1824	100.0	422	22	AAV97670	Human MCH-R3 prote
19	1824	100.0	422	22	AAB85894	Human long form MC
20	1824	100.0	422	23	AAU75541	Human melanin conc
21	1824	100.0	422	23	AAU75853	Human melanin conc
22	1824	100.0	422	23	AAB80491	Human SLC-1 protei
23	1824	100.0	422	23	AAG80611	Human SLC-1 protei
24	1824	100.0	709	22	AAB56396	TSHR-Gs-alpha fusi
25	1819	99.7	353	22	AAB56307	Non-endogenous hum
26	1819	99.7	422	21	AAB13440	Mutant human MCH1
27	1819	99.7	422	21	AAB13441	Mutant human MCH1
28	1819	99.7	422	23	AAU75857	Human melanin conc
29	1819	99.7	422	23	AAU75858	Human melanin conc
30	1818	99.7	353	22	AAB56297	Non-endogenous hum
31	1818	99.7	353	22	AAB56305	Non-endogenous hum
32	1817	99.6	353	22	AAB56306	Non-endogenous hum
33	1814	99.5	353	22	AAB56301	Non-endogenous hum
34	1814	99.5	353	22	AAB56303	Non-endogenous hum
35	1814	99.5	353	22	AAB85897	Human short form/m
36	1814	99.5	422	22	AAB85898	Human long form/mo
37	1814	99.5	604	22	AAB85906	Human short form/m
38	1814	99.5	673	22	AAB85907	Human long form/mo
39	1813	99.4	353	22	AAB56300	Non-endogenous hum
40	1812	99.3	353	22	AAB56298	Non-endogenous hum
41	1811	99.3	353	22	AAB56302	Non-endogenous hum
42	1811	99.3	353	22	AAB56304	Non-endogenous hum
43	1808	99.1	353	21	AAV57284	Human GPCR protein
44	1781	97.6	353	23	AAU76892	Dog melanin-concen
45	1763	96.7	353	21	AAB12778	Rat SLC-1 protein

ALIGNMENTS

RESULT 1	
AAW61370	
ID	AAW61370 standard; Protein; 353 AA.
XX	
AC	AAW61370;
XX	
DT	25-SEP-1998 (first entry)
XX	
DE	Human 11CB splice variant peptide.
XX	
KW	Human; 11CB splice variant; 7-transmembrane receptor family; asthma;
KW	HIV; cancer; diabetes; eating disorder; Parkinson's disease;
KW	heart failure; angina pectoris; myocardial infarction; osteoporosis;
KW	benign prostatic hypertrophy; psychotic disorder; neurological disorder;
KW	severe mental retardation; dyskinesias.
XX	
OS	Homo sapiens.
XX	
PN	EP848060-A2.
XX	
PD	17-JUN-1998.
XX	
PF	01-DEC-1997; 97EP-0309647.
XX	
PR	11-DEC-1996; 96US-0032763.
XX	
PA	(SMIK) SMITHKLINE BEECHAM CORP.
XX	
PI	Bergsma DJ, Ellis CE;
XX	
DR	WPI; 1998-314475/28.
DR	N-PSDB; AAV28115.
XX	

PT Human 11cb splice variant polypeptide - used for treatment of e.g.
PT bacterial, protozoal, fungal and viral infections e.g. caused by
PT human immunodeficiency virus
XX
PS Claim 11; Page 23-24; 31pp; English.
XX
CC The human 11CB splice variant protein is related to the 11CB splice
CC variant encoded by mouse cDNA and is also structurally related to other
CC member of the 7-transmembrane receptor family. Polypeptides or agonists
CC of the 11CB splice variant can be used to treat infections, such as
CC bacterial, fungal, protozoal and viral infections, particularly infection
CC caused by human immunodeficiency virus-1 or -2; pain; cancers; diabetes;
CC obesity; anorexia; bulimia; asthma; Parkinson's disease; both acute and
CC congestive heart failure; hypotension; hypertension; urinary retention;
CC osteoporosis; angina pectoris; myocardial infarction; ulcers; allergies;
CC benign prostatic hypertrophy and psychotic and neurological disorders or
CC severe mental retardation, and dyskinesias.
XX
SQ Sequence 353 AA;

Query Match 100.0%; Score 1824; DB 19; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.6e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTSGSPPTGTSISYINIMPSVFGTICLLGIGNST 60
Db 1 MDLEASLLPTGPNASNTSDGPDNLTSGSPPTGTSISYINIMPSVFGTICLLGIGNST 60
QY 61 VIFAVVKSSKSLHMCNNVDPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
Db 61 VIFAVVKSSKSLHMCNNVDPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
QY 121 AMDANSOFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSISTPVL 180
Db 121 AMDANSOFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSISTPVL 180
QY 181 YARLIPRPGGAVGCGIRLPNDTLYWFTLYQFFLAFALPFPVITAAVVRILQRMSSVA 240
Db 181 YARLIPRPGGAVGCGIRLPNDTLYWFTLYQFFLAFALPFPVITAAVVRILQRMSSVA 240
QY 241 PASQSRIRLTKRVRTAICLVFVWCWAPYVYLQTLQLSISRPITLTFVLYNNAISLG 300
Db 241 PASQSRIRLTKRVRTAICLVFVWCWAPYVYLQTLQLSISRPITLTFVLYNNAISLG 300
QY 301 YANSCLNPFYIIVLCETFRKRLVSVKPAQGOLRAVSNAGTADERTESKGT 353
Db 301 YANSCLNPFYIIVLCETFRKRLVSVKPAQGOLRAVSNAGTADERTESKGT 353

RESULT 2
ID AAY16570 standard; Protein; 353 AA.
XX
AC AAY16570;
XX
DT 10-AUG-1999 (first entry)
XX
DE Amino acid sequence of the human 11cb splice variant.
XX
KW Human 11cb splice variant; antibacterial; gene therapy; vaccine; HIV-1;
KW HIV-2; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma;
KW Parkinson's disease; heart failure; hypotension; hypertension;
KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW ulcer; allergy; benign prostatic hypertrophy; psychotic disorder;
KW neurological disorder; anxiety; schizophrenia; manic depression;
KW delirium; dementia; severe mental retardation; dyskinesia;
KW Huntington's disease; Gilles de la Tourette's syndrome;
KW bacterial adhesion.
XX
OS Homo sapiens.
XX
PN WO9928492-A1.
XX

PD 10-JUN-1999.
XX
XX 02-DEC-1998; 98WO-US25497.
PF
PR 15-APR-1998; 98US-0060504.
PR 03-DEC-1997; 97US-0984288.
PR 05-FEB-1998; 98US-0073747.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Ames RS, Bergsma D, Chambers JK, Ellis CE, Foley JJ;
PI Sarau HM;
XX
DR WPI; 1999-371132/31.
XX
DR N-PSDB; AAX60230.
PT New human 11cb splice variant polypeptide and polynucleotide
XX
XX
PS Claim 11; Fig 1B; 56pp; English.
XX
CC The present sequence represents a human 11cb splice variant polypeptide.
CC 11cb splice variant polypeptides and polynucleotides are useful for
CC diagnosing diseases due to an infection of an organism with the 11cb
CC splice variant gene. They can diagnose the stage and type of infection.
CC 11cb splice variant polypeptides are also useful for screening for
CC compounds which affect activity of the protein. These can be used in
CC treatment to inhibit (antagonist i.e. antibacterial drugs) or enhance
CC (agonist) 11cb splice variant activity, in addition to direct
CC administration of 11cb splice variant polypeptides to treat conditions
CC associated with a lack of 11cb splice variant polypeptide, or direct
CC administration of antisense sequences to prevent expression. 11cb splice
CC variant polypeptides (administered directly, in a vector i.e. gene
CC therapy, and as a vaccine) and antibodies induce an immune response to
CC immunize and prevent disease. Diseases diagnosed, prevented or treated
CC include HIV-1 or -2 infection; pain; cancer; diabetes; obesity; feeding
CC and drinking abnormalities e.g. anorexia, bulimia; asthma; Parkinson's
CC disease; acute and congestive heart failure; hypotension; hypertension;
CC urinary retention; osteoporosis; angina pectoris; myocardial infarction;
CC ulcers; allergies; benign prostatic hypertrophy and psychotic and
CC neurological disorders, including anxiety, schizophrenia, manic
CC depression, delirium, dementia or severe mental retardation, and
CC dyskinesias, such as Huntington's disease or Gilles de la Tourette's
CC syndrome. 11cb splice variant polypeptides, polynucleotides and their
CC (ant)agonists can prevent adhesion of bacteria to matrix proteins, and
CC are useful for use on wounds and body implants to prevent bacterial
CC infection.
XX
XX Sequence 353 AA;

Query Match 100.0%; Score 1824; DB 20; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.6e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTSGSPPTGTSISYINIMPSVFGTICLLGIGNST 60
Db 1 MDLEASLLPTGPNASNTSDGPDNLTSGSPPTGTSISYINIMPSVFGTICLLGIGNST 60
QY 61 VIFAVVKSSKSLHMCNNVDPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
Db 61 VIFAVVKSSKSLHMCNNVDPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
QY 121 AMDANSOFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSISTPVL 180
Db 121 AMDANSOFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSISTPVL 180
QY 181 YARLIPRPGGAVGCGIRLPNDTLYWFTLYQFFLAFALPFPVITAAVVRILQRMSSVA 240
Db 181 YARLIPRPGGAVGCGIRLPNDTLYWFTLYQFFLAFALPFPVITAAVVRILQRMSSVA 240
QY 241 PASQSRIRLTKRVRTAICLVFVWCWAPYVYLQTLQLSISRPITLTFVLYNNAISLG 300
Db 241 PASQSRIRLTKRVRTAICLVFVWCWAPYVYLQTLQLSISRPITLTFVLYNNAISLG 300

CC detecting the presence or absence of a variation in a 11cby allele in
CC an individual. Assaying for the presence or absence of a 11cby
CC polynucleotide mutation by isolating DNA from the individuals is useful
CC for screening an individual for an increased risk of developing a
CC disease or for diagnosing a disease. 11cby polynucleotides may contain
CC polymorphic markers, and are therefore useful for genetic association
CC studies searching for a disease susceptibility gene and/or therapeutic
CC response gene. Diseases treated include bacterial, fungal, protozoan and
CC viral infections, particularly infection caused by human immunodeficiency
CC virus (HIV)-1 or HIV-2, cancers, diabetes, obesity, feeding and drinking
CC abnormalities, such as anorexia and bulimia, asthma, Parkinson's disease,
CC acute and congestive heart failure, hypotension, hypertension, urinary
CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcers,
CC allergies, benign prostatic hypertrophy, psychotic and neurological
CC disorders, including anxiety, schizophrenia, manic depression, delirium,
CC Huntington's disease or Gilles de la Tourette's syndrome. The methods for
CC detecting a mutation in the 11cby gene, can therefore be further extended
CC to include genetic counselling for an individual with respect to the
CC individual's potential for developing one of the above diseases.
XX
SQ Sequence 353 AA;

Query Match 100.0%; Score 1824; DB 21; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.6e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLLGIIGNST 60
Db 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLLGIIGNST 60
OY 61 VIFAVVKKSKLHMCNNVPDIFIINLSVVDLFLGLMPFMIHQLMGNGVWHFGETMCTLIT 120
Db 61 VIFAVVKKSKLHMCNNVPDIFIINLSVVDLFLGLMPFMIHQLMGNGVWHFGETMCTLIT 120
OY 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISITPVWL 180
Db 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISITPVWL 180
OY 181 YARLIPFGGAVGCGIRLPNPDTLWFTLYQFFLAFALPFVVITAAVYRILQRMSSVA 240
Db 181 YARLIPFGGAVGCGIRLPNPDTLWFTLYQFFLAFALPFVVITAAVYRILQRMSSVA 240
OY 241 PASQSRIRLRTKRYTRTAIAICLVFVCWAPYVYLQTLQSLISRPFLTFVYLYNAAISLG 300
Db 241 PASQSRIRLRTKRYTRTAIAICLVFVCWAPYVYLQTLQSLISRPFLTFVYLYNAAISLG 300
OY 301 YANSCLNPFVYIVLCETFRKRLVLSVKPAAQGLRAVSNAQTADERTESKGT 353
Db 301 YANSCLNPFVYIVLCETFRKRLVLSVKPAAQGLRAVSNAQTADERTESKGT 353

RESULT 5
AAE07328
ID AAE07328 standard; Protein; 353 AA.
XX
AC AAE07328;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human melanin-concentrating hormone receptor variant #1.
XX
KW Human; melanin-concentrating hormone; MCH analogue; signal transduction;
KW appetite; therapy; anorexia; acquired immune deficiency syndrome; AIDS;
KW wasting; cachexia; frail elderly; weight maintenance; cancer; anorectic;
KW pain reduction; stress reduction; sexual dysfunction; variant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200157070-A1.
XX
PD 09-AUG-2001.

XX
PF 01-FEB-2001; 2001WO-US03293.
XX
PR 03-FEB-2000; 2000US-0179967.
XX
PA (MERI) MERCK & CO INC.
XX
PI Bednarek M;
XX
DR WPI; 2001-483416/52.
DR N-PSDB; AAD13652.

PT Novel peptide encoding a melanin-concentrating hormone analog useful
PT for increasing weight or appetite -
XX
PS Example 2; Page 33-34; 66pp; English.

CC The present invention relates to truncated melanin-concentrating hormone
CC (MCH) analogues active at the MCH receptor. The truncated MCH analogues
CC are optionally modified peptide derivatives of mammalian MCH. The MCH
CC analogues can bind to the MCH receptor and bring about signal
CC transduction. The MCH agonists can be used to facilitate a weight gain,
CC maintenance of weight and/or an appetite increase. The MCH agonists can
CC also be used to treat disorders such as anorexia, acquired immune
CC deficiency syndrome (AIDS), wasting, cachexia and frail elderly. The MCH
CC antagonists can be used to facilitate weight loss, appetite decrease,
CC weight maintenance, cancer treatment, pain reduction, stress reduction
CC and/or treatment of sexual dysfunction. The present sequence is a human
CC MCH receptor variant.

SQ Sequence 353 AA;
Query Match 100.0%; Score 1824; DB 22; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.6e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLLGIIGNST 60
Db 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLLGIIGNST 60
OY 61 VIFAVVKKSKLHMCNNVPDIFIINLSVVDLFLGLMPFMIHQLMGNGVWHFGETMCTLIT 120
Db 61 VIFAVVKKSKLHMCNNVPDIFIINLSVVDLFLGLMPFMIHQLMGNGVWHFGETMCTLIT 120
OY 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISITPVWL 180
Db 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISITPVWL 180
OY 181 YARLIPFGGAVGCGIRLPNPDTLWFTLYQFFLAFALPFVVITAAVYRILQRMSSVA 240
Db 181 YARLIPFGGAVGCGIRLPNPDTLWFTLYQFFLAFALPFVVITAAVYRILQRMSSVA 240
OY 241 PASQSRIRLRTKRYTRTAIAICLVFVCWAPYVYLQTLQSLISRPFLTFVYLYNAAISLG 300
Db 241 PASQSRIRLRTKRYTRTAIAICLVFVCWAPYVYLQTLQSLISRPFLTFVYLYNAAISLG 300
OY 301 YANSCLNPFVYIVLCETFRKRLVLSVKPAAQGLRAVSNAQTADERTESKGT 353
Db 301 YANSCLNPFVYIVLCETFRKRLVLSVKPAAQGLRAVSNAQTADERTESKGT 353

RESULT 6
AAE04747
ID AAE04747 standard; Protein; 353 AA.
XX
AC AAE04747;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human 11cby protein.
XX
KW 11cby; stroke; pain; neuropathy; analgesic; cerebroprotective; vaccine;
KW gene therapy; G-protein coupled receptor superfamily; MCH receptor;

KW melanin-concentrating hormone; human.
XX
OS Homo sapiens.
XX
PN WO200143759-A2.
XX
PD 21-JUN-2001.
XX
PF 12-DEC-2000; 2000WO-EP12703.
XX
PR 16-DEC-1999; 99GB-0029772.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Campbell CA, Hadingham SJ, Harrison DC, Hervieu GJ;
XX
DR WPI: 2001-398072/42.
DR N-PSDB; AAD09345.
XX
XX
PT Use of a compound selected from 11CBY polypeptide, a compound which
PT activates or inhibits the polypeptide, or a polynucleotide encoding the
PT polypeptide, for treating stroke, pain or neuropathies -
XX
XX
PS Claim 6; Page 31; 40pp; English.

CC The present invention relates to use of 11CBY polypeptides and
CC polynucleotides for the manufacture of medicament for treating stroke,
CC pain or neuropathies. The 11CBY polypeptides and polynucleotides are
CC useful for identifying compounds which may be agonists, antagonists or
CC inhibitors which are potentially useful in therapy. The polypeptide
CC is useful for inducing an immunological response in a mammal, for
CC identifying interacting proteins or other molecules, as immunogens to
CC produce antibodies, in vaccine formulation, and in a method for the
CC structure-based design of its agonist, antagonist or inhibitor. The
CC 11CBY polypeptide and polynucleotide are also useful to configure
CC screening methods for detecting the effect of added components on the
CC production of mRNA and polypeptide in cells. The present sequence is
CC human 11CBY protein. 11CBY polypeptide is a member of G-protein coupled
CC receptor superfamily and is believed to be a physiological melanin-
CC concentrating hormone (MCH) receptor.
XX
XX

SO Sequence 353 AA;

Query Match 100.0%; Score 1824; DB 22; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.6e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGISYINIMPSVFGTICLLGIIGNST 60
Db 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGISYINIMPSVFGTICLLGIIGNST 60
QY 61 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
Db 61 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
QY 121 AMDANSQFTSTYIILTAMAIIDRYLATVHPISSTKFRKPSVATVICLLMAISFISITPVWL 180
Db 121 AMDANSQFTSTYIILTAMAIIDRYLATVHPISSTKFRKPSVATVICLLMAISFISITPVWL 180
QY 181 YARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFLPFWVITAAYVRILQMTSSVA 240
Db 181 YARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFLPFWVITAAYVRILQMTSSVA 240
QY 241 PASQRSIRLRTKRVTRTAIAICLVFVCWAPRYVLQLTQLSISRPTLTFVYLYNAAISLG 300
Db 241 PASQRSIRLRTKRVTRTAIAICLVFVCWAPRYVLQLTQLSISRPTLTFVYLYNAAISLG 300
QY 301 YANSCLNPFYIVLCETFRKRLVLSVKPAQGOLRAVSNAQTADERTESKGT 353
Db 301 YANSCLNPFYIVLCETFRKRLVLSVKPAQGOLRAVSNAQTADERTESKGT 353

RESULT 7

AAY97668
ID AAY97668 standard; Protein; 353 AA.
XX
XX AAY97668;
AC
XX
XX 08-MAY-2001 (first entry)
DT
XX
XX Human MCH-R1 protein sequence.
DE
XX
XX Human; melanin-concentrating hormone receptor; MCH-R1; MCH-R2; MCH-R3;
KW weight loss; weight gain; cancer; pain; diabetes; stress; therapy;
KW sexual dysfunction.
XX
XX
OS Homo sapiens.

XX
XX WO200105947-A1.
PN
XX
XX 25-JAN-2001.
PD
XX
PF 10-JUL-2000; 2000WO-US18733.
XX
XX 14-JUL-1999; 99US-0143706.
PR
XX
XX (MERI) MERCK & CO INC.

XX
XX Howard AD;
PI
XX
XX WPI: 2001-159528/16.
DR
DR N-PSDB; AAA91187.
XX

PT Melanin-concentrating hormone receptor polypeptides for increasing or
PT decreasing appetite, reducing stress and to screen for compounds that
PT bind to the receptor -
XX
XX
PS Disclosure; Page 20-21; 43pp; English.

CC This sequence is a melanin-concentrating hormone (MCH) receptor
CC protein of the invention, designated MCH-R1. MCH receptor fragments and
CC polypeptides are useful in assays to screen for compounds that bind to
CC the MCH receptor and modulate the activity of the receptor. MCH Receptor
CC activity is modulated to achieve weight loss, weight gain, to treat
CC cancer (e.g. colon or breast), reduce pain, treat diabetes, reduce stress
CC or treat sexual dysfunction. Nucleic acid coding for the MCH receptor can
CC be used to cause an increase in appetite and to create a test system
CC (e.g. a transgenic animal) for screening for compounds affecting MCH
CC receptor expression. Inhibition of MCH receptor nucleic acid activity is
CC useful to inhibit appetite or stress.
XX
XX

SO Sequence 353 AA;

Query Match 100.0%; Score 1824; DB 22; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.6e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGISYINIMPSVFGTICLLGIIGNST 60
Db 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGISYINIMPSVFGTICLLGIIGNST 60
QY 61 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
Db 61 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
QY 121 AMDANSQFTSTYIILTAMAIIDRYLATVHPISSTKFRKPSVATVICLLMAISFISITPVWL 180
Db 121 AMDANSQFTSTYIILTAMAIIDRYLATVHPISSTKFRKPSVATVICLLMAISFISITPVWL 180
QY 181 YARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFLPFWVITAAYVRILQMTSSVA 240
Db 181 YARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFLPFWVITAAYVRILQMTSSVA 240
QY 241 PASQRSIRLRTKRVTRTAIAICLVFVCWAPRYVLQLTQLSISRPTLTFVYLYNAAISLG 300
Db 241 PASQRSIRLRTKRVTRTAIAICLVFVCWAPRYVLQLTQLSISRPTLTFVYLYNAAISLG 300

QY 301 YANSCLNPEVYIVLCETFRRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 353
Db 301 YANSCLNPEVYIVLCETFRRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 353

RESULT 8
AAB85895
ID AAB85895 standard; Protein; 353 AA.

AC AAB85895;
DT 30-NOV-2001 (first entry)

DE Human short form MCH1R sequence.

KW Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion;
KW fluorescent polypeptide; orexigenic; anabolic; food intake; MCH1R.
OS Homo sapiens.

PN WO200168706-A1.

PD 20-SEP-2001.

PF 14-MAR-2001; 2001WO-US08071.

PR 15-MAR-2000; 2000US-0189698.

PA (MERI) MERCK & CO INC.

PI Marsh DJ;

DR WPI; 2001-565791/63.
DR N-PSDB; AAH47298.

PT Fusion proteins comprising melanin concentrating hormone receptor
PT peptides and fluorescent proteins, useful for identifying appetite
PT stimulants -

PS Claim 1; Page 13; 71pp; English.

CC The invention provides melanin concentrating hormone (MCH) receptor
CC (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise
CC MCHR polypeptide regions from different species. The MCHR fusion protein
CC comprise MCHR polypeptide region and a fluorescent polypeptide region
CC joined directly, or via a linker, to the carboxy side of the MCHR
CC polypeptide region. The MCHR fusion proteins can be expressed by standard
CC recombinant methodology. MCH action promotes feeding (orexigenic) and up
CC regulation of MCH activity stimulates food intake. The present sequence
CC represents a human short form MCH1R protein sequence.

SO Sequence 353 AA;

Query Match 100.0%; Score 1824; DB 22; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.6e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTASGSPRTGSISYINIMPSVFGTICLLGIIGNST 60
Db 1 MDLEASLLPTGPNASNTSDGPDNLTASGSPRTGSISYINIMPSVFGTICLLGIIGNST 60
QY 61 VIFAVVKSKSLHMCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLLT 120
Db 61 VIFAVVKSKSLHMCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLLT 120
QY 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWL 180
Db 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWL 180
QY 181 YARLIPEPGAVGCGIRLPNPDLDYWFETLYQFLAFALPFVVTAAVYRILQRMTSVA 240
Db 181 YARLIPEPGAVGCGIRLPNPDLDYWFETLYQFLAFALPFVVTAAVYRILQRMTSVA 240

QY 241 PASQSRIRLRTKRVTRTAIAICLVFFVCWAPYVYLQTLQLSISRPTLTFVLYNNAISLG 300
Db 241 PASQSRIRLRTKRVTRTAIAICLVFFVCWAPYVYLQTLQLSISRPTLTFVLYNNAISLG 300

QY 301 YANSCLNPEVYIVLCETFRRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 353
Db 301 YANSCLNPEVYIVLCETFRRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 353

RESULT 9
AAU76893
ID AAU76893 standard; Protein; 353 AA.

AC AAU76893;

DT 05-JUN-2002 (first entry)

DE Human melanin-concentrating hormone (MCH) receptor.

KW Dog; melanin-concentrating hormone; MCH; receptor; weight loss; cancer;
KW weight gain; colon; breast; pain; stress; sexual dysfunction; anorexia;
KW bulimia; cancer cachexia; wasting; chemotherapy; radiation therapy;
KW immobilisation; dialysis; cytostatic; anorectic; analgesic; endocrine;
KW immunomodulatory; human.

OS Homo sapiens.

PN WO200208290-A1.

PD 31-JAN-2002.

PF 17-JUL-2001; 2001WO-US22458.

PR 21-JUL-2000; 2000US-219669P.

PA (MERI) MERCK & CO INC.

PI Tan CP;

DR WPI; 2002-257333/30.
DR N-PSDB; ABK10702.

PT New dog MCH receptor polypeptides and nucleic acids, useful for
PT achieving weight loss or gain, treating cancer (e.g. colon or breast),
PT reducing pain or stress, or treating sexual dysfunction -

PS Example 1; Fig 1; 36pp; English.

CC The invention relates to a dog melanin-concentrating hormone (MCH)
CC receptor and the polynucleotide encoding the polypeptide. The sequences
CC are useful for achieving weight loss or gain, treating cancer (e.g. of
CC the colon or breast), reducing pain or stress, or treating sexual
CC dysfunction. They are also useful for treating a patient having a disease
CC or disorder, or under going a treatment accompanied by weight loss.
CC Examples of diseases or disorders accompanied by weight loss include
CC anorexia, bulimia, cancer cachexia, and wasting in frail elderly.
CC Examples of treatments accompanied by weight loss include chemotherapy,
CC radiation therapy, temporary or permanent immobilisation, and dialysis.
CC The nucleic acid is useful as a hybridisation probe or a PCR primer used
CC to identify the presence of dog MCH nucleic acid, to identify or clone a
CC nucleic acid encoding a receptor related to the MCH receptor from a
CC different source, or for the recombinant expression of a dog MCH receptor
CC polypeptide. This sequence represents the human MCH receptor.

SO Sequence 353 AA;

Query Match 100.0%; Score 1824; DB 23; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.6e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTASGSPRTGSISYINIMPSVFGTICLLGIIGNST 60
Db 1 MDLEASLLPTGPNASNTSDGPDNLTASGSPRTGSISYINIMPSVFGTICLLGIIGNST 60

Db 1 MDLEASLLPTGPNASNTSDGPDNLTSAGSPPRTGSSISYINIIMPSVFGTICLLGIIGNST 60
QY 61 VIFAVYKSKSLHWCNNVPDIFIINLSVVDLFLLGMPFMIHQMGNGVWHFGETMCTLIT 120
Db 61 VIFAVYKSKSLHWCNNVPDIFIINLSVVDLFLLGMPFMIHQMGNGVWHFGETMCTLIT 120
QY 121 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSISTPVWL 180
Db 121 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSISTPVWL 180
QY 181 YARLIPEPGGAVGCGIRLPNPDIDLWFTLYQFFLAFALPFWVITAAVYRILQRTSSVA 240
Db 181 YARLIPEPGGAVGCGIRLPNPDIDLWFTLYQFFLAFALPFWVITAAVYRILQRTSSVA 240
QY 241 PASQRSIRLTKRVTRTAIAICLVFVCWAPYVYLQTLQLSISRPTLTFVYLYNAAISLG 300
Db 241 PASQRSIRLTKRVTRTAIAICLVFVCWAPYVYLQTLQLSISRPTLTFVYLYNAAISLG 300
QY 301 YANSCLNPFVYIVLCETFRKRLVSVKPAAGQLRAVSNAQTADERTESKGT 353
Db 301 YANSCLNPFVYIVLCETFRKRLVSVKPAAGQLRAVSNAQTADERTESKGT 353
RESULT 10
AAU75859 standard; Protein; 353 AA.
AC AAU75859;
XX 08-MAY-2002 (first entry)
DT Human melanin concentrating hormone receptor, MCH1, B0120 mutant.
XX Human melanin concentrating hormone receptor; MCH1;
DE Human melanin concentrating hormone receptor; MCH1, B0120 mutant.
XX Human; melanin concentrating hormone receptor; MCH1;
KW steroid hormone disorder; pituitary hormone disorder; B0120;
KW epinephrine release disorder; gastrointestinal disorder; mutcin;
KW cardiovascular disorder; hypertension; diabetes; respiratory disorder;
KW asthma; reproductive function disorder; immune disorder; mutant;
KW musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
KW memory disorder; motor coordination disorder; obesity; eating disorder;
KW dopaminergic function disorder; pain; psychosis; opiate addiction;
KW affective disorder; migraine; transgenic.
XX Homo sapiens.
OS Synthetic.
OS Homo sapiens.
XX WO200202744-A2.
PN 10-JAN-2002.
XX 05-JUL-2001; 2001WO-US21350.
PD 05-JUL-2000; 2000US-0610635.
XX (SYNA-) SYNAPTIC PHARM CORP.
PA Salon JA, Laz TM, Nagorny R, Wilson AE;
XX WPI; 2002-164532/21.
DR Purified human melanin concentrating hormone receptor protein and
XX polynucleotides for screening modulator useful for treating memory
PT disorder, sensory modulation and transmission disorder, motor
PT coordination disorder -
XX Claim 10; Fig 15; 524pp; English.
PS The invention relates to a purified human melanin concentrating hormone
XX (MCH1) receptor protein and its encoding nucleic acid (or mutant
CC activated by MCH or its analogue or homologue). Also included are
CC expression vectors, probes, transformed insect cells, antisense
CC oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting
CC the binding of the antibody to MCH1, a transgenic animal expressing the

CC protein, or a homologous knockout or antisense complementary to the MCH1
CC nucleic acid, ant/agonists of MCH1, and methods of isolating chemical
CC compounds which activate MCH1. The protein, nucleic acid, antibody,
CC ant/agonists and compound are useful for diagnosing and treating a
CC steroid or pituitary hormone disorder, an epinephrine release disorder, a
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder, sensory modulation and transmission disorder, motor
CC coordination disorder, sensory integration disorder, motor integration
CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder,
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC represents human MCH1 mutant encoded by plasmid B0120, where
CC residues 1-70 of the wild-type MCH1 have been deleted and residue
CC 71 replaced by a new initiator methionine.
XX Sequence 353 AA;
SQ Query Match 100.0%; Score 1824; DB 23; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.6e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLEASLLPTGPNASNTSDGPDNLTSAGSPPRTGSSISYINIIMPSVFGTICLLGIIGNST 60
Db 1 MDLEASLLPTGPNASNTSDGPDNLTSAGSPPRTGSSISYINIIMPSVFGTICLLGIIGNST 60
QY 61 VIFAVYKSKSLHWCNNVPDIFIINLSVVDLFLLGMPFMIHQMGNGVWHFGETMCTLIT 120
Db 61 VIFAVYKSKSLHWCNNVPDIFIINLSVVDLFLLGMPFMIHQMGNGVWHFGETMCTLIT 120
QY 121 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSISTPVWL 180
Db 121 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSISTPVWL 180
QY 181 YARLIPEPGGAVGCGIRLPNPDIDLWFTLYQFFLAFALPFWVITAAVYRILQRTSSVA 240
Db 181 YARLIPEPGGAVGCGIRLPNPDIDLWFTLYQFFLAFALPFWVITAAVYRILQRTSSVA 240
QY 241 PASQRSIRLTKRVTRTAIAICLVFVCWAPYVYLQTLQLSISRPTLTFVYLYNAAISLG 300
Db 241 PASQRSIRLTKRVTRTAIAICLVFVCWAPYVYLQTLQLSISRPTLTFVYLYNAAISLG 300
QY 301 YANSCLNPFVYIVLCETFRKRLVSVKPAAGQLRAVSNAQTADERTESKGT 353
Db 301 YANSCLNPFVYIVLCETFRKRLVSVKPAAGQLRAVSNAQTADERTESKGT 353
RESULT 11
AAE07329 standard; Protein; 417 AA.
ID AAE07329;
XX AAE07329;
AC 06-NOV-2001 (first entry)
XX Human melanin-concentrating hormone receptor variant #2.
DE Human melanin-concentrating hormone; MCH analogue; signal transduction;
XX appetite; therapy; anorexia; acquired immune deficiency syndrome; AIDS;
KW wasting; cachexia; frail elderly; weight maintenance; cancer; anorectic;
KW pain reduction; stress reduction; sexual dysfunction; variant.
XX Homo sapiens.
OS Synthetic.
OS Homo sapiens.
XX WO200157070-A1.
PN 09-AUG-2001.
XX

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PF 01-FEB-2001; 2001WO-US03293.
XX
XX 03-FEB-2000; 2000US-0179967.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Bednarek M;
XX
XX WPI; 2001-483416/52.
XX
XX N-PSDB; AAD13653.
XX
XX
XX Novel peptide encoding a melanin-concentrating hormone analog useful
XX for increasing weight or appetite -
XX
XX PS Disclosure; Page 34-35; 66pp; English.
XX
XX The present invention relates to truncated melanin-concentrating hormone
XX (MCH) analogues active at the MCH receptor. The truncated MCH analogues
XX are optionally modified peptide derivatives of mammalian MCH. The MCH
XX analogues can bind to the MCH receptor and bring about signal
XX transduction. The MCH agonists can be used to facilitate a weight gain,
XX maintenance of weight and/or an appetite increase. The MCH agonists can
XX also be used to treat disorders such as anorexia, acquired immune
XX deficiency syndrome (AIDS), wasting, cachexia and frail elderly. The MCH
XX antagonists can be used to facilitate weight loss, appetite decrease,
XX weight maintenance, cancer treatment, pain reduction, stress reduction
XX and/or treatment of sexual dysfunction. The present sequence is a human
XX MCH receptor variant.
XX
XX SQ Sequence 417 AA;

Query Match 100.0%; Score 1824; DB 22; Length 417;
Best Local Similarity 100.0%; Pred. No. 2e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTSGSPRRTGSISYINIIIMPVFGTICLLGIIGNST 60
DB 65 MDLEASLLPTGPNASNTSDGPDNLTSGSPRRTGSISYINIIIMPVFGTICLLGIIGNST 124

QY 61 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
DB 125 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 184

QY 121 AMDANSQFTSTYILTAAMADRYLATVHPISSTKFRKPSVATLVICLMAISFISTPVMWL 180
DB 185 AMDANSQFTSTYILTAAMADRYLATVHPISSTKFRKPSVATLVICLMAISFISTPVMWL 244

QY 181 YARLIPFGAVGCGIRLPNPDLDLYWFTLYQFFLAFALPFEVVTAAVYRILQMTSSVA 240
DB 245 YARLIPFGAVGCGIRLPNPDLDLYWFTLYQFFLAFALPFEVVTAAVYRILQMTSSVA 304

QY 241 PASQSRIRLRTKRYTRTAIAICLVFVCWAPYVYLQTLQSLISRPTLTFVLYNAAISLG 300
DB 305 PASQSRIRLRTKRYTRTAIAICLVFVCWAPYVYLQTLQSLISRPTLTFVLYNAAISLG 364

QY 301 YANSCLNPFVYIVLCETFRKRLVLSVKPPAOGQLRAVSNAGTADERTESKGT 353
DB 365 YANSCLNPFVYIVLCETFRKRLVLSVKPPAOGQLRAVSNAGTADERTESKGT 417

RESULT 12
AAY97669
ID AAY97669 standard; Protein; 417 AA.
XX
XX AAY97669;
XX
XX 08-MAY-2001 (first entry)
XX
XX Human MCH-R2 protein sequence.
XX
XX Human; melanin-concentrating hormone receptor; MCH-R1; MCH-R2; MCH-R3;
XX weight loss; weight gain; cancer; pain; diabetes; stress; therapy;
XX sexual dysfunction.
```

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XX
XX OS Homo sapiens.
XX
XX PN WO200105947-A1.
XX
XX PD 25-JAN-2001.
XX
XX PF 10-JUL-2000; 2000WO-US18733.
XX
XX PR 14-JUL-1999; 99US-0143706.
XX
XX PA (MERI ) MERCK & CO INC.
XX
XX PI Howard AD;
XX
XX DR WPI; 2001-159528/16.
XX
XX DR N-PSDB; AAA91188.
XX
XX
XX Melanin-concentrating hormone receptor polypeptides for increasing or
XX decreasing appetite, reducing stress and to screen for compounds that
XX bind to the receptor -
XX
XX PS Claim 20; Page 21-22; 43pp; English.
XX
XX This sequence is a melanin-concentrating hormone (MCH) receptor
XX protein of the invention, designated MCH-R2. MCH receptor fragments and
XX polypeptides are useful in assays to screen for compounds that bind to
XX the MCH receptor and modulate the activity of the receptor. MCH Receptor
XX activity is modulated to achieve weight loss, weight gain, to treat
XX cancer (e.g. colon or breast), reduce pain, treat diabetes, reduce stress
XX or treat sexual dysfunction. Nucleic acid coding for the MCH receptor can
XX be used to cause an increase in appetite and to create a test system
XX (e.g. a transgenic animal) for screening for compounds affecting MCH
XX receptor expression. Inhibition of MCH receptor nucleic acid activity is
XX useful to inhibit appetite or stress.
XX
XX SQ Sequence 417 AA;

Query Match 100.0%; Score 1824; DB 22; Length 417;
Best Local Similarity 100.0%; Pred. No. 2e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTSGSPRRTGSISYINIIIMPVFGTICLLGIIGNST 60
DB 65 MDLEASLLPTGPNASNTSDGPDNLTSGSPRRTGSISYINIIIMPVFGTICLLGIIGNST 124

QY 61 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
DB 125 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 184

QY 121 AMDANSQFTSTYILTAAMADRYLATVHPISSTKFRKPSVATLVICLMAISFISTPVMWL 180
DB 185 AMDANSQFTSTYILTAAMADRYLATVHPISSTKFRKPSVATLVICLMAISFISTPVMWL 244

QY 181 YARLIPFGAVGCGIRLPNPDLDLYWFTLYQFFLAFALPFEVVTAAVYRILQMTSSVA 240
DB 245 YARLIPFGAVGCGIRLPNPDLDLYWFTLYQFFLAFALPFEVVTAAVYRILQMTSSVA 304

QY 241 PASQSRIRLRTKRYTRTAIAICLVFVCWAPYVYLQTLQSLISRPTLTFVLYNAAISLG 300
DB 305 PASQSRIRLRTKRYTRTAIAICLVFVCWAPYVYLQTLQSLISRPTLTFVLYNAAISLG 364

QY 301 YANSCLNPFVYIVLCETFRKRLVLSVKPPAOGQLRAVSNAGTADERTESKGT 353
DB 365 YANSCLNPFVYIVLCETFRKRLVLSVKPPAOGQLRAVSNAGTADERTESKGT 417

RESULT 13
AAB12779
ID AAB12779 standard; Protein; 422 AA.
XX
XX AAB12779;
XX
```

DT 22-NOV-2000 (first entry)
XX
DE Human SLC-1 protein sequence SEQ ID NO:11.
XX
KW SLC-1; MHC; melanin concentrating hormone; screening; eating;
KW appetite stimulator; appetite regulator; period pain; atonic bleeding;
KW caesarean section; milk congestion; antiobestic agent; drug;
KW foetal asphyxia; cervical rupture; premature birth; uterine rupture;
KW Prader-Willi syndrome; anorectic; gynaecological; abortifaciant;
KW antoanaemia; anabolic; orphan G protein-couple receptor protein.
XX
OS Homo sapiens.
XX
PN WO200040725-A1.
XX
PD 13-JUL-2000.
XX
PF 27-DEC-1999; 99WO-JP07336.
XX
PR 28-DEC-1998; 98JP-0374454.
PR 28-APR-1999; 99JP-0122688.
PR 02-SEP-1999; 99JP-0249300.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Mori M, Shimomura Y, Takekawa S, Sugo T, Ishibashi Y, Kitada C;
PI Suzuki N;
XX
DR WPI; 2000-475832/41.
DR N-PSDB; AAA72918.
XX
XX
PT Screening methods for compounds as SLC-1 (ant)agonists useful in the
PT treatment of eating disorders and as preventives and remedies for e.g.
PT atonic bleeding and Prader-Willi syndrome -
XX
XX
PS Claim 6; Page 111-113; 123pp; Japanese.
XX
XX
CC The present invention describes a method for screening components (I) or
CC their salts that can alter the binding properties of melanin-
CC concentrating hormone (MCH) or its derivative or salt to SLC-1 or its
CC salt. Compounds identified by (I) are useful as SLC-1 (ant)agonists in
CC eating disorders and as preventives and remedies for e.g. period pains,
CC uterine recovery failure, caesarean section, artificial interruption of
CC pregnancy, galactostosis, tonic uterine contraction, foetal asphyxia,
CC rupture of uterus, cervical rupture, premature birth and Prader-Willi
CC syndrome. The present sequence represents the human SLC-1 protein
CC sequence, which is used in an example from the present invention.
XX
SQ Sequence 422 AA;

Query Match 100.0%; Score 1824; DB 21; Length 422;
Best Local Similarity 100.0%; Pred. No. 2e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTASGSPRTGSIYINIIMPSVFGTICLIGTGNST 60
Db 70 MDLEASLLPTGPNASNTSDGPDNLTASGSPRTGSIYINIIMPSVFGTICLIGTGNST 129

QY 61 VIFAVVKKSKLHWCNNVDPDIFIINLSVDLLFLGMPFMIHQLMNGVWHFGFTMCTLLIT 120
Db 130 VIFAVVKKSKLHWCNNVDPDIFIINLSVDLLFLGMPFMIHQLMNGVWHFGFTMCTLLIT 189

QY 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFTISITPVWL 180
Db 190 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFTISITPVWL 249

QY 181 VARLIPEPGGAVGCGIRLPNDPTDLYWFTLYQFLAFALPFEVITAAYVRIQRMSTSSVA 240
Db 250 VARLIPEPGGAVGCGIRLPNDPTDLYWFTLYQFLAFALPFEVITAAYVRIQRMSTSSVA 309

QY 241 PASQSRIRLRTKRVTRTAIAICLVFVCWAPYVYLQTLQSLISRPPTLTFYVLYNAAISLIG 300
Db 310 PASQSRIRLRTKRVTRTAIAICLVFVCWAPYVYLQTLQSLISRPPTLTFYVLYNAAISLIG 369

QY 301 YANSCINPFVYIVLCETFRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 353
Db 370 YANSCINPFVYIVLCETFRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 422

RESULT 14
AAB13436
ID AAB13436 standard; Protein; 422 AA.
AC AAB13436;
XX
DT 17-NOV-2000 (first entry)
XX
DE Human MCH1 receptor.
XX
KW Human; MCH1 receptor; melanin concentrating hormone; neuroregulator;
KW G-protein coupled; PEXJ.HR-TL231; feeding; water balance;
KW energy metabolism; arousal; attention; memory; cognitive function;
KW psychiatric disorder; stress; sexual activity; hormone disorder;
KW hypertension; diabetes; cardiovascular; gastrointestinal;
KW electrolyte balance; respiratory; asthma; reproductive function;
KW immune; endocrine; musculoskeletal; Alzheimer's disease;
KW sensory modulation; transmission; motor coordination;
KW Parkinson's disease; olfaction; urinary; depression; seizure; pain;
KW schizophrenia; morphine tolerance; opiate addiction; migraine.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FH Region 110..135
FT /label= Transmembrane_region_1
FT Region 149..169
FT /label= Transmembrane_region_2
FT Region 193..208
FT /label= Transmembrane_region_3
FT Region 228..262
FT /label= Transmembrane_region_4
FT Region 274..301
FT /label= Transmembrane_region_5
FT Region 323..349
FT /label= Transmembrane_region_6
FT Region 358..383
FT /label= Transmembrane_region_7
XX
XX
XX WO200039279-A2.
XX
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US31169.
XX
PR 31-DEC-1998; 98US-0224426.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
PI Salon JA, Laz TM, Nagorny R, Wilson AE;
XX
DR WPI; 2000-548644/50.
DR N-PSDB; AAA63240.
XX
XX
PT Novel nucleic acid encoding human melanin concentrating hormone
PT receptor useful for treating cardiovascular disorders, hypertension and
PT diabetes, whose mutant form is activated by melanin concentrating
PT hormone -
XX
PS Claim 7; Fig 2; 173pp; English.

Neuroregulators modulate communication in the nervous system. Melanin
concentrating hormone 1 (MCH1) is one such neuroregulator. MCH may serve
as an intergrative neuropeptide, involved in stress response, feeding
regulation and sexual activity. Also, MCH is thought to participate in
water balance regulation, energy metabolism, general arousal/ attention
state, memory and cognitive functions and psychiatric disorders. The

CC present sequence is the human MCH1 receptor. The present sequence is a
CC G-protein coupled receptor and has 7 transmembrane regions. MCH1 receptor
CC may be used in the therapy for a variety of disorders: steroid or
CC pituitary hormone disorder, epinephrine release disorder,
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder e.g. Alzheimer's disease, sensory modulation and
CC transmission disorder, motor coordination disorder, sensory integration
CC disorder, dopaminergic function disorder e.g. Parkinson's disease,
CC olfaction disorder, sympathetic innervation disorder, depression, stress,
CC fluid-imbalance disorder, urinary disorder e.g. urinary incontinence,
CC seizure, pain, psychotic behaviour e.g. schizophrenia, morphine
CC tolerance, opiate addiction or migraine. The coding sequence for the
CC present protein is also contained in plasmid pEX1.HR-TL231 (ATCC 203197).
XX SQ Sequence 422 AA;

Query Match 100.0%; Score 1824; DB 21; Length 422;
Best Local Similarity 100.0%; Pred. No. 2e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTSGSPPRGTSISYINIIMPSVFGTICLLGIGNST 60
DB 70 MDLEASLLPTGPNASNTSDGPDNLTSGSPPRGTSISYINIIMPSVFGTICLLGIGNST 129

QY 61 VIFAVVKKSKLHMCNNVPDIFIINLSVVDLFLGLMPFMIHQLMNGVWHFGETMCTLIIT 120
DB 130 VIFAVVKKSKLHMCNNVPDIFIINLSVVDLFLGLMPFMIHQLMNGVWHFGETMCTLIIT 189

QY 121 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFSITPWVL 180
DB 190 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFSITPWVL 249

QY 181 YARLIPEPGGAVGCGIRLPNDTDLWFTLYQFFLAFAFPVVITAAYVRILQMTSSVA 240
DB 250 YARLIPEPGGAVGCGIRLPNDTDLWFTLYQFFLAFAFPVVITAAYVRILQMTSSVA 309

QY 241 PASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNNAISLG 300
DB 310 PASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNNAISLG 369

QY 301 YANSCINPFVYIVLCETFRKRLVLSVKPAAQGQLRAVSNAQTADERTESKGT 353
DB 370 YANSCINPFVYIVLCETFRKRLVLSVKPAAQGQLRAVSNAQTADERTESKGT 422

RESULT 15
AAE07330
ID AAE07330 standard; Protein; 422 AA.

XX AC AAE07330;
XX DT 06-NOV-2001 (first entry)

XX DE Human melanin-concentrating hormone receptor variant #3.
XX KW Human; melanin-concentrating hormone; MCH analogue; signal transduction;
KW appetite; therapy; anorexia; acquired immune deficiency syndrome; AIDS;
KW wasting; cachexia; frail elderly; weight maintenance; cancer; anorectic;
KW pain reduction; stress reduction; sexual dysfunction; variant.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200157070-A1.
XX PD 09-AUG-2001.
XX PF 01-FEB-2001; 2001WO-US03293.
XX PR 03-FEB-2000; 2000US-0179967.

XX PA (MERI) MERCK & CO INC.
XX PI Bednarek M;
XX DR WPI; 2001-483416/52.
XX DR N-PSDB; AAD13654.
XX PT Novel peptide encoding a melanin-concentrating hormone analog useful
XX for increasing weight or appetite
XX PS Disclosure; Page 35-36; 66pp; English.

CC The present invention relates to truncated melanin-concentrating hormone
CC (MCH) analogues active at the MCH receptor. The truncated MCH analogues
CC are optionally modified peptide derivatives of mammalian MCH. The MCH
CC analogues can bind to the MCH receptor and bring about signal
CC transduction. The MCH agonists can be used to facilitate a weight gain,
CC maintenance of weight and/or an appetite increase. The MCH agonists can
CC also be used to treat disorders such as anorexia, acquired immune
CC deficiency syndrome (AIDS), wasting, cachexia and frail elderly. The MCH
CC antagonists can be used to facilitate weight loss, appetite decrease,
CC weight maintenance, cancer treatment, pain reduction, stress reduction
CC and/or treatment of sexual dysfunction. The present sequence is a human
CC MCH receptor variant.
XX SQ Sequence 422 AA;

Query Match 100.0%; Score 1824; DB 22; Length 422;
Best Local Similarity 100.0%; Pred. No. 2e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTSGSPPRGTSISYINIIMPSVFGTICLLGIGNST 60
DB 70 MDLEASLLPTGPNASNTSDGPDNLTSGSPPRGTSISYINIIMPSVFGTICLLGIGNST 129

QY 61 VIFAVVKKSKLHMCNNVPDIFIINLSVVDLFLGLMPFMIHQLMNGVWHFGETMCTLIIT 120
DB 130 VIFAVVKKSKLHMCNNVPDIFIINLSVVDLFLGLMPFMIHQLMNGVWHFGETMCTLIIT 189

QY 121 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFSITPWVL 180
DB 190 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFSITPWVL 249

QY 181 YARLIPEPGGAVGCGIRLPNDTDLWFTLYQFFLAFAFPVVITAAYVRILQMTSSVA 240
DB 250 YARLIPEPGGAVGCGIRLPNDTDLWFTLYQFFLAFAFPVVITAAYVRILQMTSSVA 309

QY 241 PASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNNAISLG 300
DB 310 PASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNNAISLG 369

QY 301 YANSCINPFVYIVLCETFRKRLVLSVKPAAQGQLRAVSNAQTADERTESKGT 353
DB 370 YANSCINPFVYIVLCETFRKRLVLSVKPAAQGQLRAVSNAQTADERTESKGT 422

Search completed: February 13, 2003, 13:58:02
Job time : 29.0159 secs

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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:56:21 ; Search time 10.3216 Seconds
(without alignments)
1006.264 Million cell updates/sec

Title: US-09-885-478-28
Perfect score: 1824
Sequence: 1 MDLEASLPTGPNASNTSDG.....LRAVSNAGTADERTESKGT 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	1824	100.0	353	3 US-08-984-288-2	Sequence 2, Appl1
2	1824	100.0	353	4 US-09-218-467B-2	Sequence 2, Appl1
3	1824	100.0	422	4 US-09-224-426-2	Sequence 2, Appl1
4	1824	100.0	422	4 US-09-478-601-2	Sequence 2, Appl1
5	1824	100.0	422	4 US-09-478-602-2	Sequence 2, Appl1
6	1763	96.7	353	4 US-09-224-426-4	Sequence 4, Appl1
7	1763	96.7	353	4 US-09-478-601-4	Sequence 4, Appl1
8	1763	96.7	353	4 US-09-478-602-4	Sequence 4, Appl1
9	1687	92.5	402	3 US-08-602-809-2	Sequence 2, Appl1
10	1676	91.9	400	5 PCT-US95-16472-2	Sequence 2, Appl1
11	532.5	29.2	369	4 US-08-120-601B-9	Sequence 9, Appl1
12	530.5	29.1	369	1 US-07-816-283-6	Sequence 6, Appl1
13	530.5	29.1	369	1 US-08-417-103-6	Sequence 6, Appl1
14	530.5	29.1	369	1 US-08-417-103-16	Sequence 16, Appl1
15	529.5	29.0	369	1 US-07-816-283-8	Sequence 8, Appl1
16	529.5	29.0	369	1 US-08-417-103-8	Sequence 8, Appl1
17	524.5	28.8	369	2 US-08-411-859-3	Sequence 3, Appl1
18	524.5	28.8	369	4 US-08-387-707-9	Sequence 9, Appl1
19	524.5	28.8	369	4 US-08-405-271A-9	Sequence 9, Appl1
20	504.5	27.7	418	1 US-07-816-283-10	Sequence 10, Appl1
21	504.5	27.7	418	1 US-08-417-103-10	Sequence 10, Appl1
22	502	27.5	391	4 US-08-120-601B-8	Sequence 8, Appl1
23	496.5	27.2	391	1 US-07-816-283-2	Sequence 2, Appl1
24	496.5	27.2	391	1 US-07-816-283-4	Sequence 4, Appl1
25	496.5	27.2	391	1 US-08-417-103-2	Sequence 2, Appl1
26	496.5	27.2	391	1 US-08-417-103-4	Sequence 4, Appl1
27	496.5	27.2	391	1 US-08-417-103-14	Sequence 14, Appl1

28	494.5	27.1	384	3 US-09-071-434-3	Sequence 3, Appl1
29	494	27.1	389	4 US-08-430-286A-7	Sequence 7, Appl1
30	472	25.9	428	1 US-07-816-283-12	Sequence 12, Appl1
31	472	25.9	428	1 US-08-417-103-12	Sequence 12, Appl1
32	456	25.0	370	4 US-08-405-271A-21	Sequence 21, Appl1
33	449	24.6	400	4 US-08-188-275A-2	Sequence 2, Appl1
34	449	24.6	400	4 US-09-351-198-2	Sequence 2, Appl1
35	449	24.6	400	4 US-08-113-426-2	Sequence 2, Appl1
36	449	24.6	415	4 US-08-405-271A-20	Sequence 20, Appl1
37	447.5	24.5	372	4 US-08-120-601B-7	Sequence 7, Appl1
38	446.5	24.5	367	2 US-08-454-549-4	Sequence 4, Appl1
39	446.5	24.5	367	3 US-08-454-552-4	Sequence 4, Appl1
40	446.5	24.5	367	3 US-08-676-351-3	Sequence 3, Appl1
41	446.5	24.5	372	4 US-08-188-275A-4	Sequence 4, Appl1
42	446.5	24.5	372	4 US-09-351-198-4	Sequence 4, Appl1
43	446.5	24.5	372	4 US-09-113-426-4	Sequence 4, Appl1
44	446	24.5	372	4 US-08-430-286A-6	Sequence 6, Appl1
45	444	24.3	400	3 US-08-889-108-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-08-984-288-2
; Sequence 2, Application us/08984288
; Patent No. 6033872
; GENERAL INFORMATION:
; APPLICANT: BERGSMÄ, DERK
; APPLICANT: ELLIS, CATHERINE
; TITLE OF INVENTION: NOVEL HUMAN 11CB SPLICE V
; TITLE OF INVENTION: ARIANT
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RÄTNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,288
; FILING DATE: 03-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,763
; FILING DATE: 11-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: P50599
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-984-288-2

Query Match 100.0%; Score 1824; DB 3; Length 353;
Best local Similarity 100.0%; Pred. No. 3.2e-159;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTSGSPRRTGSIYINIMPSVFGTICLLGIIGNST 60
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Db 1 MDLEASLLPTGPNASNTSDGPDNLTSGSPRRTGSIYINIMPSVFGTICLLGIIGNST 60
QY 61 VIFAVVKSKLHWCNNVPDIFIINLSVDDLFLGMPFMIHQMGVWHFGETMCTLIT 120
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Db 61 VIFAVVKSKLHWCNNVPDIFIINLSVDDLFLGMPFMIHQMGVWHFGETMCTLIT 120
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Db 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSITPVWL 180
QY 181 VARLIPFGGAVGCGIRLPNDPTDLYWFTLYQFFLAFLPFFVITAAVVRILQRMSTSSVA 240
| | | | |
Db 181 VARLIPFGGAVGCGIRLPNDPTDLYWFTLYQFFLAFLPFFVITAAVVRILQRMSTSSVA 240
QY 241 PASORSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQSLISRPTLTFVYLYNNAISLG 300
| | | | |
Db 241 PASORSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQSLISRPTLTFVYLYNNAISLG 300
QY 301 YANSCINPFVYIVLCETFRKRLVSVKPAAGQLRAVSNACOTADEERTESKGT 353
| | | | |
Db 301 YANSCINPFVYIVLCETFRKRLVSVKPAAGQLRAVSNACOTADEERTESKGT 353

RESULT 2
US-09-218-467B-2
; Sequence 2, Application US/09218467B
; Patent No. 6362326
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: HALSEY, WENDY
; APPLICANT: BERGSMAN, DEBK
; TITLE OF INVENTION: 11cby Genomic Sequence
; FILE REFERENCE: GP-50010
; CURRENT APPLICATION NUMBER: US/09/218,467B
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-218-467B-2

Query Match 100.0%; Score 1824; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 3.2e-159;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTSGSPRRTGSIYINIMPSVFGTICLLGIIGNST 60
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Db 61 VIFAVVKSKLHWCNNVPDIFIINLSVDDLFLGMPFMIHQMGVWHFGETMCTLIT 120
QY 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSITPVWL 180
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Db 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSITPVWL 180
QY 181 VARLIPFGGAVGCGIRLPNDPTDLYWFTLYQFFLAFLPFFVITAAVVRILQRMSTSSVA 240
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Db 181 VARLIPFGGAVGCGIRLPNDPTDLYWFTLYQFFLAFLPFFVITAAVVRILQRMSTSSVA 240
QY 241 PASORSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQSLISRPTLTFVYLYNNAISLG 300
| | | | |
Db 241 PASORSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQSLISRPTLTFVYLYNNAISLG 300
QY 301 YANSCINPFVYIVLCETFRKRLVSVKPAAGQLRAVSNACOTADEERTESKGT 353
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Db 301 YANSCINPFVYIVLCETFRKRLVSVKPAAGQLRAVSNACOTADEERTESKGT 353

RESULT 3
US-09-224-426-2
; Sequence 2, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453/JPW/JHB
; CURRENT APPLICATION NUMBER: US/09/224,426
; CURRENT FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-224-426-2

Query Match 100.0%; Score 1824; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 3.9e-159;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 70 MDLEASLLPTGPNASNTSDGPDNLTSGSPRRTGSIYINIMPSVFGTICLLGIIGNST 129
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QY 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSITPVWL 180
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Db 190 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSITPVWL 249
QY 181 VARLIPFGGAVGCGIRLPNDPTDLYWFTLYQFFLAFLPFFVITAAVVRILQRMSTSSVA 240
| | | | |
Db 250 VARLIPFGGAVGCGIRLPNDPTDLYWFTLYQFFLAFLPFFVITAAVVRILQRMSTSSVA 309
QY 241 PASORSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQSLISRPTLTFVYLYNNAISLG 300
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Db 310 PASORSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQSLISRPTLTFVYLYNNAISLG 369
QY 301 YANSCINPFVYIVLCETFRKRLVSVKPAAGQLRAVSNACOTADEERTESKGT 353
| | | | |
Db 370 YANSCINPFVYIVLCETFRKRLVSVKPAAGQLRAVSNACOTADEERTESKGT 422

RESULT 4
US-09-478-601-2
; Sequence 2, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453z\JPW
; CURRENT APPLICATION NUMBER: US/09/478,601
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 422

TYPE: PRT
ORGANISM: Homo sapiens
US-09-478-601-2

Query Match 100.0%; Score 1824; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 3.9e-159;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
Db 130 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLIT 189
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Db 190 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWL 249
QY 181 YARLIPPGGAVGCGIRLPNPDLDLYWFTLYQFLAFALPFEVVTAAVVRILQRMSSVA 240
Db 250 YARLIPPGGAVGCGIRLPNPDLDLYWFTLYQFLAFALPFEVVTAAVVRILQRMSSVA 309
QY 241 PASQSRIRLTKRVRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVYLYNAAISLG 300
Db 310 PASQSRIRLTKRVRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVYLYNAAISLG 369
QY 301 YANSCLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 353
Db 370 YANSCLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 422

RESULT 5
US-09-478-602-2
Sequence 2, Application US/09478602
Patent No. 6291195
GENERAL INFORMATION:
APPLICANT: Salon, John A.
APPLICANT: Laz, Thomas M.
APPLICANT: Nagorny, Raisa
APPLICANT: Wilson, Amy E.
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
FILE REFERENCE: 57453Y/JPW
CURRENT APPLICATION NUMBER: US/09/478, 602
CURRENT FILING DATE: 2000-01-06
EARLIER APPLICATION NUMBER: 09/224, 426
EARLIER FILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 2
LENGTH: 422
TYPE: PRT
ORGANISM: Homo sapiens
US-09-478-602-2

Query Match 100.0%; Score 1824; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 3.9e-159;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSSISYINIMPSVFGTICLLGIIGNST 60
Db 70 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSSISYINIMPSVFGTICLLGIIGNST 129
QY 61 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
Db 130 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLIT 189
QY 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWL 180
Db 190 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWL 249

QY 181 YARLIPPGGAVGCGIRLPNPDLDLYWFTLYQFLAFALPFEVVTAAVVRILQRMSSVA 240
Db 250 YARLIPPGGAVGCGIRLPNPDLDLYWFTLYQFLAFALPFEVVTAAVVRILQRMSSVA 309
QY 241 PASQSRIRLTKRVRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVYLYNAAISLG 300
Db 310 PASQSRIRLTKRVRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVYLYNAAISLG 369
QY 301 YANSCLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 353
Db 370 YANSCLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 422

RESULT 6
US-09-224-426-4
Sequence 4, Application US/09224426
Patent No. 6221613
GENERAL INFORMATION:
APPLICANT: Salon, John A.
APPLICANT: Laz, Thomas M.
APPLICANT: Nagorny, Raisa
APPLICANT: Wilson, Amy E.
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
FILE REFERENCE: 57453/JPW/JHB
CURRENT APPLICATION NUMBER: US/09/224, 426
CURRENT FILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentln Ver. 2.0 - beta
SEQ ID NO 4
LENGTH: 353
TYPE: PRT
ORGANISM: rat
US-09-224-426-4

Query Match 96.7%; Score 1763; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 1.2e-153;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSSISYINIMPSVFGTICLLGIIGNST 60
Db 1 MDLQTSLSLSTGPNASNISDQDNLTLPGSPRTGSSVSYINIMPSVFGTICLLGIIGNST 60
QY 61 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
Db 61 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
QY 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWL 180
Db 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSMATLVICLLMALSFISITPVWL 180
QY 181 YARLIPPGGAVGCGIRLPNPDLDLYWFTLYQFLAFALPFEVVTAAVVRILQRMSSVA 240
Db 181 YARLIPPGGAVGCGIRLPNPDLDLYWFTLYQFLAFALPFEVVTAAVVRILQRMSSVA 240
QY 241 PASQSRIRLTKRVRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVYLYNAAISLG 300
Db 241 PASQSRIRLTKRVRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVYLYNAAISLG 300
QY 301 YANSCLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 353
Db 301 YANSCLPFVYIVLCETFRKRLVLSVKPAAGQLRTVSNAQTADERTESKGT 353

RESULT 7
US-09-478-601-4
Sequence 4, Application US/09478601
Patent No. 6221616
GENERAL INFORMATION:
APPLICANT: Salon, John A.
APPLICANT: Laz, Thomas M.
APPLICANT: Nagorny, Raisa
APPLICANT: Wilson, Amy E.

; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453z\JPW
; CURRENT APPLICATION NUMBER: US/09/478,601
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-478-601-4

Query Match 96.7%; Score 1763; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 1.2e-153;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTSGSPRTGSISYINIMPSVFETICLLGIGNST 60
Db 1 MDLQTSLLSTGPNASNTSDGQDNLTLPSPRTGSVSYINIMPSVFETICLLGIVGNST 60
QY 61 VIFAVVKKSKLHWCNNVPDIFIINLSVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
Db 61 VIFAVVKKSKLHWCNNVPDIFIINLSVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
QY 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFSITPWVL 180
Db 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSMATLVICLWALSFSITPWVL 180
QY 181 YARLIPPPGAVGCGIRLPNDTDLWFTLYQFLAFALPFWVITAAYVRIQMTSSVA 240
Db 181 YARLIPPPGAVGCGIRLPNDTDLWFTLYQFLAFALPFWVITAAYVKILQMTSSVA 240
QY 241 PASQSRIRLTKRVRTAIAICLVFVCWAPYYVLQTLQLSISRPTLFVYLYNNAISLG 300
Db 241 PASQSRIRLTKRVRTAIAICLVFVCWAPYYVLQTLQLSISRPTLFVYLYNNAISLG 300
QY 301 YANCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 353
Db 301 YANCLNPFVYIVLCETFRKRLVLSVKPAAGQLRTVSNAQTADERTESKGT 353

RESULT 8
US-09-478-602-4
; Sequence 4, Application US/09478602
; Patent No. 6291195
; GENERAL INFORMATION:
; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453y\JPW
; CURRENT APPLICATION NUMBER: US/09/478,602
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-478-602-4

Query Match 96.7%; Score 1763; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 1.2e-153;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTSGSPRTGSISYINIMPSVFETICLLGIGNST 60

Db 1 MDLQTSLLSTGPNASNTSDGQDNLTLPSPRTGSVSYINIMPSVFETICLLGIVGNST 60
QY 61 VIFAVVKKSKLHWCNNVPDIFIINLSVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
Db 61 VIFAVVKKSKLHWCNNVPDIFIINLSVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
QY 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFSITPWVL 180
Db 121 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSMATLVICLWALSFSITPWVL 180
QY 181 YARLIPPPGAVGCGIRLPNDTDLWFTLYQFLAFALPFWVITAAYVRIQMTSSVA 240
Db 181 YARLIPPPGAVGCGIRLPNDTDLWFTLYQFLAFALPFWVITAAYVKILQMTSSVA 240
QY 241 PASQSRIRLTKRVRTAIAICLVFVCWAPYYVLQTLQLSISRPTLFVYLYNNAISLG 300
Db 241 PASQSRIRLTKRVRTAIAICLVFVCWAPYYVLQTLQLSISRPTLFVYLYNNAISLG 300
QY 301 YANCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 353
Db 301 YANCLNPFVYIVLCETFRKRLVLSVKPAAGQLRTVSNAQTADERTESKGT 353

RESULT 9
US-08-602-809-2
; Sequence 2, Application US/08602809
; Patent No. 6008012
; GENERAL INFORMATION:
; APPLICANT: BERGMA, DERK
; APPLICANT: ELLIS, CATHERINE
; TITLE OF INVENTION: HUMAN SOMATOSTATIN-LIKE R
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestlia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: US
; ZIP: 19482-0980
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,809
; FILING DATE: 13-JUN-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16472
; FILING DATE: 15-DEC-1995
; APPLICATION NUMBER: US 08/357,675
; FILING DATE: 16-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestlia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: P50277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 601-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-602-809-2

Query Match 92.5%; Score 1687; DB 3; Length 402;

Best Local Similarity	99.1%;	Pred. No. 1.2e-146;							
Matches	327;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;

OY	24	LT	SAGSPFRG	SISYINIIMPSVEGTICLLGIIGNSTVIRAVYKSKLHWCNNVPDIFII	83
Dd	73	LLCPGSPPRTGISIYINIIIMP	SVEGTICLLGIIGNSTVIRAVYKSKLHWCNNVPDIFII	1322	
OY	84	NLSVVDLFLF	LGMPEMIHOLMGNGVWHFGETMCTLLITAMANSQFTSTYILTAMADRYL	143	
Dd	133	NLSVVDLFLF	LGMPEMIHOLMGNGVWHFGETMCTLLITAMANSQFTSTYILTAMADRYL	192	
OY	144	ATVHPISSTFKRKP	SVATLVICLLMAISFISITPVMYLARLIPEPGAVGCGRLENDPT	203	
Dd	193	ATVHPISSTFKRKP	SVATLVICLLMAISFISITPVMYLARLIPEPGAVGCGRLENDPT	252	
OY	204	DLYWETLYQEFLA	FALPFVVITAAYVRILOMTSSVAPASQRSIRLTRKRVTRATAICL	263	
Dd	253	DLYWETLYQEFLA	FALPFVVITAAYVRILOMTSSVAPASQRSIRLTRKRVTRATAICL	312	
OY	264	VFFVCWAPRYVLQ	LTLQLSISRPTLFVYLLYNAAISLGANSCUNPFVYIVLCETERKRLV	323	
Dd	313	VFFVCWAPRYVLQ	LTLQLSISRPTLFVYLLYNAAISLGANSCUNPFVYIVLCETERKRLV	372	
OY	324	LSVKPAOQGOLRA	VSNNAQTADEERTESKGT	353	
Dd	373	LSVKPAOQGOLRA	VSNNAQTADEERTESKGT	402	

RESULT 10
PCT-US95-16472-2

```

1Sequence 2, Application PC/TUS9516472
2GENERAL INFORMATION:
3APPLICANT: Bergsma, Derk J
4APPLICANT: Ellis, Catherine E
5TITLE OF INVENTION: Human Somatostatin Receptor
6NUMBER OF SEQUENCES: 3
7CORRESPONDENCE ADDRESS:
8ADDRESSEE: SmithKline Beecham Corporation/Corporate
9ADDRESSEE: Intellectual Proper
10STREET: P. O. Box 1539-UW2220
11CITY: King of Prussia
12STATE: Pennsylvania
13COUNTRY: USA
14ZIP: 19406-0939
15COMPUTER READABLE FORM:
16MEDIUM TYPE: Floppy disk
17COMPUTER: IBM PC compatible
18OPERATING SYSTEM: PC-DOS/MS-DOS
19SOFTWARE: PatentIn Release #1.0, Version #1.25
20CURRENT APPLICATION DATA:
21APPLICATION NUMBER: PCT/US95/16472
22FILING DATE:
23CLASSIFICATION:
24ATTORNEY/AGENT INFORMATION:
25NAME: Sutton, Jeffrey A
26REGISTRATION NUMBER: 34,028
27REFERENCE/DOCKET NUMBER: P50277
28TELECOMMUNICATION INFORMATION:
29TELEPHONE: 610 270 5024
30TELEFAX: 610 270 5090
31INFORMATION FOR SEQ ID NO: 2:
32SEQUENCE CHARACTERISTICS:
33LENGTH: 400 amino acids
34TYPE: amino acid
35STRANDEDNESS: single
36TOPOLOGY: linear
37MOLECULE TYPE: protein
38PCT-US95-16472-2

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Query Match	91.98;	Score 1676;	DB 5;	Length 400;
Best Local Similarity	99.18;	Pred. No. 1.3e-145;		
Matches 325; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

[illegible]

RESULT 11
US-08-120-601B-9

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: Sequence 9, Application US/08120601B
: Patent No. 6235496
: GENERAL INFORMATION:
: APPLICANT: Yu, lei
: TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND
: TITLE OF INVENTION: METHODS
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/120,601B
: FILING DATE: 13-SEP-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Wilson, Mark B.
: REGISTRATION NUMBER: 37,259
: REFERENCE/DOCKET NUMBER: INDA:002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512/418-3000
: TELEFAX: 512/474-7577
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 369 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
:
US-08-120-601B-9

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Query Match	29.2%;	Score 532.5;	DB 4;	Length 369;
Best Local Similarity	31.8%;	Pred. No. 4.4e-41;		
Matches 114;	Conservative 75;	Mismatches 128;	Indels 41;	Gaps 8;

```

OY      2 DLEASLPTGENASNTSDGPDNITSAGSPRIGSISYINIIMPSVEGICLLGIGNSTV 61
         || || | : || :: || | : : || : : || : || : |
Db      20 DLNGSLGPS--NGSNQTEPYMTS-----NAVLTFLFYVVCVGLCGNTLV 64

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[illegible]

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RESULT 12
; US-07-816-283-6
; Sequence 6, Application US/07816283
; Patent No. 5436155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Saino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/816, 283
; FILING DATE: 19911231
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-816-283-6

Query Match          29.1%; Score 530.5; DB 1; length 369;
Best Local Similarity 31.8%; Pred. No. 6.7e-41;
Matches 114; Conservative 75; Mismatches 128; Indels 41; Gaps

QY      2 DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLGIGNSTV 61
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      20 DLNGSVST--NTSNQTEPYDLT-----NAVLTFIYFVVCIIIGLCNTLV 64

QY      62 IFAVVKRSKLIHWCNNVPDIFIINLSVDLLFLGMF-----MIHOLMGNGVWHFGETM 115
    |:::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      65 IYVILRYAKM---KTITNIYILNLAIDELFMGLGPLAMQVALVH-----WPGKAI 114

```

```

QY 116 CTLITAMDANSQSTSTYIILTAMAIIDRIATVHPISSTKFRKSVATLVICLMLWLSFISI 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 CRVMTVDGINDEFTSIECLTVMSIDRIYLAVHPIKSAKWRRPRTAKMITMAVWGVSLLVI 174

QY 176 TPWVLYARLIPFGGAVGCGIRLPNPDIDLY-WETLYQFELAFALPFVVITAAVRIIR 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 LPIMITYAGLRSNQWRSSCTINWPGESGAMYTGFIIYTFIDGLVPLPILICLCYFLIIK 234

QY 235 MTSSVAPASQSRISRLRTRKVRTALAICLVEFVCWAPYYVLTQLTQLSIS-RPTLFEVLY 293
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 VKSSGIRVGSKRKKSEKKVTRMVSIVAVFIFCWLPEYIFNVSVSMAISPALRGME 294

QY 294 NAAISLGYANSCINPFVYIVLCETFRKRLVSVKPAAGOLRAVNSNAOTADEERTESK 351
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 DFVVVLTYANSCANPILYAFLSDNEFK-----SFQNVLCIVKVGSGTDGERSJSK 344

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RESULT 13
US-08-417-103-6
; Sequence 6, Application US/08417103
; Patent No. 5723299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Saino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,103
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/816,283
; FILING DATE: 01-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-417-103-6

Query Match      29.1%; Score 530.5; DB 1; Length 369;
Best Local Similarity 31.8%; Pred. No. 6.7e-41;
Matches 114; Conservative 75; Mismatches 128; Indels 41; Gaps 8;

QY    2 DLEASLLPTGPNASNTSDGPDNLTSAGSPPRGTGISYSYNIIMPSVFGTICLIGNSTV 61
      | | : : | | | : : ||| | : : : : || : : : : MIHOLMGNGVWHFGETM 115
      | : : : | : : : : | : | : | : | : | : | : | : | : | : | : | :
DB    20 DLNLSVST--NTSNOTPEPYDLTS-----NAVLTFTFYFWVCITGLCGNTLV 64

QY    62 IFAVVKSKSLKHCNNVPDIFILNSVDLLFLGMPE-----MIHOLMGNGVWHFGETM 115
      | : : : | : : : : | : | : | : | : | : | : | : | : | : | : | :
DB    65 IVYLIRYAKM---KTITNYILNLAIADLEMLGIPLAMQVALVH-----WPF GKAI 114

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Thu Feb 20 11:32:52 2003

us-09-885-478-28.ra1

Page 8

[illegible]

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Job time : 11.3216 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:56:21 ; Search time 12.3392 Seconds
(without alignments)
1006.264 Million cell updates/sec

Title: US-09-885-478-2
Perfect score: 2212
Sequence: 1 MSVGAMKKGVGRAVGLGGGS.....LRAYSNAQTADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2212	100.0	422	4	US-09-224-426-2	Sequence 2, Appli
2	2212	100.0	422	4	US-09-478-601-2	Sequence 2, Appli
3	2212	100.0	422	4	US-09-478-602-2	Sequence 2, Appli
4	1824	82.5	353	3	US-08-984-288-2	Sequence 2, Appli
5	1824	82.5	353	4	US-09-218-467B-2	Sequence 2, Appli
6	1763	79.7	353	4	US-09-224-426-4	Sequence 4, Appli
7	1763	79.7	353	4	US-09-478-601-4	Sequence 4, Appli
8	1763	79.7	353	4	US-09-478-602-4	Sequence 4, Appli
9	1691	76.4	402	3	US-08-602-809-2	Sequence 2, Appli
10	1680	75.9	400	5	PCT-US95-16472-2	Sequence 2, Appli
11	535	24.2	369	1	US-08-120-601B-9	Sequence 9, Appli
12	533	24.1	369	1	US-07-816-283-8	Sequence 8, Appli
13	533	24.1	369	1	US-08-417-103-8	Sequence 8, Appli
14	531.5	24.0	369	1	US-07-816-283-6	Sequence 6, Appli
15	531.5	24.0	369	1	US-08-417-103-6	Sequence 6, Appli
16	531.5	24.0	369	1	US-08-417-103-16	Sequence 16, Appli
17	527	23.8	369	2	US-08-411-859-3	Sequence 9, Appli
18	527	23.8	369	4	US-08-387-707-9	Sequence 9, Appli
19	527	23.8	369	4	US-08-405-271A-9	Sequence 2, Appli
20	514	23.2	391	1	US-07-816-283-2	Sequence 2, Appli
21	514	23.2	391	1	US-08-417-103-2	Sequence 14, Appli
22	514	23.2	391	1	US-07-816-283-4	Sequence 4, Appli
23	508	23.0	391	1	US-08-417-103-4	Sequence 10, Appli
24	504.5	22.8	418	1	US-07-816-283-10	Sequence 10, Appli
25	504.5	22.8	418	1	US-08-417-103-10	Sequence 8, Appli
26	502	22.7	391	4	US-08-120-601B-8	
27						

28	496.5	22.4	389	4	US-08-430-286A-7	Sequence 7, Appli
29	494.5	22.4	384	3	US-09-071-434-3	Sequence 3, Appli
30	472	21.3	428	1	US-07-816-283-12	Sequence 12, Appli
31	472	21.3	428	1	US-08-417-103-12	Sequence 12, Appli
32	456.5	20.6	370	4	US-08-405-271A-21	Sequence 21, Appli
33	453	20.5	400	4	US-08-188-275A-2	Sequence 2, Appli
34	453	20.5	400	4	US-09-351-198-2	Sequence 2, Appli
35	453	20.5	400	4	US-08-113-426-2	Sequence 20, Appli
36	452.5	20.5	415	4	US-08-405-271A-20	Sequence 5, Appli
37	452.5	20.5	398	1	US-08-149-093A-5	Sequence 2, Appli
38	452.5	20.5	398	2	US-08-911-245-5	Sequence 5, Appli
39	452.5	20.5	398	3	US-08-889-108-2	Sequence 2, Appli
40	452.5	20.5	398	4	US-08-120-601B-2	Sequence 16, Appli
41	452.5	20.5	398	4	US-08-387-707-16	Sequence 5, Appli
42	452.5	20.5	398	4	US-09-510-473-5	Sequence 16, Appli
43	452.5	20.5	398	4	US-08-405-271A-16	Sequence 2, Appli
44	452.5	20.5	391	2	PCT-US94-10358-2	Sequence 3, Appli
45	451.5	20.4			US-08-454-549-3	

ALIGNMENTS

RESULT 1
US-09-224-426-2
; Sequence 2, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salon, John A
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453/JFW/JHB
; CURRENT APPLICATION NUMBER: US/09/224, 426
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-224-426-2

Query Match 100.0%; Score 2212; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 9.5e-174;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSVGAMKKGVGRAVGLGGSGCOATEDEPLDCACAPGCGRRRLPQPAWEGSSARL	60
DB	1	MSVGAMKKGVGRAVGLGGSGCOATEDEPLDCACAPGCGRRRLPQPAWEGSSARL	60
QY	61	WEGATGTGMDLEASLPTGPNASNTSDGPDNLTSGASPPRTGISYINIMPSVFGTIC	120
DB	61	WEGATGTGMDLEASLPTGPNASNTSDGPDNLTSGASPPRTGISYINIMPSVFGTIC	120
QY	121	LLGIIGNSTVIFAVYKSKLHWCNVDPDIFINLSVDLLELLGMPFMIHQMGNGVWHF	180
DB	121	LLGIIGNSTVIFAVYKSKLHWCNVDPDIFINLSVDLLELLGMPFMIHQMGNGVWHF	180
QY	181	GETWCTLTITAMDANSQFTSTYIITAMALDKRLATVHPISSTFKRKPVSATLVICLLMALS	240
DB	181	GETWCTLTITAMDANSQFTSTYIITAMALDKRLATVHPISSTFKRKPVSATLVICLLMALS	240
QY	241	FISTPVLWLYARLPPFGGAVGCGIRLPNDTDLYWFTLYQFFLAFLPFVVITAAVRI	300
DB	241	FISTPVLWLYARLPPFGGAVGCGIRLPNDTDLYWFTLYQFFLAFLPFVVITAAVRI	300
QY	301	LQRMSSVAPASQSRIRLTKRVTRTATACLVFEVCAWAPYVYLQTLQSLISRPULTFVY	360
DB	301	LQRMSSVAPASQSRIRLTKRVTRTATACLVFEVCAWAPYVYLQTLQSLISRPULTFVY	360

OY 361 LYNAAISLGYANCLNPFVYIVLCETFRKRLVLSVKPAAOGQLRAVSNAQTADERTESK 420
| | | | |
Db 361 LYNAAISLGYANCLNPFVYIVLCETFRKRLVLSVKPAAOGQLRAVSNAQTADERTESK 420
OY 421 GT 422
| |
Db 421 GT 422

RESULT 2
US-09-478-601-2
; Sequence 2, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453z\JPW
; CURRENT APPLICATION NUMBER: US/09/478,601
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-478-601-2

Query Match 100.0%; Score 2212; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 9.5e-174;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGOGGRRWRLPQPAWEGSSARL 60
| | | | |
Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGOGGRRWRLPQPAWEGSSARL 60
OY 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIIMPSVFGTTC 120
| | | | |
Db 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIIMPSVFGTTC 120
OY 121 LGGTIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
| | | | |
Db 121 LGGTIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
OY 181 GETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLMAIS 240
| | | | |
Db 181 GETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLMAIS 240
OY 241 FISTIPVWLVARLIPPGAVGCGIRLPNPDLDLYWFTLYQFFLAFAALPFVITAAYRI 300
| | | | |
Db 241 FISTIPVWLVARLIPPGAVGCGIRLPNPDLDLYWFTLYQFFLAFAALPFVITAAYRI 300
OY 301 LQMTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLFVY 360
| | | | |
Db 301 LQMTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLFVY 360
OY 361 LYNAAISLGYANCLNPFVYIVLCETFRKRLVLSVKPAAOGQLRAVSNAQTADERTESK 420
| | | | |
Db 361 LYNAAISLGYANCLNPFVYIVLCETFRKRLVLSVKPAAOGQLRAVSNAQTADERTESK 420
OY 421 GT 422
| |
Db 421 GT 422

RESULT 3
US-09-478-602-2
; Sequence 2, Application US/09478602

; Patent No. 6291195
; GENERAL INFORMATION:
; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453y\JPW
; CURRENT APPLICATION NUMBER: US/09/478,602
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-478-602-2

Query Match 100.0%; Score 2212; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 9.5e-174;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGOGGRRWRLPQPAWEGSSARL 60
| | | | |
Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGOGGRRWRLPQPAWEGSSARL 60
OY 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIIMPSVFGTTC 120
| | | | |
Db 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIIMPSVFGTTC 120
OY 121 LGGTIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
| | | | |
Db 121 LGGTIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
OY 181 GETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLMAIS 240
| | | | |
Db 181 GETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLMAIS 240
OY 241 FISTIPVWLVARLIPPGAVGCGIRLPNPDLDLYWFTLYQFFLAFAALPFVITAAYRI 300
| | | | |
Db 241 FISTIPVWLVARLIPPGAVGCGIRLPNPDLDLYWFTLYQFFLAFAALPFVITAAYRI 300
OY 301 LQMTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLFVY 360
| | | | |
Db 301 LQMTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLFVY 360
OY 361 LYNAAISLGYANCLNPFVYIVLCETFRKRLVLSVKPAAOGQLRAVSNAQTADERTESK 420
| | | | |
Db 361 LYNAAISLGYANCLNPFVYIVLCETFRKRLVLSVKPAAOGQLRAVSNAQTADERTESK 420
OY 421 GT 422
| |
Db 421 GT 422

RESULT 4
US-08-984-288-2
; Sequence 2, Application US/08984288
; Patent No. 6033872
; GENERAL INFORMATION:
; APPLICANT: BERGSM, DEK
; APPLICANT: ELLIS, CATHERINE
; TITLE OF INVENTION: NOVEL HUMAN 11CB SPLICE V
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA

```

; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,288
; FILING DATE: 03-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,763
; FILING DATE: 11-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: P50599
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-984-288-2

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Query Match 82.5%; Score 1824; DB 3; Length 353;
Best Local Similarity 100.0%; Pred. No. 4.9e-142;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 70 MDLEASLLPTGPNASNTSDGPDNLTSAAGSPRTGSIYINIMPSVFGTICLLGIGNST 129
Db 1 MDLEASLLPTGPNASNTSDGPDNLTSAAGSPRTGSIYINIMPSVFGTICLLGIGNST 60
QY 130 VIFAVVKKSKLHWCNNVPDIFINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 189
Db 61 VIFAVVKKSKLHWCNNVPDIFINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
QY 190 AMDANSQFTSYILLTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSITPVWL 249
Db 121 AMDANSQFTSYILLTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSITPVWL 180
QY 250 YARLIPPGGAVGCGIRLPNDTDLWFTLYQFFLAFALPFVYITAAVRIILQRMSSVA 309
Db 181 YARLIPPGGAVGCGIRLPNDTDLWFTLYQFFLAFALPFVYITAAVRIILQRMSSVA 240
QY 310 PASQRSIRLRTRKRTAATAICLVFVWCWAPYYVQLTQLSISRPTLTFVYLYNAISLG 369
Db 241 PASQRSIRLRTRKRTAATAICLVFVWCWAPYYVQLTQLSISRPTLTFVYLYNAISLG 300
QY 370 YANSCINPFYIVLCETFRKRLVLSVKPAAQQLRAVSNAQTADERTESKGT 422
Db 301 YANSCINPFYIVLCETFRKRLVLSVKPAAQQLRAVSNAQTADERTESKGT 353

```

RESULT 5
US-09-218-467B-2
; Sequence 2, Application US/09218467B
; Patent No. 6362326
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: HALSEY, WENDY
; APPLICANT: BERGSMAN, DEK
; TITLE OF INVENTION: 11cby Genomic Sequence
; FILE REFERENCE: GP-50010
; CURRENT APPLICATION NUMBER: US/09/218,467B
; CURRENT FILING DATE: 2001-06-22

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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-218-467B-2

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Query Match 82.5%; Score 1824; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 4.9e-142;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 70 MDLEASLLPTGPNASNTSDGPDNLTSAAGSPRTGSIYINIMPSVFGTICLLGIGNST 129
Db 1 MDLEASLLPTGPNASNTSDGPDNLTSAAGSPRTGSIYINIMPSVFGTICLLGIGNST 60
QY 130 VIFAVVKKSKLHWCNNVPDIFINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 189
Db 61 VIFAVVKKSKLHWCNNVPDIFINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
QY 190 AMDANSQFTSYILLTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSITPVWL 249
Db 121 AMDANSQFTSYILLTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSITPVWL 180
QY 250 YARLIPPGGAVGCGIRLPNDTDLWFTLYQFFLAFALPFVYITAAVRIILQRMSSVA 309
Db 181 YARLIPPGGAVGCGIRLPNDTDLWFTLYQFFLAFALPFVYITAAVRIILQRMSSVA 240
QY 310 PASQRSIRLRTRKRTAATAICLVFVWCWAPYYVQLTQLSISRPTLTFVYLYNAISLG 369
Db 241 PASQRSIRLRTRKRTAATAICLVFVWCWAPYYVQLTQLSISRPTLTFVYLYNAISLG 300
QY 370 YANSCINPFYIVLCETFRKRLVLSVKPAAQQLRAVSNAQTADERTESKGT 422
Db 301 YANSCINPFYIVLCETFRKRLVLSVKPAAQQLRAVSNAQTADERTESKGT 353

```

RESULT 6
US-09-224-426-4
; Sequence 4, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salton, John A
; APPLICANT: Laz, Thomas M
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453/JPW/JHB
; CURRENT APPLICATION NUMBER: US/09/224,426
; CURRENT FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: rat
; US-09-224-426-4

Query Match 79.7%; Score 1763; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 4.9e-137;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

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QY 70 MDLEASLLPTGPNASNTSDGPDNLTSAAGSPRTGSIYINIMPSVFGTICLLGIGNST 129
Db 1 MDLQTSLLSTGPNASNTSDGPDNLTLPSPRTGSIYINIMPSVFGTICLLGIGNST 60
QY 130 VIFAVVKKSKLHWCNNVPDIFINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 189
Db 61 VIFAVVKKSKLHWCNNVPDIFINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
QY 190 AMDANSQFTSYILLTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSITPVWL 249

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Db 121 AMDANSQFTSTYILTAMTIDRYLATVHPISSTKFRKPSMATLVICLLMALSFISTIPVWL 180
QY 250 YARLIPFGGAVGCGIRLPNDPDTLWFTLYQFFLAFALPFFVITTAAYVRILOMTSSVA 309
Db 181 YARLIPFGGAVGCGIRLPNDPDTLWFTLYQFFLAFALPFFVITTAAYVKILOMTSSVA 240
QY 310 PASQSRIRLTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVLYXNAISLG 369
Db 241 PASQSRIRLTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVLYXNAISLG 300
QY 370 YANSCINPFYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 422
Db 301 YANSCINPFYIVLCETFRKRLVLSVKPAAGQLRTVSNAGTADERTESKGT 353

RESULT 7
US-09-478-601-4
; Sequence 4, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salom, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453z\JPW
; CURRENT APPLICATION NUMBER: US/09/478,601
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-478-601-4

Query Match 79.7%; Score 1763; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 4.9e-137;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 70 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGTSISYINIMPSVFGTICLGIIGNST 129
Db 1 MDLQTSLSITGPNASNISDGDNLTLPGSPRTGTSVSYINIMPSVFGTICLGIIGNST 60
QY 130 VIFAVYKSKLHWCNNVPDIFILNLSVDLLEFLGMPFMIHQLMNGVWHFGETMCTLIT 189
Db 61 VIFAVYKSKLHWCNNVPDIFILNLSVDLLEFLGMPFMIHQLMNGVWHFGETMCTLIT 120
QY 190 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISTIPVWL 249
Db 121 AMDANSQFTSTYILTAMTIDRYLATVHPISSTKFRKPSMATLVICLLMALSFISTIPVWL 180
QY 250 YARLIPFGGAVGCGIRLPNDPDTLWFTLYQFFLAFALPFFVITTAAYVRILOMTSSVA 309
Db 181 YARLIPFGGAVGCGIRLPNDPDTLWFTLYQFFLAFALPFFVITTAAYVKILOMTSSVA 240
QY 310 PASQSRIRLTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVLYXNAISLG 369
Db 241 PASQSRIRLTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVLYXNAISLG 300
QY 370 YANSCINPFYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 422
Db 301 YANSCINPFYIVLCETFRKRLVLSVKPAAGQLRTVSNAGTADERTESKGT 353

RESULT 8
US-09-478-602-4
; Sequence 4, Application US/09478602
; Patent No. 629195
; GENERAL INFORMATION:

; APPLICANT: Salom, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453y\JPW
; CURRENT APPLICATION NUMBER: US/09/478,602
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-478-602-4

Query Match 79.7%; Score 1763; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 4.9e-137;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 70 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGTSISYINIMPSVFGTICLGIIGNST 129
Db 1 MDLQTSLSITGPNASNISDGDNLTLPGSPRTGTSVSYINIMPSVFGTICLGIIGNST 60
QY 130 VIFAVYKSKLHWCNNVPDIFILNLSVDLLEFLGMPFMIHQLMNGVWHFGETMCTLIT 189
Db 61 VIFAVYKSKLHWCNNVPDIFILNLSVDLLEFLGMPFMIHQLMNGVWHFGETMCTLIT 120
QY 190 AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISTIPVWL 249
Db 121 AMDANSQFTSTYILTAMTIDRYLATVHPISSTKFRKPSMATLVICLLMALSFISTIPVWL 180
QY 250 YARLIPFGGAVGCGIRLPNDPDTLWFTLYQFFLAFALPFFVITTAAYVRILOMTSSVA 309
Db 181 YARLIPFGGAVGCGIRLPNDPDTLWFTLYQFFLAFALPFFVITTAAYVKILOMTSSVA 240
QY 310 PASQSRIRLTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVLYXNAISLG 369
Db 241 PASQSRIRLTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVLYXNAISLG 300
QY 370 YANSCINPFYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 422
Db 301 YANSCINPFYIVLCETFRKRLVLSVKPAAGQLRTVSNAGTADERTESKGT 353

RESULT 9
US-08-602-809-2
; Sequence 2, Application US/08602809
; Patent No. 6008012
; GENERAL INFORMATION:
; APPLICANT: BERGMA, DEER
; APPLICANT: ELLIS, CATHERINE
; TITLE OF INVENTION: HUMAN SOMATOSTATIN-LIKE R
; TITLE OF INVENTION: ECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: US
; ZIP: 19482-0980
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,809
; FILING DATE: 13-JUN-1997


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; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16472
; FILING DATE: 15-DEC-1995
; APPLICATION NUMBER: US 08/357,675
; FILING DATE: 16-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: P50277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 601-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-602-809-2

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Query Match          76.4%; Score 1691; DB 3; Length 402;
Best Local Similarity 82.9%; Pred. No. 4.5e-131;
Matches 340; Conservative 7; Mismatches 15; Indels 48; Gaps 4;

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QY 50 PAWVEGS--SARLMEQATGTGWMDLASLLPTGPNASNTSDGPDN----- 92
Db 4 PSKTDGSGHSGRIHQETHGEGKRD-----KISN-SEGRENGBRGFMNGSLEAE 52
QY 93 -----LTSAGSPRTGSIYINIMPSVFGTICLLGIIGNSTVIF 132
Db 53 HASRMSVLRAPKPMNSQRLLLCPGSPRTGISYINIMPSVFGTICLLGIIGNSTVIF 112
QY 133 AVVKSSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLLITAMD 192
Db 113 AVVKSSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLLITAMD 172
QY 193 ANSOFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISTIPVWLYAR 252
Db 173 ANSOFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISTIPVWLYAR 232
QY 253 LIPEPGAVGCGIRLPNDTDLWFTLYQFFLAFALPEVVITAAYVRILQRMSTSSVAPAS 312
Db 233 LIPEPGAVGCGIRLPNDTDLWFTLYQFFLAFALPEVVITAAYVRILQRMSTSSVAPAS 292
QY 313 QRSIRLRTKRVTRTAIAICLVEFVCWAPYYVQLTQLSISRPTLTFFVYLYNNAISLGYAN 372
Db 293 QRSIRLRTKRVTRTAIAICLVEFVCWAPYYVQLTQLSISRPTLTFFVYLYNNAISLGYAN 352
QY 373 SCLNPFVYIVLCETFRKRLVLSVKPAAQGQLRAVSNAQTADERTESKGT 422
Db 353 SCLNPFVYIVLCETFRKRLVLSVKPAAQGQLRAVSNAQTADERTESKGT 402

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RESULT 10
PCT-US95-16472-2
; Sequence 2, Application PC/TUS9516472
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk J
; APPLICANT: Ellis, Catherine E
; TITLE OF INVENTION: Human Somatostatin Receptor
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation/Corporate
; ADDRESS: Intellectual Proper
; STREET: P. O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16472
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5024
; TELEFAX: 610 270 5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-16472-2

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Query Match          75.9%; Score 1680; DB 5; Length 400;
Best Local Similarity 82.8%; Pred. No. 3.6e-130;
Matches 338; Conservative 7; Mismatches 15; Indels 48; Gaps 4;

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QY 50 PAWVEGS--SARLMEQATGTGWMDLASLLPTGPNASNTSDGPDN----- 92
Db 4 PSKTDGSGHSGRIHQETHGEGKRD-----KISN-SEGRENGBRGFMNGSLEAE 52
QY 93 -----LTSAGSPRTGSIYINIMPSVFGTICLLGIIGNSTVIF 132
Db 53 HASRMSVLRAPKPMNSQRLLLCPGSPRTGISYINIMPSVFGTICLLGIIGNSTVIF 112
QY 133 AVVKSSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLLITAMD 192
Db 113 AVVKSSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLLITAMD 172
QY 193 ANSOFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISTIPVWLYAR 252
Db 173 ANSOFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISTIPVWLYAR 232
QY 253 LIPEPGAVGCGIRLPNDTDLWFTLYQFFLAFALPEVVITAAYVRILQRMSTSSVAPAS 312
Db 233 LIPEPGAVGCGIRLPNDTDLWFTLYQFFLAFALPEVVITAAYVRILQRMSTSSVAPAS 292
QY 313 QRSIRLRTKRVTRTAIAICLVEFVCWAPYYVQLTQLSISRPTLTFFVYLYNNAISLGYAN 372
Db 293 QRSIRLRTKRVTRTAIAICLVEFVCWAPYYVQLTQLSISRPTLTFFVYLYNNAISLGYAN 352
QY 373 SCLNPFVYIVLCETFRKRLVLSVKPAAQGQLRAVSNAQTADERTESK 420
Db 353 SCLNPFVYIVLCETFRKRLVLSVKPAAQGQLRAVSNAQTADERTESK 400

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RESULT 11
US-08-120-601B-9
; Sequence 9, Application US/08120601B
; Patent No. 6235496
; GENERAL INFORMATION:
; APPLICANT: Yu, lei
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSOTIONS AND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210

```

Thu Feb 20 11:32:10 2003

us-09-885-478-2.ra1

Page 6

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/120,601B
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA:002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-120-601B-9

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Best Local Similarity	31.7%;	Pred. No. 2.3e-36;		
Matches 118;	Conservative 77;	Mismatches 131;	Indels 46;	Gaps 10;

QY	62	EQATGTG-WM----	DLEASLLPTGPASANTSDGPDNLTSAGSPRTGISYINIMPSVF	116
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Db	6	EOFNQSQVWIPSPFDLNGSLGPS--	NGSNQTEPYDMTS-----	NAVLTETIY 50
QY	117	GTICLLGIIGNSTVFAVVKKS	KLHMCNNVPDIFINISVDLFLGMPF-----	MH 1700
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Db	51	FVVCVVGLCGNLTIVYILRYAKM--	KTITNITYILNAIDELFMGLPFLANQVALYH	107
QY	171	QLMGNGVWHFEGETMCCLLITAMDANSQ	ETSTYIILTAMADRYLATVHPISSTKFRKPSVAT	230
		: : : :	: : : :	
Db	108	-----WPEGKAICRAYMTVDG	INQETSI FCLTYWMSIDRYLAVVHPISAKWRRPRIAK	160
QY	231	LVTCLLMALSFISIEPVWLXARLIP	EPGAVGCGIRLNPDTDLY--WETLYQEF	LALP 289
		: : : :	: : : :	
Db	161	MINAVMGVSLVILIPIMITYAGLR	SNQWRSSCTINMPGESGAWYTGFIYA	FILGLVP 220
QY	290	FVVITAAVYRILQRM	TVSSVAPASQSRITRLTKRVT	RAIAICLVFVCWAPYVYLQTLQ 349
		: : : :	: : : :	
Db	221	LTIICLCYLRIIIKVKS	SGIRVGSKRKSEKKVTRMVSIVAVEIFC	WLPFEYIENVSIV 280
QY	350	SIS--RPTLTFFVLYLNAASIS	LGYANSCINPFVYIVLCETFRKRLVL	SVKPAAQQLRAVSN 408
		: : : :	: : : :	
Db	281	SVAISPTPALKGMEFV	VILTYANSCANPILYAFLSDNFKK-----	SQNVLCIVKY 332
QY	409	AQTADERTESK 420		
		: : :		
Db	333	SGAEDGERSDSK 344		

RESULT 12
US-07-816-283-8
; Sequence 8, Application US/07816283
; Patent No. 5436155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA

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; ZIP: 77210
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/07/816,283
;
; FILING DATE: 19911231
;
; CLASSIFICATION: 435
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: McDaniel, C. Steven
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 713-787-1400
;
; TELEFAX: 713-789-2679
;
; TELEX: 79-0924
;
; INFORMATION FOR SEQ ID NO: 8:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 369 amino acids
;
; TYPE: AMINO ACID
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
US-07-816-283-8

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Query Match	24.1%;	Score 533;	DB 1;	Length 369;
Best Local Similarity	31.7%;	Pred. No. 3.3e-36;		
Matches 118; Conservative	77;	Mismatches 131;	Indels 46;	Gaps 10

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0Y      EQAQGTG-WM---DIEASLPTGPNASNTSDGPDNLTSGSPPRGTGSISYINIIMPSVF 116
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Db      6 EQLNGSQVWVSSPFIDNGLGSPS--NGSNQTEPYDMTS-----NAVLTFTY 50

0Y      117 GTICLLIGIIGNSTVIFAVVKSSKLLHMCNNVPDIFIINISVDLFLGMPF-----MH 170
      | : : : | | : | | : : : | : : | | : | | : | | : | | : | |
Db      51 FVVCVVGCGCNLTLYVILRYAKM--KITINILMTAIDELFMGLPFLAQVALYH 107

0Y      171 QLMGNGVWHFGEETMCTLLITAMDANSQFTSYILITAMAIDRYLATVHPJSTSKFRKPSVAT 230
      | | : : | : : : | : | | : | | : | | | | | | | | : | |
Db      108 -----WPFKAICRAVMTVDGINQFTSIFCLTYMSIDRYLAVHPITSAKMRRPRIRK 160

0Y      231 LVICLLMALSFISTPFVWLYARLIRPFGAGVCGGIRLEPNPTDLY-WETLYQFFLAFLAP 289
      | : | : | : | : | : | | | | | | | | | | | | | | : | |
Db      161 MINAVWCVSLVLIEPIMITYAGLRNSQWGRSSCTINMGESGAWYTGFIYAFILGFLVP 220

0Y      290 FVVITAAVRILORMSSVAPASORSIRLRTKRVTRAIACLVFVCAAPYVLQTLQ 349
      | : | : | : : | | : : | | : | | | : | | : | | : | |
Db      221 LTIICLCYLIITIKVKSSGIRVGSRRKSEKKVTRMYSIVAVEIFCWLFPYIFNVSSV 280

0Y      350 SIS-RPTLTFVYLYNAISLGYANSCLNPFVYIVLCETFRKRLVLVSYPAAQOLRAVSN 408
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Db      281 SVAISPTPALKGMDFEVLITYANSCANPILYAFLSDNFKK-----SFQNVLCIVKV 332

0Y      409 AQTADEERTESK 420
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Db      333 SGTEGERSDSK 344

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RESULT 13
US-08-417-103-8
; Sequence 8, Application US/08417103
; Patent No. 5723299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America

Thu Feb 20 11:32:10 2003

us-09-885-478-2.ra1

Page 7

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: ZIP: 77210
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: COMPUTER READABLE FORM:
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: MEDIUM TYPE: Floppy disk
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: COMPUTER: IBM PC compatible
:
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/08/417,103
:
: FILING DATE: 05-APR-1995
:
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
:
: APPLICATION NUMBER: US 07/816,283
:
: FILING DATE: 01-DEC-1991
:
: ATTORNEY/AGENT INFORMATION:
:
: NAME: Wilson, Mark B.
:
: REGISTRATION NUMBER: 37,259
:
: REFERENCE/DOCKET NUMBER: ARCD:144
:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: (512) 418-3000
:
: TELEFAX: (512) 474-7577
:
: INFORMATION FOR SEQ ID NO: 8:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 369 amino acids
:
: TYPE: amino acid
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: US-08-417-103-8

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Query Match	24.18;	Score 533;	DB 1;	Length 369;
Best Local Similarity	31.78;	Pred. No. 3.3e-36;		
Matches 118; Conservative	77;	Mismatches 131;	Indels 46;	Gaps 10;

[illegible]

RESULT 14
 US-07-816-283-6
 ; Sequence 6, Application US/07816283
 ; Patent No. 5436155
 ; GENERAL INFORMATION:
 ; APPLICANT: Bell, Graeme I.
 ; APPLICANT: Yamada, Yuichiro
 ; APPLICANT: Selnio, Susumu
 ; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee

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; STREET: PO Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/816,283
; FILING DATE: 19911231
;
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-07-816-283-6

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Query Match	24.0%;	Score 531.5;	DB 1;	Length 369;
Best Local Similarity	31.6%;	Pred. No. 4.4e-36;		
Matches 115; Conservative	76;	Mismatches 128;	Indels 45;	Gaps 9;

[illegible]

RESULT 15
 US-08-417-103-6
 ; Sequence 6, Application US/08417103
 ; Patent No. 5723299
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Bell, Graeme I.
 ;
 ; APPLICANT: Yamada, Yuichiro
 ;
 ; APPLICANT: Seino, Susumu
 ;
 ; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
 ;
 ; NUMBER OF SEQUENCES: 16
 ;
 ; CORRESPONDENCE ADDRESS:
 ;
 ; ADDRESSEE: Arnold, White & Durkee
 ;

Thu Feb 20 11:32:10 2003

us-09-885-478-2.ra1

Page 8

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: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: United States of America
: ZIP: 77210
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: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/417,103
: FILING DATE: 05-APR-1995
:
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/816,283
: FILING DATE: 01-DEC-1991
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Wilson, Mark B.
: REGISTRATION NUMBER: 37,259
: REFERENCE/DOCKET NUMBER: ARCD:144
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (512) 474-7577
:
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 369 amino acids
: TYPE: amino acid
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: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
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: US-08-417-103-6

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Query Match	24.0%;	Score 531.5;	DB 1;	Length 369;
Best Local Similarity	31.6%;	Pred. No. 4.4e-36;		
Matches 115;	Conservative 76;	Mismatches 128;	Indels 45;	Gaps 9;

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Db	14	WLSIPFD	LNGSVST--	NTSNQTE	PEYD	LTS-----	NAVL	TEYF	EV	CI	58
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QY	125	IGNSTV	IFAVVKKSKL	HWCN	NVPD	FIINLS	VDL	FL	GM	PF----	MIHQ
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		:	:	:	:	:	:	:	:	:	
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Db	59	CGNTLV	IYILRYAKM--	KTITN	IYIL	NLAID	ELF	MLG	PEL	MAQ	VALVH-----
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QY	179	HGE	TC	FL	TAM	DANS	QFT	ST	VIL	TAMA	IDRY
		:	:	:	:	:	:	:	:	:	
		:	:	:	:	:	:	:	:	:	
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Db	109	PFG	KAIC	RVM	TVD	G	IN	Q	F	T	SIF
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QY	239	LSF	SIT	P	W	L	Y	A	R	L	I
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QY	298	VRI	LQ	R	M	T	S	S	V	A	P
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Job time : 14.3392 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2003, 09:26:46 ; Search time 62 Seconds
(without alignments)
6276.981 Million cell updates/sec

Title: US-09-885-478-1
Perfect score: 1269
Sequence: 1 atgtcagtggagccatgaa.....cagaagcacaagcactga 1269

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1237.4	97.5	1385	3	US-08-984-288-1 Sequence 1, Appli
5	984.4	77.6	3488	4	US-09-218-467B-1 Sequence 1, Appli
6	983	77.5	1316	3	US-08-602-809-1 Sequence 1, Appli
7	983	77.5	1316	5	PCT-US95-16472-1 Sequence 1, Appli
8	980	77.2	980	4	US-09-218-467B-6 Sequence 6, Appli
9	912.8	71.9	1214	4	US-09-224-426-3 Sequence 3, Appli
10	912.8	71.9	1214	4	US-09-478-601-3 Sequence 3, Appli
11	912.8	71.9	1214	4	US-09-478-602-3 Sequence 3, Appli
12	207	16.3	775	4	US-09-218-467B-3 Sequence 3, Appli
13	147.4	11.6	1147	1	US-08-417-103-15 Sequence 15, Appli
14	147.4	11.6	1351	1	US-07-816-283-5 Sequence 5, Appli
15	147.4	11.6	1351	1	US-08-417-103-5 Sequence 5, Appli
16	136.2	10.7	1244	1	US-07-816-283-7 Sequence 7, Appli
17	136.2	10.7	1244	1	US-08-417-103-7 Sequence 7, Appli
18	129.4	10.2	1265	1	US-07-816-283-3 Sequence 3, Appli
19	129.4	10.2	1265	1	US-08-417-103-3 Sequence 3, Appli
20	127	10.0	1205	1	US-08-417-103-13 Sequence 13, Appli
21	127	10.0	1634	1	US-07-816-283-1 Sequence 1, Appli
22	127	10.0	1634	1	US-08-417-103-1 Sequence 1, Appli
23	119.6	9.4	1296	1	US-07-816-283-9 Sequence 9, Appli
24	119.6	9.4	1296	1	US-08-417-103-9 Sequence 9, Appli
25	105.4	8.3	1054	1	US-08-148-215A-1 Sequence 1, Appli
26	98.4	7.8	1829	2	US-08-411-859-1 Sequence 1, Appli
27	98.4	7.8	1829	4	US-08-387-707-7 Sequence 7, Appli

28	98.4	7.8	1829	4	US-08-405-271A-7	Sequence 7, Appli
29	97.2	7.7	1142	3	US-08-765-743-1	Sequence 1, Appli
30	96.8	7.6	2272	3	US-08-147-592A-3	Sequence 3, Appli
31	96.8	7.6	2272	4	US-08-292-694A-3	Sequence 3, Appli
32	95.2	7.5	1518	1	US-08-148-215A-3	Sequence 3, Appli
33	94.2	7.4	1805	4	US-08-405-271A-18	Sequence 18, Appli
34	88.2	7.0	1618	3	US-08-889-108-1	Sequence 1, Appli
35	88.2	7.0	1618	3	US-08-889-108-3	Sequence 3, Appli
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37	88.2	7.0	1618	4	US-08-120-601B-3	Sequence 3, Appli
38	88.2	7.0	1618	5	PCT-US94-10358-1	Sequence 1, Appli
39	88.2	7.0	1618	5	PCT-US94-10358-3	Sequence 3, Appli
40	88.2	7.0	2135	5	US-08-430-286A-1	Sequence 1, Appli
41	86.6	6.8	1796	1	US-07-816-283-11	Sequence 11, Appli
42	86.6	6.8	1796	1	US-08-417-103-11	Sequence 11, Appli
43	86	6.8	1179	4	US-08-148-708-3	Sequence 3, Appli
44	86	6.8	1378	1	US-08-759-848-2	Sequence 2, Appli
45	86	6.8	1378	4	US-08-148-708-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-224-426-1
; Sequence 1, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salon, John A
; APPLICANT: Laz, Thomas M
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453/JPM/JHB
; CURRENT APPLICATION NUMBER: US/09/224,426
; CURRENT FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 1
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-224-426-1

Query Match	100.0%;	Score 1269;	DB 4;	Length 1269;
Best Local Similarity	100.0%;	Pred. No. 7.5e-283;		
Matches 1269;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGTCAGTGGAGGACCATGAGAGGAGAGTGGGAGGGCAGTTGGCTTGAGGCGGACGC	60	
Db	1	ATGTCAGTGGAGGACCATGAGAGGAGAGTGGGAGGGCAGTTGGCTTGAGGCGGACGC	60	
QY	61	GGCTGCCAGGCTACGGAGGAGAGACCCCTTCCCGACTGCCGGGCTTGCGCTCCGGACAA	120	
Db	61	GGCTGCCAGGCTACGGAGGAGAGACCCCTTCCCGACTGCCGGGCTTGCGCTCCGGACAA	120	
QY	121	GGTGCAGGCGCTGGAGGCTGCCAGCCTGCGTGGGTGAGGGGAGCTCAGCTCGGTTG	180	
Db	121	GGTGCAGGCGCTGGAGGCTGCCAGCCTGCGTGGGTGAGGGGAGCTCAGCTCGGTTG	180	
QY	181	TGGAGCAGGCGACCGGACCTGGATGGATGACCTGGAAGCCTCGCTGCCACCTGGT	240	
Db	181	TGGAGCAGGCGACCGGACCTGGATGGATGACCTGGAAGCCTCGCTGCCACCTGGT	240	
QY	241	CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCATTTCAGCAGATCACCTCTCT	300	
Db	241	CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCATTTCAGCAGATCACCTCTCT	300	
QY	301	CGCAGCGGGAGCATCTCTTACATCAACATCATCATGCTTGGTTCGGTTCGGACCATCTGC	360	
Db	301	CGCAGCGGGAGCATCTCTTACATCAACATCATCATGCTTGGTTCGGTTCGGACCATCTGC	360	

QY 361 CTCCTGGCATCATCGGGAACTCCACGGTCACTTCGCGGTGCTGAAGAAGTCCAAAGCTG 420
|||||
Db 361 CTCCTGGCATCATCGGGAACTCCACGGTCACTTCGCGGTGCTGAAGAAGTCCAAAGCTG 420
QY 421 CACTGCTGCACAACAGCTCCCGACATCTTCATCATCAACCTCTCGTAGTAGATCTCTC 480
|||||
Db 421 CACTGCTGCACAACAGCTCCCGACATCTTCATCATCAACCTCTCGTAGTAGATCTCTC 480
QY 481 TTCTCTCTGGGCAATGCCCTTCATGATCCACAGCTCATGGGCAATGGGGTGTGGCACTT 540
|||||
Db 481 TTCTCTCTGGGCAATGCCCTTCATGATCCACAGCTCATGGGCAATGGGGTGTGGCACTT 540
QY 541 GGGGAGACCATGTGCAACCCCTCATCACGGCCATGGATGCCAATAGTCAGTTCAACAGCACC 600
|||||
Db 541 GGGGAGACCATGTGCAACCCCTCATCACGGCCATGGATGCCAATAGTCAGTTCAACAGCACC 600
QY 601 TACATCCTGACCCGCAATGGCCATTTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC 660
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Db 601 TACATCCTGACCCGCAATGGCCATTTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC 660
QY 661 ACGAAGTTCGGAAGCCCTCTGTGGCCACCCCTGGTGAATCGCCCTCTGGGCCCTCTCC 720
|||||
Db 661 ACGAAGTTCGGAAGCCCTCTGTGGCCACCCCTGGTGAATCGCCCTCTGGGCCCTCTCC 720
QY 721 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGTGA 780
|||||
Db 721 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGTGA 780
QY 781 GTGGGCTGCGGCATACGCCCTGCCCCAACCCAGACACTGACCTCTACTGTTCACCCCTGTAC 840
|||||
Db 781 GTGGGCTGCGGCATACGCCCTGCCCCAACCCAGACACTGACCTCTACTGTTCACCCCTGTAC 840
QY 841 CAGTTTTCCTGGCCCTTTTGCCCTGCTTTGTGTGTCATCACAGCCGCATACGTGAGAGATC 900
|||||
Db 841 CAGTTTTCCTGGCCCTTTTGCCCTGCTTTGTGTGTCATCACAGCCGCATACGTGAGAGATC 900
QY 901 CTGCAGCGCATGACGTCTCAGTGGCCCCCGCTCCAGCGCAGCATCCGGCTGCGGACA 960
|||||
Db 901 CTGCAGCGCATGACGTCTCAGTGGCCCCCGCTCCAGCGCAGCATCCGGCTGCGGACA 960
QY 961 AAGAGGGTGACCCGCAAGCCATCGCCATCTGTCTGTCTTTGTGTGTGGGCAACC 1020
|||||
Db 961 AAGAGGGTGACCCGCAAGCCATCGCCATCTGTCTGTCTTTGTGTGTGGGCAACC 1020
QY 1021 TACTATGTGCTACAGCTGACCCAGTTGTTCATCAGCCGCGCCGACCTCACCCTTTGTAC 1080
|||||
Db 1021 TACTATGTGCTACAGCTGACCCAGTTGTTCATCAGCCGCGCCGACCTCACCCTTTGTAC 1080
QY 1081 TTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAAGCTGCTCAACCCCTTTGTAC 1140
|||||
Db 1081 TTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAAGCTGCTCAACCCCTTTGTAC 1140
QY 1141 ATCGTGTCTGTGAGACGTTCGCAAAACGCTGTCTGTCTGTGAAAGCCTGCAGCCAG 1200
|||||
Db 1141 ATCGTGTCTGTGAGACGTTCGCAAAACGCTGTCTGTCTGTGAAAGCCTGCAGCCAG 1200
QY 1201 GGGCAGCTTCGCGCTGTCAAGCAACGCTCAGACGGCTGACGAGAGAGACAGAAAGCAAA 1260
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Db 1201 GGGCAGCTTCGCGCTGTCAAGCAACGCTCAGACGGCTGACGAGAGAGACAGAAAGCAAA 1260
QY 1261 GGCACCTGA 1269
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Db 1261 GGCACCTGA 1269

RESULT 2
US-09-478-601-1
; Sequence 1, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa

; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453z\JPW
; CURRENT APPLICATION NUMBER: US/09/478, 601
; EARLIER FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224, 426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-478-601-1

Query Match 100.0%; Score 1269; DB 4; Length 1269;
Best Local Similarity 100.0%; Pred. No. 7.5e-283;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCAAGTGGAGGACCATGAAGAAGGAGAGTGGGAGGGGAGTGGGCTTGAAGGCGGACG 60
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Db 1 ATGTCAAGTGGAGGACCATGAAGAAGGAGAGTGGGAGGGGAGTGGGCTTGAAGGCGGACG 60
QY 61 GGCTGCCAGGCTACGGAGGAGAACCCCTTCCGACCTGCGGGGCTTGCCTCCGGGACAA 120
|||||
Db 61 GGCTGCCAGGCTACGGAGGAGAACCCCTTCCGACCTGCGGGGCTTGCCTCCGGGACAA 120
QY 121 GGTGGCAGGCGCTGGAGGCTGCCGACAGCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTTG 180
|||||
Db 121 GGTGGCAGGCGCTGGAGGCTGCCGACAGCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTTG 180
QY 181 TGGAGCAGGCGGACCGGACCTGGCTGGATGAGCTGGAAGCCCTGCTGCTGCCACTGTG 240
|||||
Db 181 TGGAGCAGGCGGACCGGACCTGGCTGGATGAGCTGGAAGCCCTGCTGCTGCCACTGTG 240
QY 241 CCCAATGCCAGCAACACCTCTGATGAGCCCGGATAAACCCTCACTTCAGCAGATCACTCT 300
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Db 241 CCCAATGCCAGCAACACCTCTGATGAGCCCGGATAAACCCTCACTTCAGCAGATCACTCT 300
QY 301 CGCAGCGGGAGCATCTCCTACATCAACATCATCATGCTTCCGCTGTCGGGCAACATCTGC 360
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Db 301 CGCAGCGGGAGCATCTCCTACATCAACATCATCATGCTTCCGCTGTCGGGCAACATCTGC 360
QY 361 CTCCTGGGATCATCGGGAATCCACGGTCACTTTCGGGCTGTAAGAAGTCCAAGCTG 420
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Db 361 CTCCTGGGATCATCGGGAATCCACGGTCACTTTCGGGCTGTAAGAAGTCCAAGCTG 420
QY 421 CACTGCTGCACAACAGTCCCGACATCTTCATCATCAACCTCTCGTAGTAGATCTCTC 480
|||||
Db 421 CACTGCTGCACAACAGTCCCGACATCTTCATCATCAACCTCTCGTAGTAGATCTCTC 480
QY 481 TTTCTCTGGGATGCCCTTCATGATCCACAGCTCATGGGCAATGGGGTGTGGCACTT 540
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Db 481 TTTCTCTGGGATGCCCTTCATGATCCACAGCTCATGGGCAATGGGGTGTGGCACTT 540
QY 541 GGGAGACCATGTGCAACCCCTCATCAAGCCCATGATGCCAATAGTCAAGTCAACAGCACC 600
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Db 541 GGGAGACCATGTGCAACCCCTCATCAAGCCCATGATGCCAATAGTCAAGTCAACAGCACC 600
QY 601 TACATCCTGACCCGCAATGGCCATTTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC 660
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Db 601 TACATCCTGACCCGCAATGGCCATTTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC 660
QY 661 ACGAAGTTCGGAAGCCCTCTGTGGCCACCCCTGGTGAATCGCCCTCTGGGCCCTCTCC 720
|||||
Db 661 ACGAAGTTCGGAAGCCCTCTGTGGCCACCCCTGGTGAATCGCCCTCTGGGCCCTCTCC 720
QY 721 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGTGA 780
|||||
Db 721 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGTGA 780
QY 781 GTGGGCTGCGGCATACGCCCTGCCCAACCCAGACACTGACCTTACTGTGTTACCCCTGTAC 840

|||||
Db 781 GTGGGCTGCGCATACGCCCTGCCCCAACCCAGACACTGACCTCTACTGTTACACCCCTGTAC 840
QY 841 CAGTTTTTCTGGCCTTTGGCCTTGCCCTTTTGTGTGTCATCAACGCCGATACGTAGAGATC 900
|||||
Db 841 CAGTTTTTCTGGCCTTTGGCCTTGCCCTTTTGTGTGTCATCAACGCCGATACGTAGAGATC 900
QY 901 CTGCAGCGCATGACGTCCTTCAGTAGTGGCCCCCGCCTCCACGCCAGCATCCGGCTGCGGACA 960
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Db 901 CTGCAGCGCATGACGTCCTTCAGTAGTGGCCCCCGCCTCCACGCCAGCATCCGGCTGCGGACA 960
QY 961 AAGAGGGTGACCCGACACGCCATCGCCATCTGTCTGTCTTCTTGTGTGCTGGGACACC 1020
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Db 961 AAGAGGGTGACCCGACACGCCATCGCCATCTGTCTGTCTTCTTGTGTGCTGGGACACC 1020
QY 1021 TACTATGTGCTACAGCTGACGCCAGTTGTCATCAGCCGCCGACCCCTCACCTTTGTGTAC 1080
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Db 1021 TACTATGTGCTACAGCTGACGCCAGTTGTCATCAGCCGCCGACCCCTCACCTTTGTGTAC 1080
QY 1081 TTATACAATGCGGCATGACGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTGTGTAC 1140
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Db 1081 TTATACAATGCGGCATGACGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTGTGTAC 1140
QY 1141 ATCGTGCTCTGTGAGACGTCCTCCGCAAAACGCTTGGTCCCTGTGCGGTGAAGCCTGCAGCCACG 1200
|||||
Db 1141 ATCGTGCTCTGTGAGACGTCCTCCGCAAAACGCTTGGTCCCTGTGCGGTGAAGCCTGCAGCCACG 1200
QY 1201 GGGCAGCTTCGCGCTGTACAGAACGCTCAGACGGCTGACGAGGAGAGACAGAAAGCAAA 1260
|||||
Db 1201 GGGCAGCTTCGCGCTGTACAGAACGCTCAGACGGCTGACGAGGAGAGACAGAAAGCAAA 1260
QY 1261 GGCACCTGA 1269
|||||
Db 1261 GGCACCTGA 1269

RESULT 3
US-09-478-602-1
; Sequence 1, Application US/09478602
; Patent No. 6291195
; GENERAL INFORMATION:
; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Wilson, Amy E.
; APPLICANT: Nagorny, Raisa
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453Y\JPW
; CURRENT APPLICATION NUMBER: US/09/478, 602
; EARLIER FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224, 426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-478-602-1

Query Match 100.0%; Score 1269; DB 4; Length 1269;
Best Local Similarity 100.0%; Pred. No. 7.5e-283;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCACTGGGAGCCATGAAGAAGGAGAGTGGGAGGGGACAGTTGGGCTTGAGGGCGGACG 60
|||||
Db 1 ATGTCACTGGGAGCCATGAAGAAGGAGAGTGGGAGGGGACAGTTGGGCTTGAGGGCGGACG 60
QY 61 GGTGCCAGGCTACGGAGGAAGACCCCTTCCGACTGCGGGCTTGCGCTCCGGGACAA 120
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Db 61 GGTGCCAGGCTACGGAGGAAGACCCCTTCCGACTGCGGGCTTGCGCTCCGGGACAA 120
QY 121 GGTGCCAGGCGCTGGAGGCTGCCGACGCTGCGTGGTGAGGGGAGGCTCAGCTCGGTTG 180

|||||
Db 121 GTGGCAGGCGCTGGAGGCTGCCGACGCTGCGTGGGTGAGGGGAGCTCAGCTCGGTTG 180
QY 181 TGGAGCAGGGGACCGGCACCTGGCTGGATGAGCCTGGAAGCCCTGCTGCTGCCACTGGT 240
|||||
Db 181 TGGAGCAGGGGACCGGCACCTGGCTGGATGAGCCTGGAAGCCCTGCTGCTGCCACTGGT 240
QY 241 CCCATGCCAGCAACACCTCTGATGGCCCCGATTAACCTCACTTCAGCAGGATCACCTCCT 300
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Db 241 CCCATGCCAGCAACACCTCTGATGGCCCCGATTAACCTCACTTCAGCAGGATCACCTCCT 300
QY 301 CGCAGGGGAGCATCTCCTACATCAACATCATATGCGCTTGCGGTGTTGCGCACCATCTGC 360
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Db 301 CGCAGGGGAGCATCTCCTACATCAACATCATATGCGCTTGCGGTGTTGCGCACCATCTGC 360
QY 361 CTCTGGGCATCATCGGGAACCTGCAGGTCATCTTCGCGGTGCTGAAGAAGTCCAAGCTG 420
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Db 361 CTCTGGGCATCATCGGGAACCTGCAGGTCATCTTCGCGGTGCTGAAGAAGTCCAAGCTG 420
QY 421 CACTGTGCAACAACAGTCCCGGACATCTTCATCATCAACCTCTGCGGTAGTAGATCTCTC 480
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Db 421 CACTGTGCAACAACAGTCCCGGACATCTTCATCATCAACCTCTGCGGTAGTAGATCTCTC 480
QY 481 TTTCTCTGGGCATGCCCCCTTCATGATCCACCAAGCTCATGGGCAATGGGGTGTGGCACTTT 540
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Db 481 TTTCTCTGGGCATGCCCCCTTCATGATCCACCAAGCTCATGGGCAATGGGGTGTGGCACTTT 540
QY 541 GGGGAGCATTGTGCACCCCTCATCAGCGCCATGGATGCCAATAGTCAGTTCACCAGCACC 600
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Db 541 GGGGAGCATTGTGCACCCCTCATCAGCGCCATGGATGCCAATAGTCAGTTCACCAGCACC 600
QY 601 TACATCTGACCGGCATGGCCATGTGACCGCTACCTGGGCCACTGTCCACCCCATCTCTCC 660
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Db 601 TACATCTGACCGGCATGGCCATGTGACCGCTACCTGGGCCACTGTCCACCCCATCTCTCC 660
QY 661 ACGAAGTTCCGGAAGCCCTGTGTGGCCACCCCTGTGATCTGCTTGTGGCCCTCTCC 720
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Db 661 ACGAAGTTCCGGAAGCCCTGTGTGGCCACCCCTGTGATCTGCTTGTGGCCCTCTCC 720
QY 721 TTCAATCAGCATCAACCCCTGTGTGCTGTATGCCAGACTCATCCCTTCCAGGAGTGCA 780
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Db 721 TTCAATCAGCATCAACCCCTGTGTGCTGTATGCCAGACTCATCCCTTCCAGGAGTGCA 780
QY 781 GTGGGCTGGGCATACGCGCTGCCCCAACCCAGACACTGACCTGACTGCTTCAACCCCTGTAC 840
|||||
Db 781 GTGGGCTGGGCATACGCGCTGCCCCAACCCAGACACTGACCTGACTGCTTCAACCCCTGTAC 840
QY 841 CAGTTTTTCTTGCCCTTTTGCCCTGCTTGTGTCATCAACGCCGATACGTAGAGATC 900
|||||
Db 841 CAGTTTTTCTTGCCCTTTTGCCCTGCTTGTGTCATCAACGCCGATACGTAGAGATC 900
QY 901 CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTCCAGCGGACGATCCGGCTGCGGACA 960
|||||
Db 901 CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTCCAGCGGACGATCCGGCTGCGGACA 960
QY 961 AAGAGGTGAACCCGACAGCCATCGCCATCTGTGCTTCTTGTGTGCTGGGACACC 1020
|||||
Db 961 AAGAGGTGAACCCGACAGCCATCGCCATCTGTGCTTCTTGTGTGCTGGGACACC 1020
QY 1021 TACTATGTGCTACAGCTGACCCAGTTGTTCATCAGCGCGCCGACCCCTCACCTTGTGTAC 1080
|||||
Db 1021 TACTATGTGCTACAGCTGACCCAGTTGTTCATCAGCGCGCCGACCCCTCACCTTGTGTAC 1080
QY 1081 TTATACAATGCGGCATCAGCTTGGGCTATGCCAACAGCTGCTCAACCCCTTGTGTAC 1140
|||||
Db 1081 TTATACAATGCGGCATCAGCTTGGGCTATGCCAACAGCTGCTCAACCCCTTGTGTAC 1140
QY 1141 ATCGTGCTGTGAGACGTTCCGCAAAACGCTTGTCTGTGCTGTAAGCCTGCAGCCACG 1200
|||||
Db 1141 ATCGTGCTGTGAGACGTTCCGCAAAACGCTTGTCTGTGCTGTAAGCCTGCAGCCACG 1200
QY 1201 GGGCAGCTTCGCGCTGTACGAACGCTCAGACGGCTGACGAGGAGAGACAGAAAGCAAA 1260
|||||


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; GENERAL INFORMATION:
; APPLICANT: SATHI, GANESH
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: HALSEY, WENDY
; APPLICANT: BERGSMAN, DEREK
; TITLE OF INVENTION: 11cby Genomic Sequence
; FILE REFERENCE: GP-50010
; CURRENT APPLICATION NUMBER: US/09/218,467B
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 1
; LENGTH: 3488
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; US-09-218-467B-1
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Query Match 77.6%; Score 984.4; DB 4; Length 3488;
Best Local Similarity 99.4%; Pred. No. 2.6e-217;
Matches 988; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY 276 CCTCACTTCAGCAGGATCACTCTCGCAGGGGAGCATCTCTACATCAACATCATCAT 335
Db 2056 CCTTCTGTCCCGAGATCACTCTCGCAGGGGAGCATCTCTACATCAACATCATCAT 2115
QY 336 GCCTTCGGTGTTCGACCATCTGCTCTGCGCATCATCGGAACTCCACGGTCACTCT 395
Db 2116 GCCTTCGGTGTTCGACCATCTGCTCTGCGCATCATCGGAACTCCACGGTCACTCT 2175
QY 396 CGCGGTGCTGAAGAAGTCCAAAGCTGACATGTCACAAACAGTCCCGACATCTTCATCAT 455
Db 2176 CGCGGTGCTGAAGAAGTCCAAAGCTGACATGTCACAAACAGTCCCGACATCTTCATCAT 2235
QY 456 CAACCTCTCGGTAGATCTCTCTTCTCTGCGCATGCGCTTCATGATCCACAGCT 515
Db 2236 CAACCTCTCGGTAGATCTCTCTTCTCTGCGCATGCGCTTCATGATCCACAGCT 2295
QY 516 CATGGGCAATGGGGTGGGCACTTTGGGGAGACATGTGACCCCTCATCAACGGCCATGGA 575
Db 2296 CATGGGCAATGGGGTGGGCACTTTGGGGAGACATGTGACCCCTCATCAACGGCCATGGA 2355
QY 576 TGCCATATAGTCAAGTCAACGACCATCATCTGACCGCCATGGCCATGACCGCTACCT 635
Db 2356 TGCCATATAGTCAAGTCAACGACCATCATCTGACCGCCATGGCCATGACCGCTACCT 2415
QY 636 GGGCACTGTCCACCCCATCTCTTCACACGAAGTCCGGAAAGCCCTCTGTGGCCACCCCTGGT 695
Db 2416 GGGCACTGTCCACCCCATCTCTTCACACGAAGTCCGGAAAGCCCTCTGTGGCCACCCCTGGT 2475
QY 696 GATCTGCCCTCTGTGGGCTCTCTCTCATCATGACATCAACCCCTGTGTGGCTGTATGCCAG 755
Db 2476 GATCTGCCCTCTGTGGGCTCTCTCTCATCATGACATCAACCCCTGTGTGGCTGTATGCCAG 2535
QY 756 ACTCATCCCTTCCAGAGAGTGCAGTGGGCTGGGCGCATACGCCCTGCCCCAACCCAGACAC 815
Db 2536 ACTCATCCCTTCCAGAGAGTGCAGTGGGCTGGGCGCATACGCCCTGCCCCAACCCAGACAC 2595
QY 816 TGAACCTCTACTGTTCAACCTGTACAGTTTTCCTGGCCCTTGGCCCTTTTGTGGT 875
Db 2596 TGAACCTCTACTGTTCAACCTGTACAGTTTTCCTGGCCCTTGGCCCTTTTGTGGT 2655
QY 876 CATCACAGCCGCATAGTGAAGATCCTGCAGCGCATGACGTCTCAGTGGCCCCCGCCCTC 935
Db 2656 CATCACAGCCGCATAGTGAAGATCCTGCAGCGCATGACGTCTCAGTGGCCCCCGCCCTC 2715
QY 936 CCAAGCGAGCATCCGGCTCGGAGCAAGAAGGTTGACCCGACAGCCATGCCATCTGTCT 995
Db 2716 CCAAGCGAGCATCCGGCTCGGAGCAAGAAGGTTGACCCGACAGCCATGCCATCTGTCT 2775
QY 996 GGCTCTCTTTGTGTGTGGGCAACCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAG 1055
Db 2776 GGCTCTCTTTGTGTGTGGGCAACCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAG 2835
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QY 1056 CCGCCCGACCCCTCACTTGTCTACTTATACAATGCGGCCATCAGCTTGGCTATGCCAA 1115
Db 2836 CCGCCCGACCCCTCACTTGTCTACTTATACAATGCGGCCATCAGCTTGGCTATGCCAA 2895
QY 1116 CAGCTGCCCTCAACCCCTTGTGTATCATGCTGCTGTGAGACGTTCCGCAACGCTTGGT 1175
Db 2896 CAGCTGCCCTCAACCCCTTGTGTATCATGCTGCTGTGAGACGTTCCGCAACGCTTGGT 2955
QY 1176 CCGTTCGGTGAAGCTGCAGCCCGAGGGGAGCTTGGCGCTGTACGCAACGCTCAGACGGC 1235
Db 2956 CCGTTCGGTGAAGCTGCAGCCCGAGGGGAGCTTGGCGCTGTACGCAACGCTCAGACGGC 3015
QY 1236 TGACGAGGAGAGAGCAAGCAAGGCACTGA 1269
Db 3016 TGACGAGGAGAGAGCAAGCAAGGCACTGA 3049
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RESULT 6
US-08-602-809-1
; Sequence 1, Application US/08602809
; Patent No. 6008012
; GENERAL INFORMATION:
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; APPLICANT: BERGSMAN, DEREK
; APPLICANT: ELLIS, CATHERINE
; TITLE OF INVENTION: HUMAN SOMATOSTATIN-LIKE R
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: US
; ZIP: 19482-0980
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,809
; FILING DATE: 13-JUN-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16472
; FILING DATE: 15-DEC-1995
; APPLICATION NUMBER: US 08/357,675
; FILING DATE: 16-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: P50277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 601-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1316 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-602-809-1
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Query Match 77.5%; Score 983; DB 3; Length 1316;
Best Local Similarity 100.0%; Pred. No. 4e-217;
Matches 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 287 CAGGATCACTCTCTCGACGGGAGGAGCATCTCTACATCAACATCATCATGCTTGGTGT 346
Db 253 CAGGATCACTCTCTCGACGGGAGGAGCATCTCTACATCAACATCATCATGCTTGGTGT 312
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QY 347 TCGGCACCATCTGCTCCTGGGCATTCGGGAACTCAGGGTCATCTCCGGGTGCTGA 406
Db 313 TCGGCACCATCTGCTCCTGGGCATTCGGGAACTCAGGGTCATCTCCGGGTGCTGA 372
QY 407 AGAAGTCCAAAGCTGCACCTGGTGCACAAACGCTCCCGACATCTTCATCATCAACCTCTCGG 466
Db 373 AGAAGTCCAAAGCTGCACCTGGTGCACAAACGCTCCCGACATCTTCATCATCAACCTCTCGG 432
QY 467 TAGTAGATCTCCTCTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATG 526
Db 433 TAGTAGATCTCCTCTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATG 492
QY 527 GGGTGTGGCACTTTGGGGAGACCATGTGCACCCCTCATCAGGGCCATGGATGCCAATAGTC 586
Db 493 GGGTGTGGCACTTTGGGGAGACCATGTGCACCCCTCATCAGGGCCATGGATGCCAATAGTC 552
QY 587 AGTTCACCAAGCACTACATCCTGACCCCATGGCCATGACCGCTACCTGGCCACTGTCC 646
Db 553 AGTTCACCAAGCACTACATCCTGACCCCATGGCCATGACCGCTACCTGGCCACTGTCC 612
QY 647 ACCCCATCTCTTCCACGAAGTTCGGAGAGCCCTCTGTGGCCACCCCTGGTGTCTGCCCTCC 706
Db 613 ACCCCATCTCTTCCACGAAGTTCGGAGAGCCCTCTGTGGCCACCCCTGGTGTCTGCCCTCC 672
QY 707 TGTGGGCCCTCTCCTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCT 766
Db 673 TGTGGGCCCTCTCCTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCT 732
QY 767 TCCCAGGAGGTGAGTGGGCTGCGGATACGCCCTGCCCAACCCAGACACTGACCTTACT 826
Db 733 TCCCAGGAGGTGAGTGGGCTGCGGATACGCCCTGCCCAACCCAGACACTGACCTTACT 792
QY 827 GGTTCACCCCTGTACCAAGTTCCTGGCCCTTTGCCCTGCCCTTTTGTGTCTCATCAGCCG 886
Db 793 GGTTCACCCCTGTACCAAGTTCCTGGCCCTTTGCCCTGCCCTTTTGTGTCTCATCAGCCG 852
QY 887 CATACGTGAGGATTCCTGCAGCGCATGACGTCTCAGTGGCCCCGCCCTCCAGCGCAGCA 946
Db 853 CATACGTGAGGATTCCTGCAGCGCATGACGTCTCAGTGGCCCCGCCCTCCAGCGCAGCA 912
QY 947 TCCGGCTGCGGCAAAAGAGGGTGAACCCCGCACAGCCATGCCATCTGTCTGTCTTCTTG 1006
Db 913 TCCGGCTGCGGCAAAAGAGGGTGAACCCCGCACAGCCATGCCATCTGTCTGTCTTCTTG 972
QY 1007 TGTGCTGGGCAACCTACTATGTGTACAGCTGACCCAGTTTCCATCAGCGCCCGCAGCC 1066
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Db 1033 TCACCTTTGTCTACTTATACAATGGGCGCATCAGCTTGGGCTATGCCAAGACTGCCCTCA 1092
QY 1127 ACCCCTTTGTCTACTGTCGTGTGAAGCTTCCGCAACGCTTGTCTGTCTGTGTA 1186
Db 1093 ACCCCTTTGTCTACTGTCGTGTGAAGCTTCCGCAACGCTTGTCTGTCTGTGTA 1152
QY 1187 AGCCTGACGCGGAGGGGAGAGCTTCCGCTGTGACAGCAAGCTCAGACGCTGACGAGAGA 1246
Db 1153 AGCCTGACGCGGAGGGGAGAGCTTCCGCTGTGACAGCAAGCTCAGACGCTGACGAGAGA 1212
QY 1247 GGACAGAAAGCAAGGCACTGA 1269
Db 1213 GGACAGAAAGCAAGGCACTGA 1235

RESULT 7

PCT-US95-16472-1
; Sequence 1, Application PC/TUS9516472
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk J
; APPLICANT: Ellis, Catherine E
; TITLE OF INVENTION: Human Somatostatin Receptor
; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation/Corporate
; ADDRESSEE: Intellectual Proper
; STREET: P. O. Box 1539-UW2220
; CITY: King Of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16472
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5024
; TELEFAX: 610 270 5090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1316 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 27..1232
; OTHER INFORMATION: /note= "The coding sequence is from
; OTHER INFORMATION: nucleotides 27 to 1232."
PCT-US95-16472-1

Query Match 77.5%; Score 983; DB 5; Length 1316;
Best local Similarity 100.0%; Pred. No. 4e-217;
Matches 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 287 CAGGATCACCTCCTCGCAGCGGGAGCATCTCCTACATCAACATCATCATGCTTGGGT 346
Db 253 CAGGATCACCTCCTCGCAGCGGGAGCATCTCCTACATCAACATCATCATGCTTGGGT 312
QY 347 TCGGCACCATCTGCTCCTGGGCATTCGGAACCTCCAGCGGTGCTGA 406
Db 313 TCGGCACCATCTGCTCCTGGGCATTCGGAACCTCCAGCGGTGCTGA 372
QY 407 AGAAGTCCAAAGCTGCACCTGGTGCACAAACGCTCCCGCATCTTCATCATCAACCTCTCGG 466
Db 373 AGAAGTCCAAAGCTGCACCTGGTGCACAAACGCTCCCGCATCTTCATCATCAACCTCTCGG 432
QY 467 TAGTAGATCTCCTCTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATG 526
Db 433 TAGTAGATCTCCTCTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATG 492
QY 527 GGGTGTGGCACTTTGGGGAGACCATGTGCACCCCTCATCAGGGCCATGGATGCCAATAGTC 586
Db 493 GGGTGTGGCACTTTGGGGAGACCATGTGCACCCCTCATCAGGGCCATGGATGCCAATAGTC 552
QY 587 AGTTCACCAAGCACTACATCCTGACCCCATGGCCATGACCGCTACCTGGCCACTGTCC 646
Db 553 AGTTCACCAAGCACTACATCCTGACCCCATGGCCATGACCGCTACCTGGCCACTGTCC 612
QY 647 ACCCCATCTCTTCCACGAAGTTCGGAGAGCCCTCTGTGGCCACCCCTGGTGTCTGCCCTCC 706
Db 613 ACCCCATCTCTTCCACGAAGTTCGGAGAGCCCTCTGTGGCCACCCCTGGTGTCTGCCCTCC 672
QY 707 TGTGGGCCCTCTCCTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCT 766
Db 673 TGTGGGCCCTCTCCTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCT 732

QY 767 TCCACGAGAGGTGCAGTGGGCTGCGGCATACGCCCTGCCCAACCCAGACACTGACCTCTACT 826
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Db 733 TCCACGAGAGGTGCAGTGGGCTGCGGCATACGCCCTGCCCAACCCAGACACTGACCTCTACT 792
QY 827 GGTTCACCCCTGTACCACTTTTCTCTGGCCCTTGCCCTGCTTTTGTGGTCATCACAGCCG 886
|||||
Db 793 GGTTCACCCCTGTACCACTTTTCTCTGGCCCTTGCCCTGCTTTTGTGGTCATCACAGCCG 852
QY 887 CATACGTGAGGATCCTGCAGCGCATGACGTCTCAGTGGCCCCCGCCTCCAGCGCAGCA 946
|||||
Db 853 CATACGTGAGGATCCTGCAGCGCATGACGTCTCAGTGGCCCCCGCCTCCAGCGCAGCA 912
QY 947 TCCGCGCTGCGGACAAAGAGGGTGAACCCGACAGCCATCGCCATCTGTCTGTTCTTTG 1006
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Db 913 TCCGCGCTGCGGACAAAGAGGGTGAACCCGACAGCCATCGCCATCTGTCTGTTCTTTG 972
QY 1007 TGTGCTGGGACACCCCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCGACCC 1066
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Db 973 TGTGCTGGGACACCCCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCGACCC 1032
QY 1067 TCACCTTTTGTCTACTTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCTCA 1126
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Db 1033 TCACCTTTTGTCTACTTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCTCA 1092
QY 1127 ACCCTTTTGTGTACATCGTGTCTGTGAGACGTTCCGCAACCGCTTGTCTCTGCGGTGA 1186
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Db 1093 ACCCTTTTGTGTACATCGTGTCTGTGAGACGTTCCGCAACCGCTTGTCTCTGCGGTGA 1152
QY 1187 AGCTGACAGCCCGAGGGGAGCTTGGCGCTGTACGCAACGCTCAGACGGCTGACGAGAGA 1246
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Db 1153 AGCTGACAGCCCGAGGGGAGCTTGGCGCTGTACGCAACGCTCAGACGGCTGACGAGAGA 1212
QY 1247 GGACAGAAAGCAAAAGGCACCTGA 1269
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Db 1213 GGACAGAAAGCAAAAGGCACCTGA 1235

RESULT 8
US-09-218-467B-6
; Sequence 6, Application US/09218467B
; Patent No. 6362326
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: ELIS, CATHERINE
; APPLICANT: HALSEY, WENDY
; APPLICANT: BERGSMAN, DEK
; TITLE OF INVENTION: 11cby Genomic Sequence
; FILE REFERENCE: GP-50010
; CURRENT APPLICATION NUMBER: US/09/218,467B
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 980
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-218-467B-6

Query Match 77.2%; Score 980; DB 4; Length 980;
Best Local Similarity 100.0%; Pred. No. 1.8e-216;
Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 290 GATCACCCTCTCGCAGCGGGAGCATCTCTTACATCAACATCATCATGCGCTTGGTGTG 349
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Db 1 GATCACCCTCTCGCAGCGGGAGCATCTCTTACATCAACATCATCATGCGCTTGGTGTG 60
QY 350 GCACCATCTGCTCTCTGGGATCATCGGGAATCCAGGGTCACTCTTCCGGTGTGAAGA 409
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Db 61 GCACCATCTGCTCTCTGGGATCATCGGGAATCCAGGGTCACTCTTCCGGTGTGAAGA 120
QY 410 AGTCAAGCTGACGTGTGCAACAACGCTCCCGCATCTTCATCATCAACCTCTCGGTAG 469
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Db 121 AGTCAAGCTGACGTGTGCAACAACGCTCCCGGACATCTTCATCATCAACCTCTCGGTAG 180
QY 470 TAGATCTCTCTTCTCTCTGGGATGCCCTTCATGATCCACAGCTCATGGCAATGGG 529
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Db 181 TAGATCTCTCTTCTCTCTGGGATGCCCTTCATGATCCACAGCTCATGGCAATGGG 240
QY 530 TGTGGCACTTTGGGAGACCATGTGACCCCTCATACAGGGCCATGATGCCAATAGTCACT 589
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Db 241 TGTGGCACTTTGGGAGACCATGTGACCCCTCATACAGGGCCATGATGCCAATAGTCACT 300
QY 590 TCACAGCACCTTACATCCTGACCGCCATGGCCATTGACCGGCTACCTGGCCACTGTCCACC 649
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Db 301 TCACAGCACCTTACATCCTGACCGCCATGGCCATTGACCGGCTACCTGGCCACTGTCCACC 360
QY 650 CCATCTCTTCCACGAAGTCCCGAAGCCCTCTGTGGCCACCCTGGTGAATCTGCCTCTGT 709
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Db 361 CCATCTCTTCCACGAAGTCCCGAAGCCCTCTGTGGCCACCCTGGTGAATCTGCCTCTGT 420
QY 710 GGGCCCTCTCTCTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCC 769
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Db 421 GGGCCCTCTCTCTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCC 480
QY 770 CAGAGGTGAGTGGGCTGCGGCATACGCCCTGCCCAACCCAGACACTGACCTCTACTGT 829
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Db 481 CAGAGGTGAGTGGGCTGCGGCATACGCCCTGCCCAACCCAGACACTGACCTCTACTGT 540
QY 830 TCACCCCTGTACAGTTTCTCTGCGCTTGGCCCTGCTTTTGTGTGATCATCAGCCGAT 889
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Db 541 TCACCCCTGTACAGTTTCTCTGCGCTTGGCCCTGCTTTTGTGTGATCATCAGCCGAT 600
QY 890 ACGTGAGATCTGACGCGCATGACGTCTCAGTGGCCCCCGCCTCCAGCGCAGCATCC 949
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Db 601 ACGTGAGATCTGACGCGCATGACGTCTCAGTGGCCCCCGCCTCCAGCGCAGCATCC 660
QY 950 GGCTGCGAAGAGAGGGGTGACCCGACAGCCATGCCATCTGTCTGTCTTCTTGTGT 1009
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Db 661 GGCTGCGAAGAGAGGGGTGACCCGACAGCCATGCCATCTGTCTGTCTTCTTGTGT 720
QY 1010 GCTGGGACCCCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCGGACCTCA 1069
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Db 721 GCTGGGACCCCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCGGACCTCA 780
QY 1070 CCTTGTCTACTTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCTCAACC 1129
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Db 781 CCTTGTCTACTTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCTCAACC 840
QY 1130 CCTTGTGTACATCGTCTGTGTGAGACGTTCCGCAACGCTTGTGTCTGTGCTGAAGC 1189
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Db 841 CCTTGTGTACATCGTCTGTGTGAGACGTTCCGCAACGCTTGTGTCTGTGCTGAAGC 900
QY 1190 CTGACGCCAGGGGAGCTTGGCGCTGTGAGCAACGCTCAGACGGCTGACGAGAGAAGA 1249
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Db 901 CTGACGCCAGGGGAGCTTGGCGCTGTGAGCAACGCTCAGACGGCTGACGAGAGAAGA 960
QY 1250 CAGAAAGCAAAAGGCACCTGA 1269
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Db 961 CAGAAAGCAAAAGGCACCTGA 980

RESULT 9
US-09-224-426-3
; Sequence 3, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salon, John A
; APPLICANT: Laz, Thomas M
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453/JPM/JHB
; CURRENT APPLICATION NUMBER: US/09/224,426
; CURRENT FILING DATE: 1998-12-31

; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 3
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: rat
US-09-224-426-3

Query Match 71.9%; Score 912.8; DB 4; Length 1214;
Best Local Similarity 90.1%; Pred. No. 5.3e-201;
Matches 977; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 186 GCAGGCGACCGGCACCTGGCTGGATGGACCTGGAAGCCCTGCTGCTGCCACTGTGCCAA 245
Db 1 GCAGGCGACCTGCACCGGCTGCATGGATCTGCAAAACCCTGCTGCTGCCACTGGCCCCAA 60
QY 246 TGGCAGCAACACCTCTGATGGCCCCGATAACCTCATTTCAGCAGGATCACCTCTCTCGCAC 305
Db 61 TGGCAGCAACATCTCCGATGGCCAGGATAATCTCACATTTGCCGGGGTCACTCTCTCGCAC 120
QY 306 GGGAGCATCTCTACATCAACATCATATGCTTGGTGTTCGGCACCATTGCTGCTCT 365
Db 121 AGGAGTGTCTCTCTACATCAACATCATATATGCTTCCCTTCCGTGTTGGTACCATCTCTCT 180
QY 366 GGGCATCATCGGGAACCTCCAGGCTCATCTTGGCGGTGTAAGAAGTCCAAAGCTGCACCTG 425
Db 181 GGGCATCTGTGGAAACTCCAGGTCATCTTGTGTGTGAAGAAGTCCAAGCTACACTG 240
QY 426 GTGCACAACGTTCCCGCAGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTCTTCT 485
Db 241 GTGCACAACGTTCCCGCAGACATCTTCATCATCAACCTCTCTGTGTGATCTCTCTTCT 300
QY 486 CTTGGGCATGCCCCCTTCATGATCCACAGCTCATGGGCAATGGGTTGGCACTTTGGGGA 545
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QY 546 GACCATGTGCACCCCTCATCAACAGGCCATGGATGCCAATAGTCAGTTCCACCACTACAT 605
Db 361 AACCATGTGCACCCCTCATCAACAGCCATGGACGCCAACAGTCAGTTCCACTAGCACTACAT 420
QY 606 CTTGACCGCCATGGCCATTGACCGGCTACCTGGCCACTGTCCACCCCATCTCTCCACGAA 665
Db 421 CTTGACTGGCATGACCATTTGACCGGCTACTTGGCCACCGTCCACCCCATCTCTCCACGAA 480
QY 666 GTTCCGGAAGCCCTCTGTGGCCACCCCTGTGATCTGCTCTGTGGGCCCTCTCTCTCAT 725
Db 481 GTTCCGGAAGCCCTCTGATGGCCACCCCTGTGATCTGCTCTGTGGGCCCTCTCTCTCAT 540
QY 726 CAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGCAGTGGG 785
Db 541 CAGTATCACCCCTGTGTGGCTGTACGCCAGGCTCATTCCTTCCAGAGG6GTGCTGTGGG 600
QY 786 CTGGGGCATAGCGCTGCCCCAACCCAGACATGACCTCTACTGGTTCACCCCTGTACAGTT 845
Db 601 CTGTGGCATCGCCTGCCCCAAACCCGAGACATGACCTCTACTGTTCACTCTGTACAGTT 660
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Db 661 TTTCTGTGGCTTTGCCCCCTTCCGTTTGTGTGATTAACCGCCGATACGTGAATAATACTACA 720
QY 906 GCGCATGACGTCTCAGTGGCCCCCGGCTCCAGCGCAGGATCCGGCTGCGGACAAAGAG 965
Db 721 GCGCATGACGTCTCGGTGGCCCCCAGCGCTCCCAAGCAGCATCCGGCTTCGGACAAAGAG 780
QY 966 GGTGACCCGACAGCCATCGGCATCTGTGTGCTCTTCTTGTGTGTGGGACCCCTACTA 1025
Db 781 GGTGACCCGACAGCCATTCGCATCTGTGTGCTCTTCTTGTGTGTGGGACCCCTACTA 840
QY 1026 TGTGCTACAGTGAACCAAGTTGTCCATAGCCGCCGAGCCCTCAACCTTGTCTACTTATA 1085
Db 841 TGTGCTGACGTGAACCAAGCTGTCCATAGCCGCCGAGCCCTCAAGCTTGTCTACTTATA 900
QY 1086 CAATGGCGGCATGAGCTTGGGCTATGCCAACAAGCTGCTCAACCCCTTTGTGTACATGT 1145

Db 901 CAACGGCGCCATCAGCTTGGGCTATGCTAACAGCTGCTGAACCCCTTGTGTACATAGT 960
QY 1146 GCTCTGTGACGCTTCCGCAAAAGCTTGGTCTGTGCGGTGAAGCCTGCAGCCAGGGGCA 1205
Db 961 GCTCTGTGACGCTTTCGAAAAGCCTTGGTGTGTGTCAGTGAAGCCTGCAGCCAGGGGCA 1020
QY 1206 GCTTCGCGCTGTACGAAACGCTCAGACGCTGACGAGAGAGAGACAGAAAGCAAGGCAC 1265
Db 1021 GCTCCGACGGTTCAGCAACGCTCAGACAGCTGATGAGAGAGAGACAGAAAGGCAC 1080
QY 1266 CTGA 1269
Db 1081 CTGA 1084

RESULT 10
US-09-478-601-3
; Sequence 3, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 574532\JPW
; CURRENT APPLICATION NUMBER: US/09/478, 601
; EARLIER FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224, 426
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-478-601-3

Query Match 71.9%; Score 912.8; DB 4; Length 1214;
Best Local Similarity 90.1%; Pred. No. 5.3e-201;
Matches 977; Conservative 0; Mismatches 107; Indels 0; Gaps 0;
QY 186 GCAGGCGACCGGCACCTGGCTGGATGGACCTGGAAGCCCTGCTGCTGCCACTGTGCCAA 245
Db 1 GCAGGCGACCTGCACCGGCTGCATGGATCTGCAAAACCCTGCTGCTGCCACTGGCCCCAA 60
QY 246 TGGCAGCAACACCTCTGATGGCCCCCGGATAACCTCATTTCAGCAGGATCACCTCTCTCGCAC 305
Db 61 TGGCAGCAACATCTCCGATGGCCAGGATAATCTCACATTTGCCGGGGTCACTCTCTCGCAC 120
QY 306 GGGAGCATCTCTCTACATCAACATCATATGCTTGGTGTTCGGCACCATTCTGCTCTCT 365
Db 121 AGGAGTGTCTCTCTACATCAACATCATATATGCTTCCGTTGTTGGTACCATCTCTCTCT 180
QY 366 GGGCATCATCGGGAACCTCCAGGCTCATCTTGGCGGTGTAAGAAGTCCAAAGCTGCACCTG 425
Db 181 GGGCATCTGTGGAAACTCCAGGTCATCTTGTGTGTGTGAAGAAGTCCAAGCTACACTG 240
QY 426 GTGCACAACGTTCCCGCAGACATCTTCATCAACACCTCTCGGTAGTAGATCTCTCTTCT 485
Db 241 GTGCAGCAACGTTCCCGCAGACATCTTCATCAACACCTCTCTGTGTGATCTCTCTCTCT 300
QY 486 CTTGGGCATGCCCCCTTCATGATCCACAGCTCATAGGGCAATGGGTTGGCACTTTGGGGA 545
Db 301 GCTGGGCATGCCCCCTTCATGATCCACAGCTCATAGGGGAACGGCTCTGGCACTTTGGGGA 360
QY 546 GACCATGTGCACCCCTCATCAACAGGCCATGGATGCCAATAGTCAGTTCCACCACTACAT 605
Db 361 AACCATGTGCACCCCTCATCAACAGCCATGGACGCCAACAAGTCAGTTCACTACCTACAT 420
QY 606 CTTGACCGCCATGGCCATTGACCGGCTACCTGGCCACTGTCCACCCCATCTCTCCACGAA 665

Db	421	CCTGACTGCGCATGACCATTTGACCGCTACTGTGGCCACCGTCCACCCCATCTCCTCCACCAA	480
QY	666	GTTCCGGAAGCCCTCTGTGGCCACCCCTGGTGAATCTGCTCCTGTGGCCCTCTCCTTCAT	725
Db	481	GTTCCGGAAGCCCTCCATGSGCCACCCCTGGTGAATCTGCTCCTGTGGCCCTCTCCTTCAT	540
QY	726	CAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGTGCAGTGGG	785
Db	541	CAGTATCACCCCTGTGTGGCTCTACGCCAGGCTCATCCCTTCCAGGGGGTGTGGG	600
QY	786	CTGCCGATACGCCCTGCCCCAACCCAGACACTGACCTCTACTGTTACCCCTGTACCASTT	845
Db	601	CTGTGGCATCCGCCCTGCCAAACCCGAGACACTGACCTCTACTGTTCACTCTGTACCASTT	660
QY	846	TTTCCCTGGCCTTGGCCCTGCTTGTGTGTCATCACAGCCGATACGTGAGCATCCTGCA	905
Db	661	TTTCCCTGGCCTTGGCCCTTCCGTTGTGTGTCATTACCGCCGATACGTGAATAACTACA	720
QY	906	GCGCATGACGTCCTCAGTGGCCCCCGCCTCCACGCGCAGCATCCGGCTGGCGACAAGAG	965
Db	721	GCGCATGACGTCCTCGGTGGCCCCCAGCCCTCCACGCGCAGCATCCGGCTTGGCAACAAGAG	780
QY	966	GGTGACCCCGCACGCCATTCGCCATCTGTCTGTCTTCTTTGTGTGCTGGGCACCCCTACTA	1025
Db	781	GGTGACCCCGCACGCCATTGCCATCTGTCTGTCTTCTTTGTGTGCTGGGCACCCCTACTA	840
QY	1026	TGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCGCCGACCCCTCACCCTTGTCTACTTATA	1085
Db	841	TGTGCTGACGCTGACCCAGCTGTCCATCAGCCGCGCCGACCCCTCACCCTTGTCTACTTGTATA	900
QY	1086	CAATGCCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTGTGTACTCGT	1145
Db	901	CAACGGCGCCATCAGCTTGGGCTATGCTAACAGCTGCCCTGAACCCCTTGTGTACTAGT	960
QY	1146	GCTCTGTGAGAGCTTCCGCAAAACGCTTGTGCTGTGCGGTGAAGCCTGCAGCCAGGGGCA	1205
Db	961	GCTCTGTGAGAGCTTTCGAAAAACGCTTGTGCTGTGCTGAGTGAAGCCTGCAGCCAGGGGCA	1020
QY	1206	GCTTCGGCGCTGTACGCAACGCTCAGACGGCTGACGAGGAGAGACAGAAAGCAAGGGCAC	1265
Db	1021	GCTCCGACAGGTCAGCAACGCTCAGACAGCTGATGAGGAGAGACAGAAAGCAAGGGCAC	1080
QY	1266	CTGA 1269	
Db	1081	CTGA 1084	

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RESULT 11
US-09-478-602-3
; Sequence 3, Application US/09478602
; Patent No. 6291195
; GENERAL INFORMATION:
; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453y\JPW
; CURRENT APPLICATION NUMBER: US/09/478,602
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-478-602-3

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[illegible][illegible]

Db 1021 GCTCCGACGGTCAAGCAAGCTCAGACAGCTGATGAGGAGAGACAGAAAGCAAGGAC 1080
QY 1266 CTGA 1269
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Db 1081 CTGA 1084

RESULT 12

US-09-218-467B-3
; Sequence 3, Application US/09218467B
; Patent No. 6362326
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: HALSEY, WENDY
; APPLICANT: BERGSMAN, DEBK
; TITLE OF INVENTION: 11cby Genomic Sequence
; FILE REFERENCE: GP-50010
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 775
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-218-467B-3

Query Match 16.3%; Score 207; DB 4; Length 775;
Best Local Similarity 100.0%; Pred. No. 7.4e-39;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCAGTGGAGCCATGAAGAGGAGTGGGAGGGGACAGTTGGGCTTGAGGCGGAC 60
Db 569 ATGTCAGTGGAGCCATGAAGAGGAGTGGGAGGGGACAGTTGGGCTTGAGGCGGAC 628
QY 61 GGCTGCCAGGCTACGAGAGGAGACCCCTTCCGACTGCGGGGCTTGCGCTCCGGACAA 120
Db 629 GGCTGCCAGGCTACGAGAGGAGACCCCTTCCGACTGCGGGGCTTGCGCTCCGGACAA 688
QY 121 GGTGGCAGGCGCTGAGAGGCTGCCGACAGCTGCGTGGTGAGGAGGAGCTCAGCTGGTTG 180
Db 689 GGTGGCAGGCGCTGAGAGGCTGCCGACAGCTGCGTGGTGAGGAGGAGCTCAGCTGGTTG 748
QY 181 TGGGAGCAGCGCAGCGGACCTGCGTGG 207
Db 749 TGGGAGCAGCGCAGCGGACCTGCGTGG 775

RESULT 13

US-08-417-103-15
; Sequence 15, Application US/08417103
; Patent No. 5723299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,103

; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/816,283
; FILING DATE: 01-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1147 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1121
US-08-417-103-15

Query Match 11.6%; Score 147.4; DB 1; Length 1147;
Best Local Similarity 52.6%; Pred. No. 4.1e-25;
Matches 394; Conservative 0; Mismatches 346; Indels 9; Gaps 3;

QY 430 AACACGTCCTCCGACATCTCATCATCAACCTCTCGGTAGATGCTCTCTCTCTG 489
Db 237 AAGACCATCACCAACATTTATCATCTCAACCTGGGACATCGCAGATGAGCTCTCATGCTG 296
QY 490 GGCATGCTCTCATGATCAACCAAGCTCATGGGCAATGGGGTGTGGCACTTTGGGAGACC 549
Db 297 GGTGCTGCTTTCTTGCTATGCAAG--TGGCTCTGGTCCACTGGCCCTTTGGCAAGGCC 353
QY 550 ATGTGACCCCTCATCAGCGCATGGATGCCAATAGTCAAGTTCACCAAGCACTCATCTG 609
Db 354 ATTGCGGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 413
QY 610 ACCGCAATGGCCATTTGACCGCTACCTGGCCACATGTCACCCCATCTCTTCCAGAGTTC 669
Db 414 ACAGTATGAGCATGACGACGATACCTGGCTGGTCCACCCCATCAAGTCCGCAAGTGG 473
QY 670 CGAAGCCCTCTGTGGCCACCTGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 729
Db 474 AGGAGACCCCGGACGCGGACGATGATCACCATGCTGCTGCTGCTGCTGCTGCTGCTG 533
QY 730 ATCACCCTGTGTGCTGTATGCCAGACTCATCCCTTCCAGAGAGTGCAGTGGCTGC 789
Db 534 ATCTGCGCCATCATGATATATGCTGGGCTCCGAGCAACAGTGGGGAGAGAAGCAGCTGC 593
QY 790 GGCATACGCTGCC--CAACCCAGACACTGACCTCTACTGTTACACCTGTACCAGTTT 846
Db 594 ACCATCAACTGGCCAGGTGATCTGGGGCTTGTATACACAGGTTTCATCATCACTTTC 653
QY 847 TTCTTGCCCTTTGGCCCTTTTGTGTCATCACAGCCGATACGTGAGGATCTCTGAG 906
Db 654 ATTCTGGGGTTCTGTTACCCCTCACCATCATCTCTTTGCTACCTGTTTATATCATC 713
QY 907 CGCATGACGTCCTCAGTGGCCCCCGGCTCCAGCGCAGCATCCGGCTCGGAGACAAGAGG 966
Db 714 AAGGTGAAGTCTCTGGAATCCGAGTGGGCTCTCTTAAGAGGAAAGACTCTGAAGAAGAG 773
QY 967 GTGACCCGACAGCCATGCGCATCTGTCTGCTCTTCTTGTGCTGGGACACCTACTAT 1026
Db 774 GTACCCGCAATGGTGTCCATGTTGTTGGCTGTCTTCTTCTTCTTCTTCTTCTTCTT 833
QY 1027 GTGCTACAGCTGACCCAGTTGTCAT--CAGCGCGCCGACCCCTTCTTCTTCTTCTT 1083
Db 834 ATATTCACAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 893
QY 1084 TACAATGGGCGCATCAGCTTGGGCTATGCGCAACAGCTGCTCAACCCCTTGTGTACATC 1143

Db 894 TTGACTTTGTGGTGCTCCTCACCTATGCTAACAGCTGTGCCAACCCCTATCTATATGCC 953

QY 1144 GTGCTCTGTGAGAGCTTCCGCAACGCTT 1172

Db 954 TTCTTGTCTGACACTTCAAGAAGAGCTT 982

RESULT 14

US-07-816-283-5

; Sequence 5, Application US/07816283

; Patent No. 5436155

; GENERAL INFORMATION:

; APPLICANT: Bell, Graeme I.

; APPLICANT: Yamada, Yuichiro

; APPLICANT: Saino, Susumu

; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: PO Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/816,283

; FILING DATE: 19911231

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: McDaniel, C. Steven

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 713-787-1400

; TELEFAX: 713-789-2679

; TELEX: 79-0924

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1351 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; US-07-816-283-5

Query Match 11.6%; Score 147.4; DB 1; Length 1351;

Best Local Similarity 52.6%; Pred. No. 4.3e-25;

Matches 394; Conservative 0; Mismatches 346; Indels 9; Gaps 3;

QY 430 AACAACTCCCGACATCTTCATCATCAACCTCTGGTAGTAGATCTCTTCTCTCCTG 489

Db 305 AAGACCATCACCAACATTACATCTCAACCTGGCCATGCGAGATGAGCTCTTCATGCTG 364

QY 490 GGCATGCCCTTCATGATCCAGCAGCTCATGCGCAATGGGGTGTGGCACTTTGGGAGACC 549

Db 365 GGTCTGCTTCTTCTGCTATGCAGG--TGGCTCTGTGTCACCTGGCCCTTTGGCAAGGCC 421

QY 550 ATGTGACACCTCATGATCCAGGCGCATGATGCCAATAGTCAAGTTCACACGACCTACATCCTG 609

Db 422 ATTGCGGGGTGATGACTGTGATGGCATCAATCAGTTCACGACGATCTTCTGCTG 481

QY 610 ACCGCGATGGCATGACCGGCTACCTGGCCACTGTCCACCCCATCTCTTCCACGAAGTTC 669

Db 482 ACAGTCATGAGCATGACCGGATACCTGGCTGTGTCACCCCATCAAGTCCGCAAGTGG 541

QY 670 CGGAAGCCCTCTGTGGCCACCCCTGTGATCTGCTCTCTGTGGCCCTCTCTCATCAGC 729

Db 542 AGGAGACCCCGGAGCGGCAAGATGATCACCATGCTGTGTGGGAGTCTCTCTGCTGTC 601

QY 730 ATCACCCCTGTGTGCTGTATGCCAGACTCATCCCTTCCACGAGGAGGTGACGTGGGCTGC 789

Db 602 ATCTTGCCCATCATGATATATGCTGGGCTCCGGAGCAACAGTGGGGAGAGCAGCTGC 661

QY 790 GGCATACGCCCTGCC---CACCCCAGACACTGACCTCTACTGTTCACCCCTTACCAAGTTT 846

Db 662 ACCATCAACTGGCCAGGTGAATCTGGGGCTTGGTACACAGGGTTCAATCATCTACACTTTC 721

QY 847 TTCTGGCCTTTTGCCCTGCTTTTGTGTCATCACAGCCGCATACGTAGAGATCCTGCAG 906

Db 722 ATTCTGGGGTTCTCTGTATCCCTCACCATCATCTGTCTTTGTCTACCTGTTCAATATCATC 781

QY 907 CGCATGACGTCCTCAGTGGCCCCCGCCTCCAGCGCAGCATCCGGCTGCGACAAGAG 966

Db 782 AAGGTGAAGTCTCTGGAATCCGAGTGGGCTCCTCTAAGAGGAAGAAGTCTGAGAAGAAG 841

QY 967 GTGACCCGCACAGCCATCGCCATCTGTCTGCTCTTCTTGTGTGCTGGGCAACCTACTAT 1026

Db 842 GTCACCCGAATGGTGTCCATCGTGTGGCTGTCTTCATCTTGTGCTGCCCTTCTTAC 901

QY 1027 GTGCTACAGCTGACCCAGTTGCCAT---CAGCCGCCGACCCCTCACCTTTGTCTACTTA 1083

Db 902 ATATTCAACGTTTCTTCCGTCCTCCATGGCCATCAGCCCCACCCCAAGCCCTTAAGGATG 961

QY 1084 TACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTGTGTACATC 1143

Db 962 TTGACTTTGTGGTGTGCTCCTCACCTATGCTAACAGCTGTGCCAACCCCTATCTATATGCC 1021

QY 1144 GTGCTCTGTGAGAGCTTCCGCAACGCTT 1172

Db 1022 TTCTTGTCTGACACTTCAAGAAGAGCTT 1050

RESULT 15

US-08-417-103-5

; Sequence 5, Application US/08417103

; Patent No. 5723299

; GENERAL INFORMATION:

; APPLICANT: Bell, Graeme I.

; APPLICANT: Yamada, Yuichiro

; APPLICANT: Saino, Susumu

; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/417,103

; FILING DATE: 05-APR-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/816,283

; FILING DATE: 01-DEC-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Wilson, Mark B.

; REGISTRATION NUMBER: 37,259

; REFERENCE/DOCKET NUMBER: ARCD:144

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (512) 474-7577

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1351 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:50:36 ; Search time 13.7494 Seconds
(without alignments)
1273.004 Million cell updates/sec

Title: US-09-885-478-2
Perfect score: 2212
Sequence: 1 MSVGAMKKGVRAVGLGGGS.....LRAVSNAGTADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1763	79.7	353	1 GP24_RAT	P97639 rattus norv
2	1696	76.7	402	1 GP24_HUMAN	Q99705 homo sapien
3	533	24.1	369	1 SSR2_MOUSE	P30875 mus musculu
4	531.5	24.0	369	1 SSR2_HUMAN	P30874 homo sapien
5	528	23.9	368	1 SSR2_BOVIN	P34993 bos taurus
6	527	23.8	369	1 SSR2_RAT	P30680 rattus norv
7	525.5	23.8	369	1 SSR2_PIG	P34994 sus scrofa
8	514	23.2	391	1 SSR1_HUMAN	P30872 homo sapien
9	513.5	23.2	388	1 SSR1_HUMAN	P31391 homo sapien
10	508	23.0	391	1 SSR1_MOUSE	P30873 mus musculu
11	504.5	22.8	418	1 SSR3_HUMAN	P32745 homo sapien
12	497.5	22.5	391	1 SSR1_RAT	P28646 rattus norv
13	494.5	22.4	384	1 SSR4_MOUSE	P30937 rattus norv
14	483	21.8	384	1 SSR4_MOUSE	P49660 mus musculu
15	480.5	21.7	428	1 SSR3_RAT	P30936 rattus norv
16	478.5	21.6	364	1 SSR5_HUMAN	P35346 homo sapien
17	472	21.3	428	1 SSR3_MOUSE	P30935 mus musculu
18	470.5	21.3	363	1 SSR5_RAT	P30938 rattus norv
19	457	20.7	401	1 OPRM_BOVIN	P79350 bos taurus
20	456	20.6	362	1 SSR5_MOUSE	O08858 mus musculu
21	453.5	20.5	398	1 OPRM_MOUSE	P42866 mus musculu
22	452	20.4	401	1 OPRM_PIG	Q95247 sus scrofa
23	451.5	20.4	372	1 OPRD_HUMAN	P41143 homo sapien
24	451.5	20.4	398	1 OPRM_RAT	P33535 rattus norv
25	450	20.3	400	1 OPRM_MACMU	Q9myw9 macaca mula
26	448	20.3	400	1 OPRM_HUMAN	P35372 homo sapien
27	446.5	20.2	372	1 OPRD_RAT	P33533 rattus norv
28	441	19.9	372	1 OPRD_MOUSE	P32300 mus musculu
29	435.5	19.7	380	1 OPRK_HUMAN	P41145 homo sapien
30	431.5	19.5	380	1 OPRK_CAVPO	P41144 cavia porce
31	426	19.3	370	1 OPRX_HUMAN	P47748 homo sapien
32	421	19.0	328	1 GPR7_HUMAN	P48145 homo sapien
33	420.5	19.0	380	1 OPRK_MOUSE	P33534 mus musculu

34	419	18.9	380	1 OPRK_RAT	P34975 rattus norv
35	413	18.7	370	1 OPRX_HUMAN	P41146 homo sapien
36	411.5	18.6	367	1 OPRX_MOUSE	P35377 mus musculu
37	410.5	18.6	367	1 OPRX_RAT	P35370 rattus norv
38	409.5	18.5	333	1 GPR8_HUMAN	P48146 homo sapien
39	398	18.0	370	1 OPRX_PIG	P79292 sus scrofa
40	372.5	16.8	359	1 AG2R_CHICK	P79785 gallus gall
41	372.5	16.8	359	1 AG2R_MELGA	P33396 meleagris g
42	370	16.7	363	1 AG2S_XENLA	P35373 xenopus lae
43	368	16.6	362	1 AG2R_XENLA	P32303 xenopus lae
44	359.5	16.3	352	1 P2Y7_HUMAN	Q15722 homo sapien
45	350	15.8	353	1 CKR8_MOUSE	P56484 mus musculu

ALIGNMENTS

RESULT 1					
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ID	GP24_RAT	STANDARD;	PRT;	353 AA.	
AC	P97639;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Probable G protein-coupled receptor GPR24 (SLC-1).				
GN	GPR24 OR SLC1.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=98193144; PubMed=9531978;				
RA	Lakaye B., Minet A., Zorzi W., Grisar T.;				
RT	"Cloning of the rat brain cDNA encoding for the SLC-1 G protein-				
RT	coupled receptor reveals the presence of an Intron in the gene.";				
RL	Biochim. Biophys. Acta 1401:216-220(1998).				
RP	[2]				
RP	SEQUENCE OF 143-300 FROM N.A.				
RX	MEDLINE=97131607; PubMed=8977118;				
RA	Kolakowski L.F. Jr., Jung B.P., Nguyen T., Johnson M.P., Lynch K.R.,				
RA	Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;				
RT	"Characterization of a human gene related to genes encoding				
RT	somatostatin receptors.";				
RL	FEBS Lett. 398:253-258(1996).				
CC	- - FUNCTION: ORPHAN RECEPTOR. DOES NOT SEEM TO BIND TO SOMATOSTATIN.				
CC	- - SUBCELLULAR LOCATION: Integral membrane protein.				
CC	- - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	SIMILAR TO SOMATOSTATIN RECEPTORS.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AF008650; AAC27977.1; -				
DR	EMBL; U77953; AAC14588.1; -				
DR	InterPro; IPR000276; GPCR_Rhodpsn.				
DR	InterPro; IPR004047; MCH1receptor.				
DR	Pfam; PF00001; 7tm_1; 1.				
DR	PRINTS; PRO0237; GPCR_RHODOPSN.				
DR	PRINTS; PRO1507; MCH1RECEPTOR.				
DR	PROSITE; PS00237; G_PROTEIN_REC_F1_1; FALSE_NEG.				
DR	PROSITE; PS50262; G_PROTEIN_REC_F1_2; 1.				
KW	G-protein coupled receptor; Transmembrane.				
FT	DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).				
FT	TRANSMEM 46 66 1 (POTENTIAL).				
FT	DOMAIN 67 79 CYTOPLASMIC (POTENTIAL).				
FT	TRANSMEM 80 100 2 (POTENTIAL).				

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FT DOMAIN 101 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 139 3 (POTENTIAL).
FT DOMAIN 140 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 182 4 (POTENTIAL).
FT DOMAIN 183 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 225 5 (POTENTIAL).
FT DOMAIN 226 256 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 277 6 (POTENTIAL).
FT DOMAIN 278 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 315 7 (POTENTIAL).
FT DOMAIN 316 353 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 353 AA; 39063 MW; F6EEB2DF381084A9 CRC64;

Query Match 79.7%; Score 1763; DB 1; Length 353;
Best Local Similarity 96.0%; Pred. No. 6.6e-92;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 70 MDLEASLLPTGPNASNTSDGPDNLTSAGSPPRTGSSISYINIMPSYFGTICLLGIIGNST 129
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Db 1 MDLQTSLSLTGPNASNISDGDNLTLPGSPRGTGSVSYINIMPSYFGTICLLGIVGNST 60

QY 130 VIFAVVKKSKLHMCNNVPDIFIINLSVDLLFLLGMPFMIHQMGNGVWHFGETMCTLT 189
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Db 61 VIFAVVKKSKLHMCNSNPDIIFIINLSVDLLFLLGMPFMIHQMGNGVWHFGETMCTLT 120

QY 190 AMDANSQFTSTYILTAMAIDRYLATVHPISSTKPKPSVATLVICLLMALSFISTTPWL 249
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Db 121 AMDANSQFTSTYILTAMTIDRYLATVHPISSTKPKPSMATLVICLLMALSFISTTPWL 180

QY 250 YARLIPEPGGAVCGIRLPNPDLDLYWFTLYQFELAFALPEVVTAAVYRILQRMSSVA 309
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Db 181 YARLIPEPGGAVCGIRLPNPDLDLYWFTLYQFELAFALPEVVTAAVYKILQRMSSVA 240

QY 310 PASQSRIRLRKRYRTAIAICLVFECVAPYVYLQTLQSLISRPRTLTFVYLYNAAISLG 369
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 PASQSRIRLRKRYRTAIAICLVFECVAPYVYLQTLQSLISRPRTLTFVYLYNAAISLG 300

QY 370 YANSCLNPFVYIVLCETERKRLVLSVKPAAQGLRAVSNACGTADERTESKGT 422
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Db 301 YANSCLNPFVYIVLCETERKRLVLSVKPAAQGLRTVSNACGTADERTESKGT 353

RESULT 2
GP24_HUMAN
ID GP24_HUMAN STANDARD; PRT; 402 AA.
AC Q99705;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor GPR24 (SLC-1).
GN GPR24 OR SLC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97131607; PubMed=8977118;
RA Kolakowski L.F. Jr., Jung B.P., Nguyen T., Johnson M.P., Lynch K.R.,
RA Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;
RT "Characterization of a human gene related to genes encoding
RT somatostatin receptors.";
RL FEBS Lett. 398:253-258(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
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RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclell J., McLaren S., McMuray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilmington L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.L.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA zhan M., zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wansley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelman L.,
RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tilihuh Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
CC -I- FUNCTION: ORPHAN RECEPTOR. DOES NOT SEEM TO BIND TO SOMATOSTATIN.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: GREATEST ABUNDANCE IN BRAIN, PARTICULARLY IN
CC THE FRONTAL CORTEX AND HYPOTHALAMUS. A LOWER LEVEL EXPRESSION IS
CC SEEN IN THE LIVER AND HEART.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC SIMILAR TO SOMATOSTATIN RECEPTORS.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U71092; AAC14587.1; -.
DR EMBL; Z86090; CAB62943.1; -.
DR Genew; HGNC:4479; GPR24.
DR MIM; 601751; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR004047; MCH1receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01507; MCH1RECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; FALSE_NEG.
DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 94 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 95 115 1 (POTENTIAL).
FT DOMAIN 116 128 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 129 149 2 (POTENTIAL).
FT DOMAIN 150 167 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 168 188 3 (POTENTIAL).
FT DOMAIN 189 210 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 211 231 4 (POTENTIAL).
FT DOMAIN 232 253 EXTRACELLULAR (POTENTIAL).
```

FT TRANSMEM 254 274 5 (POTENTIAL).
FT DOMAIN 275 305 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 306 326 6 (POTENTIAL).
FT DOMAIN 327 343 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 344 364 7 (POTENTIAL).
FT DOMAIN 365 402 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 402 AA; 44454 MW; 5D24B72E76CF4F82 CRC64;

Query Match 76.7%; Score 1696; DB 1; Length 402;
Best Local Similarity 83.2%; Pred. No. 4e-88;
Matches 341; Conservative 7; Mismatches 14; Indels 48; Gaps 4;

QY 50 PAWVEGS--SARLMEQATGTGMDLEASLLPTGPNASNTSDGPDN----- 92
D 4 PSKTDGSGHSGRIHQETHGEKRD-----KISN-SEGRENNGRGFOMNGSLEAE 52
QY 93 -----LTSAGSPRTGSIYINIMPSVFGTICLLGIIGNSTYIF 132
D 53 HASRMSVLRAKPMSNSQRLLLSPGSPRTGISISYINIMPSVFGTICLLGIIGNSTYIF 112
QY 133 AVYKSKSLHWCNNVPDIFINLSVDLFLGLMPFMIHQLMNGVWHFGETMCTLTAMD 192
D 113 AVYKSKSLHWCNNVPDIFINLSVDLFLGLMPFMIHQLMNGVWHFGETMCTLTAMD 172
QY 193 ANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATVLCILMALSFISITPVWLVAR 252
D 173 ANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATVLCILMALSFISITPVWLVAR 232
QY 253 LIPEPGAVGCGIRLPNPDPDLWFTLYQFELAFALPFVYITAAVYRILQRTSSVAPAS 312
D 233 LIPEPGAVGCGIRLPNPDPDLWFTLYQFELAFALPFVYITAAVYRILQRTSSVAPAS 292
QY 313 QRSIRLRTKRVTRTAIAICLVFVCWAPYVYLQTLQLSISRPTLTFVYLYNNAISLGYN 372
D 293 QRSIRLRTKRVTRTAIAICLVFVCWAPYVYLQTLQLSISRPTLTFVYLYNNAISLGYN 352
QY 373 SCLNPFVYIVLCETFRRKRLVSVKPAQOQLRAVSNAGTADERTESKGT 422
D 353 SCLNPFVYIVLCETFRRKRLVSVKPAQOQLRAVSNAGTADERTESKGT 402

RESULT 3
SSR2_MOUSE STANDARD; PRT; 369 AA.
ID SSR2_MOUSE STANDARD; PRT; 369 AA.
AC P30875; P30934;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor type 2 (SS2R) (SRIF-1) (SS2RA and SS2RB).
GN SSTR2 OR SMSTR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92108031; PubMed=1346068;
RA Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;
RT "Cloning and functional characterization of a family of human and
RT mouse somatostatin receptors expressed in brain, gastrointestinal
RT tract, and kidney."
RL Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93012001; PubMed=1397330;
RA Vanetti M., Kouba M., Wang X., Vogt G., Hoellt V.;
RT "Cloning and expression of a novel mouse somatostatin receptor
RT (SSTR2B)."
RL FEBS Lett. 311:290-294(1992).
RN [3]
RP SEQUENCE OF 99-309 FROM N.A.
RX MEDLINE=94300079; PubMed=7913111;
RA Elliott D.E., Metwali A., Blum A.M., Sandor M., Lynch R.,

RA weinstock J.V.;
RT "T lymphocytes isolated from the hepatic granulomas of schistosome-
RT infected mice express somatostatin receptor subtype II (SSTR2)
RT messenger RNA."
RL J. Immunol. 153:1180-1186(1994).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=93387480; PubMed=8104154;
RA Vanetti M., Hoellt V.;
RT "The two isoforms of the mouse somatostatin receptor (msstr2a and
RT msstr2b) differ in coupling efficiency to adenylate cyclase and in
RT agonist-induced receptor desensitization."
RL FEBS Lett. 331:260-266(1993).
CC -I- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
CC PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CC CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC -I- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (By
CC similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SS2RA (SHOWN HERE) AND SS2RB;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -I- TISSUE SPECIFICITY: CEREBRUM AND KIDNEY.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M81832; AAA58256.1; -.
DR EMBL; X68951; CAA48766.1; -.
DR EMBL; S71756; -, NOT_ANNOTATED_CDS.
DR PIR; D41795; D41795.
DR PIR; S29248; S29248.
DR HSSP; P02699; 1BOJ.
DR MGD; MGI:98328; Smstr2.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; Pf00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate; Alternative splicing.
FT DOMAIN 1 43
FT TRANSMEM 1 43
FT DOMAIN 44 67
FT TRANSMEM 68 78
FT TRANSMEM 79 103
FT DOMAIN 104 118
FT TRANSMEM 119 138
FT DOMAIN 139 161
FT TRANSMEM 162 181
FT DOMAIN 182 207
FT TRANSMEM 208 229
FT DOMAIN 230 253
FT TRANSMEM 254 278
FT DOMAIN 279 308
FT TRANSMEM 289 303
FT DOMAIN 304 369
FT CARBOHYD 9 9
FT CARBOHYD 22 22
FT CARBOHYD 29 29
FT CARBOHYD 32 32
FT DISULFID 115 193
FT LIPID 328 328
FT VARSPLIC 332 369
FT CONFLICT 179 179


```

FT   CONFLICT    305      305      S -> T (IN REF. 2).
SQ   SEQUENCE    369 AA; 41221 MW; A78845AF74823039 CRC64;

Query Match
Best Local Similarity 24.1%; Score 533; DB 1; Length 369;
Matches 118; Conservative 77; Mismatches 131; Indels 46; Gaps 10;

QY   EQATGTG-WM---DLEASLPTGPNASNTSDGPDNLTSGSPRTGSISYINIIMPSVF 116
Db   6 EQLNGSÖVWVSSPFDLNGSLGPS--NGSNÖTEPYDMTS-----NAVLTFIY 50

QY   GTICLLGIIGNSTVIFAAYKSKLHWCNVPDIFIINLSVDILFLGMFP-----MIH 170
Db   51 FVVCVVGLCGNTLVIVYLIRYAKM--KITNYILNLAIADLFMLGLPELAMÖVALVH 107

QY   QLMGNGVWHFEGETMCTLTITAMDANSÖFTSTYYILTAMADRYLATVHPISSTKERKPSVAT 230
Db   108 -----WPF GKALCRVVMTPVDGINÖFTSIFFCLTVMSIDRYLAHVHPIKSAKWRRPTAK 160

QY   LVICLLMALFSISTPWLYARLIPEPGAVGCGIRLPNPDPDLV-WETLYÖFFLAFAFP 289
Db   161 MINVAVWCVSLLVILPIMIYAGLRNQWRSSCTINWPGESGAWTGFIIYAFILGLFVP 220

QY   FVVITAAYVRILÖRMTSSVAPASÖRSIRLRTKRVTRTAIAICLVFEVCWAPYYVLÖLTÖL 349
Db   221 LTIFCLCYLFIITIKVKSSGIRVGSSKRKKSEKVTIRMVSIVAVFIEFCWLPIFYENVSSV 280

QY   SIS-RPTLTFVYLYNAAISLGYSANSCLNPFVYIVLCETERKRLVSVKPAAÖGÖLRAYSN 408
Db   281 SVAISPTPALKGMEFDEVILLTYANSCANPILYAFLSDNEFK-----SFÖNVLCIVKV 332

QY   AQTADEERTESK 420
Db   333 SGTEDEGRSDSK 344

RESULT 4
SSR2_HUMAN
AC P30874; STANDARD; PRT; 369 AA.
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor type 2 (SS2R) (SRIF-1).
GN SSR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE=92108031; Pubmed=1346068;
RA Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;
RT "Cloning and functional characterization of a family of human and
RT mouse somatostatin receptors expressed in brain, gastrointestinal
RT tract, and kidney.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=93236586; Pubmed=8386508;
RA Patel Y.C., Greenwood M., Kent G., Panetta R., Srikanth C.B.;
RT "Multiple gene transcripts of the somatostatin receptor SST2: tissue
RT selective distribution and cAMP regulation.";
RL Biochem. Biophys. Res. Commun. 192:288-294(1993).
RN [3]
RP INTERACTION WITH SHANK1.
RX MEDLINE=20020275; Pubmed=10551867;
RA Zitzler H., Hoencck H.-H., Baechner D., Richter D., Kreienkamp H.-J.;
RT "Somatostatin receptor interacting protein defines a novel family of
RT multidomain proteins present in human and rodent brain.";
RL J. Biol. Chem. 274:32997-33001(1999).
CC -!- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF

```

[illegible]

RT GH4C1 pituitary cells.";
RL Biochem. Biophys. Res. Commun. 184:131-136(1992).
RN [3]
RP ALTERNATIVE SPLICING.
RX MEDLINE=93236586; PubMed=8386508;
RA Patel Y.C., Greenwood M., Kent G., Panetta R., Srikanth C.B.;
RT "Multiple gene transcripts of the somatostatin receptor SSTR2: tissue
selective distribution and cAMP regulation."
RL Biochem. Biophys. Res. Commun. 192:288-294(1993).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC -1- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (By
similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; A (SHOWN HERE) AND B; ARE
PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: CORTEX, HIPPOCAMPUS, PITUITARY GLAND, COLON
ADRENALS, PANCREAS-DERIVED CELL LINE, AND PANCREATIC TUMOR.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; M96817; AAA42166.1; -.
DR EMBL; M93273; AAA42165.1; -.
DR PIR; A45291; A45291.
DR HSSP; P02699; IBOJ.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate; Alternative splicing.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 67 1 (POTENTIAL).
FT DOMAIN 68 78 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 79 103 2 (POTENTIAL).
FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 138 3 (POTENTIAL).
FT DOMAIN 139 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 181 4 (POTENTIAL).
FT DOMAIN 182 207 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 208 229 5 (POTENTIAL).
FT DOMAIN 230 253 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 254 278 6 (POTENTIAL).
FT DOMAIN 279 288 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 289 303 7 (POTENTIAL).
FT DOMAIN 304 369 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 9 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 115 193 BY SIMILARITY.
FT LIPID 328 328 PALMITATE (POTENTIAL).
FT VARSPLIC 332 369 VSGAEDGERSDSKQSRNLTETQRTLNGDLQTSI ->
SQ SEQUENCE 369 AA; 41199 MW; 4990EA89E88D7D19 CRC64;
Query Match 23.8%; Score 527; DB 1; Length 369;
Best Local Similarity 31.5%; Pred. No. 4.6e-23;
Matches 117; Conservative 77; Mismatches 132; Indels 46; Gaps 10;

Db 6 EQFNGSQWIPSPFDLNSLGPS--NGSNQTEPEYDMS-----NAVLFTIX 50
QY 117 GTICLLGIIGNSTVIFAVYKSKSLHWCNNVPDIFIIINLSVVDLFLGMPE-----MIH 170
Db 51 FVYCVVGLCGNTLVIVYLLRYAKM---KITFTNYIILNLAIDELFMGLPFLAMQVALVH 107
QY 171 QLMGNGVWHFGETMCTLTAMDANSQFTSTYILLTAMADRYLATVHPISSTKFRKPSVAT 230
Db 108 -----WPFKAICRVVMTVDGINQFTSIFCLTWSIDRYLAVVHPDKSAKWRPRPTAK 160
QY 231 LVICLLMALSFISTPVMYARLIPFGAGVCGIRLPNPDIDL-WFTLYQFFLAFLP 289
Db 161 MINVAVWGVSLVILPIMTYAGLRSNQWGRSSCTINWPGESGAWTGTFIYAFILGLVP 220
QY 290 FVYITAAVYRILQRMTSVAPASQSRIRLRKRYTRTAICLVFVVCWAPYVVLQTLQ 349
Db 221 LTITCLCYLFIITIKVSSGIRVSSKRRKSEKVTYRMVSVIVAVFLCMLPFYIFNVSSV 280
QY 350 SIS-RPTLTFVYLYNAISLGYANSCLNPFIYIVLCETFRKRLVSVKPAQGLRAVSN 408
Db 281 SVAISPTPALKGMFDFVILLTYANSCANPILYAFLSDNFK-----SFQNVLCVAV 332
QY 409 AQTADERTESK 420
Db 333 SGAEDGERSDSK 344
RESULT 7
SSR2_PIG STANDARD; PRT; 369 AA.
AC P34994;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor type 2 (SS2R) (SRIF-1).
GN SSTR2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94168590; PubMed=8123027;
RA Matsumoto K., Yokogoshi Y., Fujinaka Y., Zhang C., Saito S.;
RT "Molecular cloning and sequencing of porcine somatostatin receptor
2."
RL Biochem. Biophys. Res. Commun. 199:298-305(1994).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC -1- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (By
similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; D21338; BAA04810.1; -.
DR PIR; JC2083; JC2083.
DR HSSP; P02699; IBOJ.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.

[illegible]

RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA	Conlson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA	Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA	Lehvaslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA	Marsh V.L., Martin S.L., McConachle L.J., McIay K., McMurray A.A.,
RA	Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA	Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA	Skrice C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA	Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA	Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA	Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA	Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA	Rogers J.;
RT	"The DNA sequence and comparative analysis of human chromosome 20.";
RL	Nature 414:865-871(2001).
CC	-1- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS
CC	RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
CC	CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF
CC	ADENYLYL CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE
CC	RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
CC	MEDIATES ANTIPROLIFERATIVE ACTION OF SOMATOSTATIN IN TUMOR CELLS.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN FETAL AND ADULT
CC	BRAIN, LUNG TISSUE, STOMACH, AND IN LESSER QUANTITIES IN THE
CC	KIDNEY, PITUITARY, AND ADRENALS.
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC	-----
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; D16826; BAA04106.1; -.
DR	EMBL; L14856; AAA36623.1; -.
DR	EMBL; L07833; AAA60565.1; -.
DR	EMBL; L07061; -; NOT ANNOTATED_CDS.
DR	EMBL; AL049651; CAB51953.1; -.
DR	PIR; JN0605; JN0605.
DR	PIR; JN0762; JN0762.
DR	HSSP; P02699; 1BOJ.
DR	Genew; HGNC:11333; SSTR4.
DR	MTM; 182454; -.
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCR_RHODOPSIN.
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;
KW	Multigene family; Lipoprotein; Palmitate; Phosphorylation;
KW	Polymorphism.
FT	DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 47 73 1 (POTENTIAL).
FT	DOMAIN 74 83 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 84 104 2 (POTENTIAL).
FT	DOMAIN 105 120 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 121 142 3 (POTENTIAL).
FT	DOMAIN 143 161 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 162 185 4 (POTENTIAL).
FT	DOMAIN 186 208 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 209 232 5 (POTENTIAL).
FT	DOMAIN 233 260 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 261 280 6 (POTENTIAL).
FT	DOMAIN 281 291 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 292 314 7 (POTENTIAL).

FT DOMAIN 315 388 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 119 198 BY SIMILARITY.
FT LIPID 327 327 PALMITATE (POTENTIAL).
FT VARIANT 83 83 N -> T (IN DBSNP:1065191).
FT CONFLICT 284 284 /FTID=VAR_011703.
FT CONFLICT 321 321 V -> F (IN REF. 4 AND 5).
FT CONFLICT 365 365 S -> F (IN REF. 5).
SQ SEQUENCE 388 AA; 41894 MW; 8BCDD69B5F3BC2F5 CRC64;

Query Match 23.2%; Score 513.5; DB 1; Length 388;
Best Local Similarity 31.7%; Pred. No. 2.7e-22;
Matches 107; Conservative 74; Mismatches 118; Indels 39; Gaps 9;

QY 62 EQATGTGWMDEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVEGTICL 121
DB 12 EEGIGTAW-----PSAANASSAPAEAEAVAGPGDARAAGM-VAIQCIYALVCL 59
QY 122 LGIIGNSTVFAVYKSKLHWCNVPIFIINLSVVDLFLGMPFMI-----HQLMGN 175
DB 60 VGLVGNALVIFILRYAKMKTATN---IYLLNLAVADELFMLSVFVASSAALRH----- 111
QY 176 GWHFGEFMCULTITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICL 235
DB 112 --WPFGSVLCRAVLSDGLNMTSVCLTVLSVDRYVAVHPLRAATYRPSVAKLINIG 169
QY 236 LMAISFISITPVMYLARLIPFPGG-AVGCGIRLPNPDITLYW---FTLYQFLAFALPEV 291
DB 170 VWLASLVTLPIAIFADTRPARGGQAVACNLQWPHP---AWSAVEVVTYTFLLGLLPVL 225
QY 292 VITAAYVRIQMTSSVAPASQSRISILRTKRVTRTAIAICLVFVCWAPYVVLQTLQST 351
DB 226 AIGLCYLLVGMKRAVALRAGWQQRRESEKKITRLVLMVVVFLCWMPEYVVLNLNV 285
QY 352 SRPTLTFVYLYNNAISLGYANSCLNPEVYIVLCETERK 389
DB 286 TSLDAT---VNHSVLSILSYANSCANPILYGLSDNFR 320

RESULT 10

SSR1_MOUSE
ID SSR1_MOUSE STANDARD; PRT; 391 AA.
AC P30873;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Somatostatin receptor type 1 (SSIR) (SRIF-2).
GN SSTRI OR SMSTR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92108031; PubMed=1346068;
RA Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Selino S.;
RT "Cloning and functional characterization of a family of human and
RT mouse somatostatin receptors expressed in brain, gastrointestinal
RT tract, and kidney."
RL Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR
CC SOMATOSTATIN-14 THAN -28. THIS RECEPTOR IS COUPLED VIA PERTUSSIS
CC TOXIN SENSITIVE G PROTEINS TO INHIBITION OF ADENYLYL CYCLASE. IN
CC ADDITION IT STIMULATES PHOSPHOTYROSINE PHOSPHATASE AND NA+/H+
CC EXCHANGER VIA PERTUSSIS TOXIN INSENSITIVE G PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: JEJUNUM AND STOMACH.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; M81831; AAA58255.1; .
DR PIR; C41795; C41795.
DR MGI; MGI:98327; Smstr1.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate.
FT DOMAIN 1 56 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 57 84 1 (POTENTIAL).
FT DOMAIN 85 94 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 95 120 2 (POTENTIAL).
FT DOMAIN 121 131 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 132 153 3 (POTENTIAL).
FT DOMAIN 154 175 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 176 196 4 (POTENTIAL).
FT DOMAIN 197 219 5 (POTENTIAL).
FT TRANSMEM 220 244 6 (POTENTIAL).
FT DOMAIN 245 270 7 (POTENTIAL).
FT TRANSMEM 271 296 6 (POTENTIAL).
FT DOMAIN 297 303 7 (POTENTIAL).
FT TRANSMEM 304 327 7 (POTENTIAL).
FT DOMAIN 328 391 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 130 208 BY SIMILARITY.
SQ SEQUENCE 391 AA; 42718 MW; 4461673956F2BD22 CRC64;

Query Match 23.0%; Score 508; DB 1; Length 391;
Best Local Similarity 30.7%; Pred. No. 5.6e-22;
Matches 111; Conservative 73; Mismatches 134; Indels 44; Gaps 8;

QY 29 PLDDGACAPGGGRRRLPQPAWEGSSARLWEQATGTGWMDEASLLPTGPNASNTSD 88
DB 14 PSPSPSGCG-----EGACSR---GPGSGAAD---GMEEPGRNASQNGT 50
QY 89 GPDNLTAGSPRTGSIYINIMPSVEGTICLLIIGNSTVFAVYKSKLHWCNVPI 148
DB 51 LSEGQSA-----ILISFIYSVCLVGLGNSMVIYILRYAKMKTATN--- 94
QY 149 IFIINLSVVDLFLGMPFMIHQLMGNVWHGETMCTLTITAMDANSQFTSTYILITAMA 208
DB 95 IYLLNLAVADELFMLSVPLVSTILRH-WFGALLCRVLSDAVNMFTSICYLTVLSV 153
QY 209 DRYLATVHPISSTKFRKPSVATVLCILMAISFISITPVMYLARLIPFPGAVGCGIRLP 268
DB 154 DRYVAVHPIKARRYRPTVAKVNLGVWLSLVILPIVVSRTAANSQDGTVACNMLMP 213
QY 269 NP-DTLYMFTLYQFLAFALPFVVITAAYVRILQMTSSVAPASQSRISRLRTKRYTRTA 327
DB 214 EPAQRWLVGFLYTFMLGFLPVGAICLCYVLIIAKMRVVALKAGWQQRKRSERKITLMV 273
QY 328 IALCLVFVCWAPYVVLQTLQSTSRPTLTFVYLYNNAISLGYANSCLNPEVYIVLCETF 387
DB 274 MAMVAVFVLCWMPYVVLVNVRAQDDATVSQ---SVILGYANSCANPILYGLSDNF 330
QY 388 RK 389
DB 331 KR 332

RESULT 11

SSR3_HUMAN
ID SSR3_HUMAN STANDARD; PRT; 418 AA.

AC P32745; 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor type 3 (SS3R) (SSR-28).
GN SS3R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93149123; PubMed=1337145;
RA Yamada Y., Reisine T., Law S.F., Ihara Y., Kubota A., Kagimoto S.,
RT "Somatostatin receptors, an expanding gene family: cloning and
RT functional characterization of human SS3R, a protein coupled to
RT adenylyl cyclase.";
RL Mol. Endocrinol. 6:2136-2142(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93238970; PubMed=8097479;
RA Corness J.D., Demchyshyn L.L., Seeman P., van Tol H.H.M.,
RA Srikant C.B., Kent G., Patel Y.C., Niznik H.B.;
RT "A human somatostatin receptor (SS3R), located on chromosome 22,
RT displays preferential affinity for somatostatin-14 like peptides.";
RL FEBS Lett. 321:279-284(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiwich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Bartlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Griffiths M.N.D., Hall C.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths A.A.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA McClay J., McLaren S., McMuray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavlitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Mala J.E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
RA Mcdermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tliahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).

CC -!- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: BRAIN, PITUITARY AND PANCREAS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; M96738; AAA60592.1; -;
DR EMBL; Z82188; CAB45263.1; -;
DR PIR; S32501; S32501.
DR PIR; A46226; A46226.
DR HSSP; P34996; 1DDD.
DR Genew; HGNC:11332; SS3R3.
DR MIM; 182453; -;
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPE_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Polymorphism.
FT DOMAIN 1 43
FT TRANSMEM 44 69
FT DOMAIN 70 79
FT TRANSMEM 80 101
FT DOMAIN 102 116
FT TRANSMEM 117 138
FT DOMAIN 139 161
FT TRANSMEM 162 181
FT DOMAIN 182 205
FT TRANSMEM 206 231
FT DOMAIN 232 257
FT TRANSMEM 258 279
FT DOMAIN 280 293
FT TRANSMEM 294 316
FT DOMAIN 317 418
FT CARBOHYD 17 17
FT CARBOHYD 30 30
FT DISULFID 116 191
FT DOMAIN 346 360
FT VARIANT 411 411
SQ SEQUENCE 418 AA; 45847 MW; 1227095F801190C4 CRC64;
Query Match 22.8%; Score 504.5; DB 1; Length 418;
Best Local Similarity 32.5%; Pred. No. 9.2e-22;
Matches 118; Conservative 76; Mismatches 134; Indels 35; Gaps 11;
QY 81 PNASNTSDGPDNLTSAGSP-----PRTGSISYINIMPSVEGTICLIGINSTV 130
Db 6 PSSVSTSEPENASSAMPDPATLGNVSAGSPAGLAVSGVLIPLVYLVYCVGLGNSLV 65
QY 131 IFAVVKKSKLHWCNNVPDIFITINLSVVDLIFLGMPEMIHOLMGNGV--WHEGETMCTLI 188
Db 66 IYVVLRHATA---SPSVYNYIILNALADELFMLGLPFLAAQ---NALSYWPFGLMCRIV 119
QY 189 TAMDANSQFTSTYITLTAIDAIDRYLATVHPISSTFKRKPSVATLVICLLMALSFISITPVW 248
Db 120 MAVVDGINQFTSIFCLTYMSVDRYLAVVHPTRSARWRTPAVARTVSAAVWASAVVLPVV 179
QY 249 LYARLIPPGGAVGCGIRLPNPDITLYW---FTLYQFFLAFALPFVVITAAVYRILQRM 305
Db 180 VFSGV---PRGMSTCHMQWDEPAA--AWRAGFIITYTALGFFGPLLVICLCYLLIVKVR 234
QY 306 SS-----VAPASQRSIRLRTRKRVTRTAIAICLVFVCWAPYVYLQTLQLSIRP-TLTFVY 360

Db 235 SAGRWAPSCQRR-RRSERRVTRMVAVVALFVLCWMPFYVLINIVNVCPLEPEPAFFG 293
QY 361 LYNAISLGYANSCLNPFYIYVLCETFR---KRLVLSYKPAAGQLRAVSNAGTADERT 417
Db 294 LYFLVALPYANSCANPILYGLSYRFKQGFRRVLLRPSRRVRSQEPVTGPPPEKTEEDE 353
OY 418 ESK 420
Db 354 EEE 356
RESULT 12
SSRL_RAT
ID SSRL_RAT STANDARD; PRT; 391 AA.
AC P28646;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Somatostatin receptor type 1 (SSIR) (SRIF-2).
GN SSTR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=92096119; PubMed=1661599;
RA Meyerhof W., Paust H.J., Schoenrock C., Richter D.;
RT "Cloning of a cDNA encoding a novel putative G-protein-coupled
RT receptor expressed in specific rat brain regions."
RL DNA Cell Biol. 10:689-694(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93016064; PubMed=1400442;
RA Li X.-J., Forte M., North R.A., Ross C.A., Snyder S.H.;
RT "Cloning and expression of a rat somatostatin receptor enriched in
RT brain."
RL J. Biol. Chem. 267:21307-21312(1992).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR
CC SOMATOSTATIN-14 THAN -28. THIS RECEPTOR IS COUPLED TO
CC PHOSPHOTYROSINE PHOSPHATASE AND NA+/H+ EXCHANGER VIA PERTUSSIS
CC TOXIN INSENSITIVE G PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, PITUITARY, ISLET, JEJUNUM, STOMACH,
CC HEART, SPLEEN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC
DR EMBL; X62314; CAA44193.1; -.
DR EMBL; M97656; -; NOT_ANNOTATED_CDS.
DR PIR; A39297; A39297.
DR PIR; A45102; A45102.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate.
FT DOMAIN 1 56 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 57 84 1 (POTENTIAL).
FT DOMAIN 85 94 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 95 120 2 (POTENTIAL).

FT DOMAIN 121 131 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 132 153 3 (POTENTIAL).
FT DOMAIN 154 175 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 176 196 4 (POTENTIAL).
FT DOMAIN 197 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 244 5 (POTENTIAL).
FT DOMAIN 245 270 6 (POTENTIAL).
FT TRANSMEM 271 296 7 (POTENTIAL).
FT DOMAIN 297 303 6 (POTENTIAL).
FT TRANSMEM 304 327 7 (POTENTIAL).
FT DOMAIN 328 391 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 130 208 BY SIMILARITY.
FT LIPID 339 339 PALMITATE (POTENTIAL).
SQ SEQUENCE 391 AA; 42746 MW; 28ED6E894B72FBB7 CRC64;
Query Match 22.5%; Score 497.5; DB 1; Length 391;
Best Local Similarity 32.3%; Pred. No. 2.1e-21;
Matches 104; Conservative 72; Mismatches 129; Indels 17; Gaps 7;
QY 78 PTGPNASNTSDGP-----DNLTSAQ-SPPRTGSISY---INIMPSVEGFTICLLGIIGNS 128
Db 18 PGGCGEGVCSRGPSGADGMEEPGRNSSONGTLESGGSAILISFIYSVCLVGLGNS 77
QY 129 TVTFAVVKKSKLHMCNNVPDIFINLSVDLLFLGLMPFMHQLMGNGVWHFGETMCTLI 188
Db 78 MVIYILRYAKMKTATN---IYLNLAIADLMLSVFVLTSTLLRH-WPFGALLCRIV 133
QY 189 TAMDANSQFTSTYIITAMAIIDRYLATVHPISSTKFRKPSVATVYICLLMALSFSITPW 248
Db 134 LSVDAVMFTSYICLTIVLSVDRIYAVVHPKARYRRPTVAKVNVNLGVWLSLVILPIV 193
QY 249 LYARLIPEPGAVGCGIRLPNP-DTDLYWFTLYQFFLAFALPPVIVTAAYRILQRTSS 307
Db 194 VFSRTAANSDDGTVACNMLMPEPAQRMVGFVLYTFILMGFLLPVGAICLCYVLIIAKRMV 253
QY 308 VAPASQSRIRLRTKRVTRTAIAICLVFVCWAPRYVVLQTLQSLSRPTLTFFVLYNAAIS 367
Db 254 ALKAGWOQRKRSEKRTITLMVMVMVYFVICWMPFYVQLVNVFAEQDDATVSQ---SVI 310
QY 368 LGYANSCLNPFYIYVLCETFRK 389
Db 311 LGYANSCANPILYGLSLDNFKR 332
RESULT 13
SSR4_RAT
ID SSR4_RAT STANDARD; PRT; 384 AA.
AC P30937;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Somatostatin receptor type 4 (SS4R).
GN SSTR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93087484; PubMed=1360663;
RA Bruno J.F., Xu Y., Song J., Berelowitz M.;
RT "Molecular cloning and functional expression of a brain-specific
RT somatostatin receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 89:11151-11155(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Hippocampus;
RX MEDLINE=94230347; PubMed=8175684;
RA Bito H., Mori M., Sakanaka C., Takano T., Honda Z., Gotoh Y.,

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OM protein - protein search, using sw model

Run on: February 13, 2003, 14:00:22 ; Search time 14.1019 Seconds
(without alignments)
764.550 Million cell updates/sec

Title: US-09-885-478-2
Perfect score: 2212
Sequence: 1 MSVGAMKKGVGRAVGLGCGS.....LRAVSNAGTADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2212	100.0	422	10 US-09-885-478-2	Sequence 2, Appli
2	2206	99.7	422	10 US-09-885-478-26	Sequence 26, Appl
3	2200	99.5	422	10 US-09-885-478-27	Sequence 27, Appl
4	1824	82.5	353	10 US-09-925-776-2	Sequence 2, Appli
5	1824	82.5	353	10 US-09-885-478-28	Sequence 28, Appl
6	1808	81.7	353	10 US-09-895-686-2	Sequence 2, Appli
7	1763	79.7	353	10 US-09-885-478-4	Sequence 4, Appli
8	1696	76.7	402	9 US-09-990-940-19	Sequence 19, Appl
9	1224	55.3	239	10 US-09-864-761-38414	Sequence 38414, A
10	565.5	25.6	340	9 US-09-791-932-117	Sequence 117, App
11	565.5	25.6	340	9 US-09-990-940-2	Sequence 2, Appli
12	538	24.3	100	10 US-09-885-478-16	Sequence 16, Appl
13	538	24.3	100	10 US-09-885-478-17	Sequence 17, Appl
14	527	23.8	369	10 US-09-823-114-9	Sequence 9, Appli
15	514	23.2	391	9 US-09-990-940-20	Sequence 20, Appl
16	504.5	22.8	418	9 US-09-992-331-17	Sequence 17, Appl
17	498	22.5	91	10 US-09-864-761-38421	Sequence 38421, A
18	480.5	21.7	428	9 US-09-992-331-16	Sequence 16, Appl
19	472	21.3	428	9 US-09-992-331-15	Sequence 15, Appl

20	470.5	21.3	363	9 US-09-992-331-14	Sequence 14, Appl
21	458	20.7	405	10 US-09-966-871-84	Sequence 84, Appl
22	458	20.7	405	12 US-10-039-645-84	Sequence 84, Appl
23	456.5	20.6	370	10 US-09-823-114-21	Sequence 21, Appl
24	456	20.6	362	9 US-09-992-331-13	Sequence 13, Appl
25	455	20.6	382	10 US-09-993-844-4	Sequence 4, Appli
26	453.5	20.5	390	10 US-09-761-962-25	Sequence 25, Appl
27	453.5	20.5	391	10 US-09-761-962-26	Sequence 26, Appl
28	453.5	20.5	392	10 US-09-761-962-19	Sequence 19, Appl
29	453.5	20.5	398	10 US-09-761-962-29	Sequence 29, Appl
30	453.5	20.5	398	10 US-09-966-871-83	Sequence 83, Appl
31	453.5	20.5	398	12 US-10-039-645-83	Sequence 83, Appl
32	453.5	20.5	401	10 US-09-761-962-20	Sequence 20, Appl
33	453.5	20.5	409	10 US-09-761-962-27	Sequence 27, Appl
34	453.5	20.5	438	10 US-09-761-962-17	Sequence 17, Appl
35	453.5	20.5	444	10 US-09-761-962-28	Sequence 28, Appl
36	453	20.5	372	9 US-10-112-599A-4	Sequence 4, Appli
37	453	20.5	415	10 US-09-823-114-20	Sequence 20, Appl
38	452.5	20.5	398	10 US-09-823-114-16	Sequence 16, Appl
39	452.5	20.5	398	10 US-09-966-871-1	Sequence 1, Appli
40	452.5	20.5	398	12 US-10-039-645-1	Sequence 1, Appli
41	451.5	20.4	398	10 US-09-214-904-2	Sequence 2, Appli
42	451.5	20.4	398	10 US-09-966-871-79	Sequence 79, Appl
43	451.5	20.4	398	12 US-10-039-645-79	Sequence 79, Appl
44	449.5	20.3	372	10 US-09-966-871-80	Sequence 80, Appl
45	449.5	20.3	372	12 US-10-039-645-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-09-885-478-2
; Sequence 2, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-885-478-2

Query Match 100.0%; Score 2212; DB 10; Length 422;
Best Local Similarity 100.0%; Pred. No. 4.8e-182;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSVGAMKKGVGRAVGLGGSGQATEEDPLPDCGACAPGQGGRRRLPPAWEGSSARL	60
Db	1	MSVGAMKKGVGRAVGLGGSGQATEEDPLPDCGACAPGQGGRRRLPPAWEGSSARL	60
QY	61	WEQATGTGWMDEASLPTGPNASNTSDGPDNLTSGSPRTGSISYINIMPSVETIC	120
Db	61	WEQATGTGWMDEASLPTGPNASNTSDGPDNLTSGSPRTGSISYINIMPSVETIC	120
QY	121	LLGIGNSTVIFAVVKKSKLHCNNVPDIFILNLSYVDLLFLGLGPFMIHQLMGNVWHF	180
Db	121	LLGIGNSTVIFAVVKKSKLHCNNVPDIFILNLSYVDLLFLGLGPFMIHQLMGNVWHF	180
QY	181	GETMCTLITAMDANSQFTSTYILLTAMADRILATVHPISSTKFRKPSVATLVICLWALS	240

Db 181 GETMCTLITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLWALS 240
QY 241 FISTTPVWLARLIPFPGAVGCCIRLPNPDLDLYWFTLLYQFFLAFALPFVYITAAYVRI 300
Db 241 FISTTPVWLARLIPFPGAVGCCIRLPNPDLDLYWFTLLYQFFLAFALPFVYITAAYVRI 300
QY 301 LQRMSSVAPASQSRIRLTKRVRTTAIAICLVFVGCWAPYYVLQTLQLSISRPTLTFVY 360
Db 301 LQRMSSVAPASQSRIRLTKRVRTTAIAICLVFVGCWAPYYVLQTLQLSISRPTLTFVY 360
QY 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAQGLRAVSNAGTADERTESK 420
Db 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAQGLRAVSNAGTADERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 2
US-09-885-478-26
; Sequence 26, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:

; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH1
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26

; LENGTH: 422
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-26

Query Match 99.7%; Score 2206; DB 10; Length 422;
Best Local Similarity 99.8%; Pred. No. 1.6e-181;
Matches 421; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVGRAVGLGGSGQATEEDPLPDCGACAPGGGRRWRLPQPAWEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSGQATEEDPLPDCGACAPGGGRRWRLPQPAWEGSSARL 60
QY 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSA GSPRTGSISYINIIMPSVFGTIC 120
Db 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSA GSPRTGSISYINIIMPSVFGTIC 120
QY 121 LGGIIGNSTVIFA VVKKSKLHWCNNVPDIFIINLSVVDLFLLGMPFMIHQLMGNGVWHF 180
Db 121 LGGIIGNSTVIFA VVKKSKLHWCNNVPDIFIINLSVVDLFLLGMPFMIHQLMGNGVWHF 180
QY 181 GETMCTLITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLWALS 240
Db 181 GETMCTLITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLWALS 240
QY 241 FISTTPVWLARLIPFPGAVGCCIRLPNPDLDLYWFTLLYQFFLAFALPFVYITAAYVRI 300
Db 241 FISTTPVWLARLIPFPGAVGCCIRLPNPDLDLYWFTLLYQFFLAFALPFVYITAAYVRI 300
QY 301 LQRMSSVAPASQSRIRLTKRVRTTAIAICLVFVGCWAPYYVLQTLQLSISRPTLTFVY 360
Db 301 LQRMSSVAPASQSRIRLTKRVRTTAIAICLVFVGCWAPYYVLQTLQLSISRPTLTFVY 360

QY 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAQGLRAVSNAGTADERTESK 420
Db 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAQGLRAVSNAGTADERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 3
US-09-885-478-27
; Sequence 27, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:

; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27

; LENGTH: 422
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-27

Query Match 99.5%; Score 2200; DB 10; Length 422;
Best Local Similarity 99.5%; Pred. No. 5.1e-181;
Matches 420; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVGRAVGLGGSGQATEEDPLPDCGACAPGGGRRWRLPQPAWEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSGQATEEDPLPDCGACAPGGGRRWRLPQPAWEGSSARL 60
QY 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSA GSPRTGSISYINIIMPSVFGTIC 120
Db 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSA GSPRTGSISYINIIMPSVFGTIC 120
QY 121 LGGIIGNSTVIFA VVKKSKLHWCNNVPDIFIINLSVVDLFLLGMPFMIHQLMGNGVWHF 180
Db 121 LGGIIGNSTVIFA VVKKSKLHWCNNVPDIFIINLSVVDLFLLGMPFMIHQLMGNGVWHF 180
QY 181 GETMCTLITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLWALS 240
Db 181 GETMCTLITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLWALS 240
QY 241 FISTTPVWLARLIPFPGAVGCCIRLPNPDLDLYWFTLLYQFFLAFALPFVYITAAYVRI 300
Db 241 FISTTPVWLARLIPFPGAVGCCIRLPNPDLDLYWFTLLYQFFLAFALPFVYITAAYVRI 300
QY 301 LQRMSSVAPASQSRIRLTKRVRTTAIAICLVFVGCWAPYYVLQTLQLSISRPTLTFVY 360
Db 301 LQRMSSVAPASQSRIRLTKRVRTTAIAICLVFVGCWAPYYVLQTLQLSISRPTLTFVY 360
QY 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAQGLRAVSNAGTADERTESK 420
Db 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAQGLRAVSNAGTADERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 4


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US-09-925-776-2
; Sequence 2, Application US/09925776
; Patent No. US20020038007A1
; GENERAL INFORMATION:
; APPLICANT: AMES, ROBERT S. , JR.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: FOLEY, JAMES J.
; APPLICANT: BERGSM, DEBK J.
; APPLICANT: ELLIS, CATHERINE E.
; APPLICANT: CHAMBERS, JON K.
; TITLE OF INVENTION: A METHOD OF FINDING AGONIST AND
; TITLE OF INVENTION: ANTAGONIST TO HUMAN 11CB SPLICE VARIANT
; FILE REFERENCE: GP-50003-D2
; CURRENT APPLICATION NUMBER: US/09/925,776
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/032,763
; PRIOR FILING DATE: 1996-12-11
; PRIOR APPLICATION NUMBER: 08/984,288
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: 60/073,747
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 09/060,504
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-925-776-2

Query Match      82.5%; Score 1824; DB 10; Length 353;
Best Local Similarity 100.0%; Pred. No. 6.8e-149;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLLGIIGNST 129
Db 1 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLLGIIGNST 60

QY 130 VIFAVVKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 189
Db 61 VIFAVVKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120

QY 190 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFSITPVL 249
Db 121 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFSITPVL 180

QY 250 YARLIPFPGGAVGCGIRLPNDTDLWFTLYQFFLAFLALPFVVTAAVVRILQRTSSVA 309
Db 181 YARLIPFPGGAVGCGIRLPNDTDLWFTLYQFFLAFLALPFVVTAAVVRILQRTSSVA 240

QY 310 PASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNAAISLG 369
Db 241 PASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNAAISLG 300

QY 370 YANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 422
Db 301 YANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 353

RESULT 5
US-09-885-478-28
; Sequence 28, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: MAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH1
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
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; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 353
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-28

Query Match      82.5%; Score 1824; DB 10; Length 353;
Best Local Similarity 100.0%; Pred. No. 6.8e-149;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLLGIIGNST 129
Db 1 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLLGIIGNST 60

QY 130 VIFAVVKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 189
Db 61 VIFAVVKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120

QY 190 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFSITPVL 249
Db 121 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFSITPVL 180

QY 250 YARLIPFPGGAVGCGIRLPNDTDLWFTLYQFFLAFLALPFVVTAAVVRILQRTSSVA 309
Db 181 YARLIPFPGGAVGCGIRLPNDTDLWFTLYQFFLAFLALPFVVTAAVVRILQRTSSVA 240

QY 310 PASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNAAISLG 369
Db 241 PASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNAAISLG 300

QY 370 YANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 422
Db 301 YANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 353

RESULT 6
US-09-895-686-2
; Sequence 2, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020106655A1 1459432CD1
US-09-895-686-2

Query Match      81.7%; Score 1808; DB 10; Length 353;
Best Local Similarity 99.2%; Pred. No. 1.6e-147;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 70 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLLGIIGNST 129
Db 1 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLLGIIGNST 60
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RESULT 9
US-09-864-761-38414
: Sequence 38414, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: FILE REFERENCE: Aecomica-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 38414
: LENGTH: 239
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO Z86090.10
: OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.67
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.74
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
: OTHER INFORMATION: EST_HUMAN HIT: BE701073.1, EVALUE 6.00e-44
: OTHER INFORMATION: SWISSPROT HIT: Q99705, EVALUE 0.00e+00
US-09-864-761-38414
Query Match 55.3%; Score 1224; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.1e-97;
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Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 184 MCTLTITAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFS 243
Db 1 MCTLTITAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFS 60
QY 244 ITPVWLVARLIPFGGAVGCGIRLPNPDITLWFTLYQFFLAFLDPVVITAAVRIQR 303
Db 61 ITPVWLVARLIPFGGAVGCGIRLPNPDITLWFTLYQFFLAFLDPVVITAAVRIQR 120
QY 304 MTSSVAPASQSRIRLRTKVRTAIAICLVFVCWAPYVYLQTLQISRPRTLTFVLYLN 363
Db 121 MTSSVAPASQSRIRLRTKVRTAIAICLVFVCWAPYVYLQTLQISRPRTLTFVLYLN 180
QY 364 AAISLGYANSCLPFVYIVLCETFRKRLVSVKPAAGQLRAVSNQTADEERTESKGT 422
Db 181 AAISLGYANSCLPFVYIVLCETFRKRLVSVKPAAGQLRAVSNQTADEERTESKGT 239
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RESULT 10
US-09-791-932-117
: Sequence 117, Application US/09791932
: Publication No. US20030003451A1
: GENERAL INFORMATION:
: APPLICANT: Vogel, Gabriel
: APPLICANT: Parodi, Luis A.
: APPLICANT: Hiebsch, Ronald R.
: APPLICANT: Lind, Peter
: APPLICANT: Kayes, Paul S.
: APPLICANT: Huff, Valerie
: APPLICANT: Wood, Linda S.
: TITLE OF INVENTION: No. US20030003451A1e1 G Protein-Coupled Receptors Cross-Refe
: FILE REFERENCE: 00325.US1
: CURRENT APPLICATION NUMBER: US/09/791,932
: PRIOR APPLICATION NUMBER: 2001-02-23
: PRIOR FILING DATE: 2000-02-23
: PRIOR APPLICATION NUMBER: 60/184,305
: PRIOR FILING DATE: 2000-02-23
: PRIOR APPLICATION NUMBER: 60/184,304
: PRIOR FILING DATE: 2000-02-23
: PRIOR APPLICATION NUMBER: 60/184,303
: PRIOR FILING DATE: 2000-02-23
: PRIOR APPLICATION NUMBER: 60/184,397
: PRIOR FILING DATE: 2000-02-23
: PRIOR APPLICATION NUMBER: 60/184,247
: PRIOR FILING DATE: 2000-02-23
: PRIOR APPLICATION NUMBER: 60/188,880
: PRIOR FILING DATE: 2000-03-13
: PRIOR APPLICATION NUMBER: 60/217,369
: PRIOR FILING DATE: 2000-07-11
: PRIOR APPLICATION NUMBER: 60/217,370
: PRIOR FILING DATE: 2000-07-11
: PRIOR APPLICATION NUMBER: 60/218,492
: PRIOR FILING DATE: 2000-07-20
: PRIOR APPLICATION NUMBER: 60/186,810
: PRIOR FILING DATE: 2000-03-03
: PRIOR APPLICATION NUMBER: 60/188,064
: PRIOR FILING DATE: 2000-03-09
: PRIOR APPLICATION NUMBER: 60/186,457
: PRIOR FILING DATE: 2000-03-02
: PRIOR APPLICATION NUMBER: 60/213,861
: PRIOR FILING DATE: 2000-06-23
: PRIOR APPLICATION NUMBER: 60/194,344
: PRIOR FILING DATE: 2000-04-03
: PRIOR APPLICATION NUMBER: 60/218,337
: PRIOR FILING DATE: 2000-07-14
: NUMBER OF SEQ ID NOS: 184
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 117
: LENGTH: 340
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-791-932-117
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	Query Match	25.6%;	Score 565.5;	DB 9;	Length 340;
	Best Local Similarity	37.0%;	Pred. No. 4.6e-41;		
	Matches 113;	Conservative	62;	Mismatches 119;	Indels 11; Gaps
QY	110 IMPSPVEGTICLLGIIGNSTVFIFAVVKKSKLHMCNMPDIFIINLSVDLLFLGCMPEMT	169			
Dd	35 VILPSMIGIICSTGLGVGNILIVFTIIRSRK---KTVPDIIYNLAADVADLVHIAGMPFLL	90			
QY	170 HQLMGNGVWHGEETMCTLTITAMDAANSQFTSTYYILTAMAIDRYLATVHPISSTKERESVA	229			
Dd	91 HQWARGENWEFGPLCTIITSLEPTCQNCFACSAIMTWSVDRFYALVQPFRLTRWRTRYKT	1500			
QY	230 TLVTCLLMALSFSISTPWWLYARLIPEPGAVGGIRLPNDPTDLWTFLYQFFLAFALP	289			
Dd	151 IRINGLMAASFILLAPVVWYSKYIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTEFEFP	209			
QY	290 FVVITAAYRIL-----QRMTSSVAPASQRSI-RLRTKRVPRTAIAICLFVFCWAPYY	343			
Dd	210 LPLILVCYLILLCYTWMYQQNKDKARCNCNPSPVKQRMVKLKTKMYLVLVVVEFILSAAAPHV	269			
QY	344 LQTLQLSIKRFTLTFVYLYNAAISLGYSANCLNPFVYIVLCETFERKRLVSVKPPAAGOL	403			
Dd	270 IQLVNLQMEDPTLAFYVGYYSLICSITYASSSINPFYIILLSGNFQKRLLPQIQRRATEKET	329			
QY	404 RAVSN 408				
Dd	330 NMMGN 334				

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RESULT 11
US-09-990-940-2
; Sequence 2, Application US/09990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiayang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupta, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030027252A1el Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR342,
; melanin-concentrating hormone receptor 2 (MCHR2)
US-09-990-940-2

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Query Match	25.6%;	Score 565.5;	DB 9;	Length 340;
Best Local Similarity	37.0%;	Pred. No. 4.6e-41;		
Matches 113; Conservative	62;	Mismatches 119;	Indels 11;	Gaps 4;
QY 110	TTPSVFETICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFITNLSVDLFLLLGPPFMI 169			

Db	35	VILPSMIGLICSTGLVGNILIVFTIIRSRK----	KTVPDIVICNLAVADLVHIYGMPELI	90
QY	170	HQLMNGVWHHEGTMCTLITAMDANSQFTSTYIL	TAMADRYLATVHPISSTKFRKPSVA	229
Db	91	HQWARGGEWEGGPLCTIITSLDTCNOFACSAIM	TMSVDRIYFALVQPFRLTRWRIRYKT	150
QY	230	TLVICLLWALSFISTIPVWLARLIPPEGAVGCG	IRLPNPDIDLWFTLYQFFLAFLP	289
Db	151	IRINGLMAASFILALPVMVYSKVIKFDGVE	SCAFDLTSPD-DVLWYLYLTITTFEFP	209
QY	290	FVVITAAYVRIL-----QRM	TSSVAPASORSI-RLRTRKVRTRTAIAICLVEFVCMAPYYV	343
Db	210	LPILIVCYILICITYWEMYQONKDARCNCPSV	PQORVMKLTIKMYLVLVVEFILSAAPHYH	269
QY	344	LQLTQLSISRPTLFVLYLYNNAISLGYANSCIN	PFVYIVLCETFERKRLVSVKPAAGQL	403
Db	270	IQLVNLQMEQPTLAFYVGYLLSICLSYASSIN	PFLYILLSGNFQKRLPQIQRRATEKEI	329
QY	404	RAVSN	408	
Db	330	NNMGN	334	

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RESULT 12
; US-09-885-478-16
; Sequence 16, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 100
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATION CLONE
US-09-885-478-16

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Query Match	24.3%;	Score 538;	DB 10;	Length 100;
Best Local Similarity	98.0%;	Pred. No. 2.3e-39;		
Matches 98;	Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;
QY 1	MSVGA	KKKG	VGRA	VGIGGSGCQATEEDPLPDCGACAPGQGGRRWRLLQPAWVEGSSARL 60
Db 1	MSVGA	KKKG	VGTA	VGIGGSGCQATEEDPLPDCGACAPGQGGRRWRLLQPAWVEGSSARL 60
QY 61	WEQATG	TGWM	DLLE	ASLLPTGPNASNTSDGPDNLTSAGSP 100
Db 61	WEQATG	TGWM	DLLE	ASLLPTGPNASNTSDGPDNLTSAGSP 100

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RESULT 13
US-09-885-478-17
; Sequence 17, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M

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		Matches	111;	Conservative	70;	Mismatches	137;	Indels	44;	Gaps	7;
QY	29	PLPDCGACAPGQGGRWRLPQPAWVEGSSARLWEQATGTGMMDLEASLPTGPNASNTSD	88								
Db	14	PSPSPGSCGEGGSR-----GPGAGAAD--GMEEPGRNASONGT	50								
QY	89	GPDNLTSAGSPPRGTSISYINIMPSVEGTICLLIGNSTVIFAAYVKSKLHWCNVDP	148								
Db	51	LSEGQSA-----ILSFIYSVCLVGLCGNSMVIYVILRYAKMKTATN---	94								
QY	149	IFTINLSVVDLLFLGMPEMIHQLMNGVWHFGETMCTLLITAMDANSQFTSTYILTAMAI	208								
Db	95	IYILNLAIADLMLSVPELVSTLLRH-WPEGALLCRLVLSVDVNMFTSIYCLTVLSV	153								
QY	209	DRYLATVHPISSTKFRKPSVATLVICLLWALSFTSTPWLVARLIPFGAGVCGIRLP	268								
Db	154	DRYVAVVHPKARYRRPTVAKVNLGVWLSLVILPIVVESRTAANSDDGTVACNMLMP	213								
QY	269	NP-DTDLYWFTLYQFLAEALPFVVITAAYVRILQKMTSSVAPASQSRRLRTKRVTRTA	327								
Db	214	EPAQRWLVGFLVFTFLMGFLLPVGAICLCYVLLIAKMRVALKAGWQQRKRSEKRTIMV	273								
QY	328	IAICLVEFVCWAPYYVLQTLQLSISRPTLTFVYLYNAAISLGYANSCLNPFYIIVLCETF	387								
Db	274	MMVVMVEVICMPEYVQLVNVFAEQDDATVSQL---SVILGYANSCANPILYGFLSDNF	330								
QY	388	RK 389									
Db	331	KR 332									

Search completed: February 13, 2003, 14:10:31
Job time : 15.1019 secs

Db 181 TGGAGCAGGCGGACCGGCACCTGGCTGGATGGACCTGGAACCTCGCTGCTGCCACTGGT 240

QY 241 CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTCAAGAGATCACCTCCT 300

Db 241 CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTCAAGAGATCACCTCCT 300

QY 301 CGCAGCGGAGCATCTCTTACATCAACATCATCATGCTTCGGTGTTCGGACCACTCTGC 360

Db 301 CGCAGCGGAGCATCTCTTACATCAACATCATCATGCTTCGGTGTTCGGACCACTCTGC 360

QY 361 CTCTGGGCATCATCGGAACATCCACGGTTCATCTTCGGGTCGTGAAGAGTCCACGCTG 420

Db 361 CTCTGGGCATCATCGGAACATCCACGGTTCATCTTCGGGTCGTGAAGAGTCCACGCTG 420

QY 421 CACTGTGCAACAACAGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTC 480

Db 421 CACTGTGCAACAACAGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTC 480

QY 481 TTTCTCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGTCGTGCACTTT 540

Db 481 TTTCTCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGTCGTGCACTTT 540

QY 541 GGGAGACCATGTGCACCCCTCATCAAGGCGCATGATGCAATAGTCAGTTCAACGACACC 600

Db 541 GGGAGACCATGTGCACCCCTCATCAAGGCGCATGATGCAATAGTCAGTTCAACGACACC 600

QY 601 TACATCTGACCGGCATGGCCATGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCC 660

Db 601 TACATCTGACCGGCATGGCCATGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCC 660

QY 661 ACGAAGTTCGGAGACCTCTGTGGCCACCCCTGTGATCTGCTCTGCTGGGCCCTCTCC 720

Db 661 ACGAAGTTCGGAGACCCCTGTGTGGCCACCCCTGTGATCTGCTCTGCTGGGCCCTCTCC 720

QY 721 TTCAATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTTGCA 780

Db 721 TTCAATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTTGCA 780

QY 781 GTGGCTGGCGCATACGCTGCCCCCAACCCAGACACTGACCTCTACTGTTACCCCTGTAC 840

Db 781 GTGGCTGGCGCATACGCTGCCCCCAACCCAGACACTGACCTCTACTGTTACCCCTGTAC 840

QY 841 CAGTTTTTCTGGCCTTTGCCCTGCTTTTGTGTCATCAAGCCGATACGTGAGGATC 900

Db 841 CAGTTTTTCTGGCCTTTGCCCTGCTTTTGTGTCATCAAGCCGATACGTGAGGATC 900

QY 901 CTGCAGCGCATGACGTCTCAGTGGCCCCCGCTGCCAGCGACATCCGGCTGCGGACA 960

Db 901 CTGCAGCGCATGACGTCTCAGTGGCCCCCGCTGCCAGCGACATCCGGCTGCGGACA 960

QY 961 AAGAGGTTGACCCGACAGCCATCGCCATCTGTGGTCTTCTTGTGTGCTGGCCACCC 1020

Db 961 AAGAGGTTGACCCGACAGCCATCGCCATCTGTGGTCTTCTTGTGTGCTGGCCACCC 1020

QY 1021 TACTATGTGTACAGCTGACCCAGTGTCCATCAGCCGCCGACCCCTACCTTTGTCTAC 1080

Db 1021 TACTATGTGTACAGCTGACCCAGTGTCCATCAGCCGCCGACCCCTACCTTTGTCTAC 1080

QY 1081 TTATACAATGGCGGCATGAGCTTGGGCTATGCCAAGCTGCTCAACCCCTTTGTGTAC 1140

Db 1081 TTATACAATGGCGGCATGAGCTTGGGCTATGCCAAGCTGCTCAACCCCTTTGTGTAC 1140

QY 1141 ATGCTGCTGTGAGAGCTTCGCAAAAGCTGTGCTCTGTGCTGAAGCCTGACGCCAG 1200

Db 1141 ATGCTGCTGTGAGAGCTTCGCAAAAGCTGTGCTCTGTGCTGAAGCCTGACGCCAG 1200

QY 1201 GGGCAGCTTCGCGTGTCAAGAGCTCAGAGCGCTGACGAGAGAGAGACAGAAAGCAA 1260

Db 1201 GGGCAGCTTCGCGTGTCAAGAGCTCAGAGCGCTGACGAGAGAGAGACAGAAAGCAA 1260

QY 1261 GGCACCTGA 1269

Db 1261 GGCACCTGA 1269

RESULT 2

US-09-925-776-1

; Sequence 1, Application US/09925776

; Patent No. US20020038007A1

; GENERAL INFORMATION:

; APPLICANT: AMES, ROBERT S., JR.

; APPLICANT: SARAU, HENRY M.

; APPLICANT: FOLEY, JAMES J.

; APPLICANT: BERGSMAN, DEBK J.

; APPLICANT: ELLIS, CATHERINE E.

; APPLICANT: CHAMBERS, JON K.

; TITLE OF INVENTION: A METHOD OF FINDING AGONIST AND

; TITLE OF INVENTION: ANTAGONIST TO HUMAN 11CB SPLICE VARIANT

; FILE REFERENCE: GP-50003-D2

; CURRENT APPLICATION NUMBER: US/09/925,776

; CURRENT FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: 60/032,763

; PRIOR FILING DATE: 1996-12-11

; PRIOR APPLICATION NUMBER: 08/984,288

; PRIOR FILING DATE: 1997-12-03

; PRIOR APPLICATION NUMBER: 60/073,747

; PRIOR FILING DATE: 1998-02-05

; PRIOR APPLICATION NUMBER: 09/060,504

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1385

; TYPE: DNA

; ORGANISM: HOMO SAPIENS

US-09-925-776-1

Query Match 97.5%; Score 1237.4; DB 10; Length 1385;

Best Local Similarity 99.9%; Pred. No. 7.3e-285;

Matches 1238; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 31 GGGAGGCGAGTTGGGCTTGGAGGCGGACAGCGGCTGCCAGGCTACGAGGAAGACCCCTT 90

Db 66 GGGAGGCGAGTTGGGCTTGGAGGCGGACAGCGGCTGCCAGGCTACGAGGAAGACCCCTT 125

QY 91 CCCGACTGCGGGGCTTGCGCTCCGGGACAAGGTGGCAGGCGCTGGAGGCTGCCGAGCCT 150

Db 126 CCCGACTGCGGGGCTTGCGCTCCGGGACAAGGTGGCAGGCGCTGGAGGCTGCCGAGCCT 185

QY 151 GCGTGGTGGAGGGGAGCTCAGCTCGGTTGTGGGAGCAGGCGGACCGGACTGGCTGATG 210

Db 186 GCGTGGTGGAGGGGAGCTCAGCTCGGTTGTGGGAGCAGGCGGACCGGACTGGCTGATG 245

QY 211 GACCTGGAAGCCTCGCTGCTGCCCACTGTGCCAATGCGCAACACCTCTGATGGCCCC 270

Db 246 GACCTGGAAGCCTCGCTGCTGCCCACTGTGCCAATGCGCAACACCTCTGATGGCCCC 305

QY 271 GATAAAGCTTCACTTCAAGAGATCACTCTGCGACGCGGAGCATCTCTTACATCAACATC 330

Db 306 GATAAAGCTTCACTTCAAGAGATCACTCTGCGACGCGGAGCATCTCTTACATCAACATC 365

QY 331 ATCATGCTTGGGTGTGCGGACCATCTGCTCTGCGGATCATCGGAATCCACGGTTC 390

Db 366 ATCATGCTTGGGTGTGCGGACCATCTGCTCTGCGGATCATCGGAATCCACGGTTC 425

QY 391 ATCTTGGCGGTGCTGAAGAGTCCAAAGCTGCACCTGTGTCCAACAAGTCCCGACATCTT 450

Db 426 ATCTTGGCGGTGCTGAAGAGTCCAAAGCTGCACCTGTGTCCAACAAGTCCCGACATCTT 485

QY 451 ATCATCAACCTCTGCTGATGATCTCTCTTTCTTCTGCGGATGCGGCTTCTGATCCAC 510

Db 486 ATCATCAACCTCTGCTGATGATCTCTCTTTCTTCTGCGGATGCGGCTTCTGATCCAC 545

QY 511 CAGCTCATGGGCAATGGGCTGTGGCACTTTGGGAGAGCCATGTGCACCCCTCATCAGGCC 570

Db 546 CAGCTCATGGGCAATGGGCTGTGGCACTTTGGGAGAGCCATGTGCACCCCTCATCAGGCC 605

QY 571 ATGATGCCAATAGTCAGTTCCACGACACCTACATCCGTGACGCCCATGGCCATTGACCGC 630
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Db 606 ATGATGCCAATAGTCAGTTCCACGACACCTACATCCGTGACGCCCATGGCCATTGACCGC 665
QY 631 TAACCTGGCCACTGTCCACCCCATCTCTCCACGAAGTCCGGAAAGCCCTCTGTGGCCACC 690
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Db 666 TAACCTGGCCACTGTCCACCCCATCTCTCCACGAAGTCCGGAAAGCCCTCTGTGGCCACC 725
QY 691 CTGGTGAATCTGCCCTCTGTGGGCCCCCTCTCTCATCAGCATCACCCCTGTGTGGCTGTAT 750
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Db 726 CTGGTGAATCTGCCCTCTGTGGGCCCCCTCTCTCATCAGCATCACCCCTGTGTGGCTGTAT 785
QY 751 GCCAGACTCATCCCCCTCCAGAGGTGCAGTGGGCTGGCGATACGCCCTGCCCAACCCA 810
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Db 786 GCCAGACTCATCCCCCTCCAGAGGTGCAGTGGGCTGGCGATACGCCCTGCCCAACCCA 845
QY 811 GACACTGACCTCTACTGGTTCAACCCCTGTACAGTTTTCCCTGGCCCTTGGCCCTGCTTTT 870
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Db 846 GACACTGACCTCTACTGGTTCAACCCCTGTACAGTTTTCCCTGGCCCTTGGCCCTGCTTTT 905
QY 871 GGTGTATCATCAGACCCGATAGCTGAGGATCCTGCAGCGCATGACGTCTCAGTGGCCCC 930
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Db 906 GGTGTATCATCAGACCCGATAGCTGAGGATCCTGCAGCGCATGACGTCTCAGTGGCCCC 965
QY 931 GCCTCCCAAGCGAGCATCCGGCTGGGACAAAGAGGTGACCCGACACAGCCATCGCCATC 990
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Db 966 GCCTCCCAAGCGAGCATCCGGCTGGGACAAAGAGGTGACCCGACACAGCCATCGCCATC 1025
QY 991 TGTCTGTCTTCTTGTGTGTGGTGGGACACCCTACTATGTGTACAGCTGACCCAGTTGTCC 1050
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Db 1026 TGTCTGTCTTCTTGTGTGTGGTGGGACACCCTACTATGTGTACAGCTGACCCAGTTGTCC 1085
QY 1051 ATCAGCCGCCCGACCCCTCACCTTTGTCTACTTATACAAATGGGCCATCAGCTTGGGCTAT 1110
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Db 1086 ATCAGCCGCCCGACCCCTCACCTTTGTCTACTTATACAAATGGGCCATCAGCTTGGGCTAT 1145
QY 1111 GCCAACAGCTGCCTCAACCCCTTGTGTACATCGTGTGTGAGACGTTCGCAAAAGCG 1170
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Db 1146 GCCAACAGCTGCCTCAACCCCTTGTGTACATCGTGTGTGAGACGTTCGCAAAAGCG 1205
QY 1171 TTGCTCCTGTGCGTGAAGCCTGACGCCAGGGGAGCTTCGGCTGTACGAACGCTCAG 1230
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Db 1206 TTGCTCCTGTGCGTGAAGCCTGACGCCAGGGGAGCTTCGGCTGTACGAACGCTCAG 1265
QY 1231 ACGGCTGACGAGGAGAGGACAGAAAGCAAGGACCTGA 1269
|||||
Db 1266 ACGGCTGACGAGGAGAGGACAGAAAGCAAGGACCTGA 1304

RESULT 3
US-09-895-686-8
; Sequence 8, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895, 686
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 8
; LENGTH: 2138
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020106655A1 1459432CB1
US-09-895-686-8

Query Match 94.8%; Score 1203; DB 10; Length 2138;
Best Local Similarity 99.18; Pred. No. 1.2e-276;
Matches 1220; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
QY 39 AGTTGGGCTTGGAGGGCGGACGGGCTGCCAGGCTACGGAGGAAGACCCCTTCCGCACTG 98
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Db 20 AATTGGGCTTGGAGGGCGGCA-CGGCTGCCAGGCTACGGAGGTAGACCCCTTCCCAACTG 78
QY 99 CGGGGCTTGGGCTCCGGGACAAAGTGGCAGGGCGCTGAGAGGCTGCCGACGCTGGGGT 158
|||||
Db 79 CGGGGCTTGGGCTCCGGGACAAAGTGGCAGGGCGCTGAGAGGCTGCCGACGCTGGGGT 138
QY 159 GGAGGGAGCTCAGCTCGTTGTGGGAGCAGCGACCGGACACTGGCTGGATGACCTGA 218
|||||
Db 139 GGAGGGAGCTCAGCTCGTTGTGGCAGCATGCGACCGGACACTGGCTGGATGACCTGA 198
QY 219 AGCCTCGCTGCTGCCCACTGTGCCAATGCCAGCAACACCTCTGATGGCCCCGATACT 278
|||||
Db 199 AGCCTCGCTGCTGCCCACTGTGCCAATGCCAGCAACACCTCTGATGGCCCCGATACT 258
QY 279 CACTTCCAGAGGATCACCTCCTCGCAGCGGGAGCATCTCCTACATCAACATCATGCC 338
|||||
Db 259 CACTTCCAGAGGATCACCTCCTCGCAGCGGGAGCATCTCCTACATCAACATCATGCC 318
QY 339 TTGCGTGTGGGCAACCATCTGCTCTGGGATCATCGGGAATCCACGGTCACTTCCG 398
|||||
Db 319 TTGCGTGTGGGCAACCATCTGCTCTGGGATCATCGGGAATCCACGGTCACTTCCG 378
QY 399 GGTGGAAGAAAGTCCAAAGCTGACGTGTGCAACAAAGTCCCGACATCTTCATCATCAA 458
|||||
Db 379 GGTGGAAGAAAGTCCAAAGCTGACGTGTGCAACAAAGTCCCGACATCTTCATCATCAA 438
QY 459 CCTCTCGTAGTAGATCTCCTCTTCTCTGGGATGCCCTTCAATGATCCACAGCTCAT 518
|||||
Db 439 CCTCTCGTAGTAGATCTCCTCTTCTCTGGGATGCCCTTCAATGATCCACAGCTCAT 498
QY 519 GGGCAATGGGGTGTGGCACTTTGGGAGAACATGTGCACCCCTCAACAGGCCATGATGC 578
|||||
Db 499 GGGCAATGGGGTGTGGCACTTTGGGAGAACATGTGCACCCCTCAACAGGCCATGATGC 558
QY 579 CAATAGTCAGTTCACACAGCACCTACATCCTGACCGGCATGGCCATTTGACCGCTACCTGCC 638
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Db 559 CAATAGTCAGTTCACACAGCACCTACATCCTGACCGGCATGGCCATTTGACCGCTACCTGCC 618
QY 639 CACTGTCCACCCCATCTCTTCCACGAAGTCCGGAAGCCCTCTGTGGCCACCCCTGTGAT 698
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Db 619 CACTGTCCACCCCATCTCTTCCACGAAGTCCGGAAGCCCTCTGTGGCCACCCCTGTGAT 678
QY 699 CTGCTCCTGTGGGCCCTCTCTTCATCAGCATCACCCCTGTGTGCTGTATGCCAGACT 758
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Db 679 CTGCTCCTGTGGGCCCTCTCTTCATCAGCATCACCCCTGTGTGCTGTATGCCAGACT 738
QY 759 CATCCCTTCCAGGAGGTGACGTGGGCTGCGGCATACGCTGCCCAACCCAGACACTGA 818
|||||
Db 739 CATCCCTTCCAGGAGGTGACGTGGGCTGCGGCATACGCTGCCCAACCCAGACACTGA 798
QY 819 CCTCTACTGTTACCCCTGTACCACTTTTCTCTGGCCTTGGCCCTTTTGTGTGAT 878
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Db 799 CCTCTACTGTTACCCCTGTACCACTTTTCTCTGGCCTTGGCCCTTTTGTGTGAT 858
QY 879 CACAGCCGATACGTGAGGATCCTGACAGCGCATGACGTCTCAGTGGCCCCCGCTCCCA 938
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Db 859 CACAGCCGATACGTGAGGATCCTGACAGCGCATGACGTCTCAGTGGCCCCCGCTCCCA 918
QY 939 GCGCAGCATCCGGCTGCGGACAAAGAGGTGACCCGACACAGCCATCTGTCTGCT 998
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Db 919 GCGCAGCATCCGGCTGCGGACAAAGAGGTGACCCGACACAGCCATCTGTCTGCT 978
QY 999 CTTCCTTGTGTGCTGGGCAACCCCTACTATGTGCTACAGCTGACCCAGTGTTCATCAGCCG 1058
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Db 979 CTTCCTTGTGTGCTGGGCAACCCCTACTATGTGCTACAGCTGACCCAGTGTTCATCAGCCG 1038

[illegible]

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RESULT 4
US-09-864-761-9721
; Sequence 9721, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

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: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Annomax Sequence Listing Engine vers. 1.1.1
: SEQ ID NO 9721
: LENGTH: 1478
: TYPE: DNA
: ORGANISM: Homo sapiens

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; FEATURE:
; OTHER INFORMATION: MAP TO Z86090.10
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3
US-09-864-761-9721

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Query Match	77.68;	Score 984.4;	DB 10;	Length 1478;
Best Local Similarity	99.48;	Pred. No. 9.1e-225;		
Matches 988; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

QY	276	CCTCAGCTTCAGCAGGATCACCCTCCTCGCACGGGGAGCATCTCCTACATCAACATCATCAT	335
Db	406	CCTTCTGTCCCCAGGATCACCCTCCTCGCACGGGGAGCATCTCCTACATCAACATCATCAT	465
QY	336	GCCTTCGGGTGTTGCGGCACCATCTGCCTCCTGCGGCATCATCGGGAACCTCCACGGTCACTT	395
Db	466	GCCTTCGGGTGTTGCGGCACCATCTGCCTCCTGCGGCATCATCGGGAACCTCCACGGTCACTT	525
QY	396	CGCGGTGCTGAAGAAGTCCCAAGCTGCACGTGTCACAACAGCTCCCGACATCTTCATCAT	455
Db	526	CGCGGTGCTGAAGAAGTCCCAAGCTGCACGTGTCACAACAGCTCCCGACATCTTCATCAT	585
QY	456	CAACCTCTCGGTAGTAGATCTCCTTCTCCTGCGCATGCCCTTCATGATCAACAGCT	515
Db	586	CAACCTCTCGGTAGTAGATCTCCTTCTCCTGCGCATGCCCTTCATGATCAACAGCT	645
QY	516	CATGGGCAATGGGGTGTGGCACTTTGGGGAGACCATGTGCACCCTCATCACGGCCATGGA	575
Db	646	CATGGGCAATGGGGTGTGGCACTTTGGGGAGACCATGTGCACCCTCATCACGGCCATGGA	705
QY	576	TGCCAATAGTCAGTTCAACCCAGCACACCTACATCCTGACCGCCATGGCCATTGACCGCTACCT	635
Db	706	TGCCAATAGTCAGTTCAACCCAGCACACCTACATCCTGACCGCCATGGCCATTGACCGCTACCT	765
QY	636	GGCCACTGTGCCACCCCATCTCTTCCACGAAGTTCGGGAAGCCCTCTGTGGCCACCCCTGGT	695
Db	766	GGCCACTGTGCCACCCCATCTCTTCCACGAAGTTCGGGAAGCCCTCTGTGGCCACCCCTGGT	825
QY	696	GATCTGCCCTCCTGTGGGCCCTCTCCTTCATCAGCATCAACCCCTGTGTGGCTGTATGCCAG	755
Db	826	GATCTGCCCTCCTGTGGGCCCTCTCCTTCATCAGCATCAACCCCTGTGTGGCTGTATGCCAG	885
QY	756	ACTCATCCCTTCCACGAGGTGCAGTGGGCTGCGGCATACGCGCTGCCCCAACCCAGACAC	815
Db	886	ACTCATCCCTTCCACGAGGTGCAGTGGGCTGCGGCATACGCGCTGCCCCAACCCAGACAC	945
QY	816	TGACCTCTACTGTTCAACCTGTACCAAGTTTTCTCCTGCGCTTTGCCCTTGTGTGGT	875
Db	946	TGACCTCTACTGTTCAACCTGTACCAAGTTTTCTCCTGCGCTTTGCCCTTGTGTGGT	1005
QY	876	CATCACAGCCGCATACGTGAGGATCCTGCAAGCCGATGACGTCTCAGTGGCCCCCGCCTC	935
Db	1006	CATCACAGCCGCATACGTGAGGATCCTGCAAGCCGATGACGTCTCAGTGGCCCCCGCCTC	1065
QY	936	CCAGCGCAGCATCCGGCTGCGGACAAAGAGGGGTGACCCGACAGCCATCGCCATCTGTCT	995
Db	1066	CCAGCGCAGCATCCGGCTGCGGACAAAGAGGGGTGACCCGACAGCCATCGCCATCTGTCT	1125
QY	996	GGTCTTCTTTGTGTGCTGGGACACCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAG	1055
Db	1126	GGTCTTCTTTGTGTGCTGGGACACCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAG	1185
QY	1056	CCGCCCCAGCCCTCACCTTTGTCTACTTATACAATGCGGCCATCAGCTTGGGCTATGCCAA	1115
Db	1186	CCGCCCCAGCCCTCACCTTTGTCTACTTATACAATGCGGCCATCAGCTTGGGCTATGCCAA	1245
QY	1116	CAGCTGCCTCAACCCCTTGTGTGATCATGCTGCTCTGTGAGACGTTCCGCAACGCTTGGT	1175

Accession	Sequence	Position
Db	1246 CAGCTGCCTCAACCCCTTTGTGTATCATCGTGCCTGTGAGACGTTCCGCATAACGCTTGGT	1305
QY	1176 CCTGTCGTTGAAGCCTGCAGCCCAAGGGGCAGCTTCGCCCTGTCAAGCAACGCTCAGACGGC	1235
Db	1306 CCTGTCGGTGAAGCCCTGCAGCCCAAGGGGCAGCTTCGCCCTGTCAAGCAACGCTCAGACGGC	1365
QY	1236 TGACGAGGAGAGGACAGAAAGCAAAAGGCACCTGA	1269
Db	1366 TGACGAGGAGAGGACAGAAAGCAAAAGGCACCTGA	1399

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RESULT 5
US-09-885-478-3
; Sequence 3, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: MAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH1)
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: RATTUS NORVEGICUS
US-09-885-478-3

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Query Match	71.9%;	Score 912.8;	DB 10;	Length 1214;
Best Local Similarity	90.1%;	Pred. No. 8.7e-208;		
Matches 977; Conservative	0;	Mismatches 107;	Indels 0;	Gaps 0;

QY	186	GCAGGCGCAGCCGGCACTGGCGTGTGATGGACCTGGAAGCCCTCGCTGTCGCCCACTGCTGCCAA	245
'			
Db	1	GCAGGCGCACTGCACC GGCTGCATGGATCTGCAAAACTCGTTGCTGTCCACTGGCCCCAA	60
QY	246	TGCCAGCAACAACCTCTGATGGCCCCGATAACCTCACATTACAGCAGGATCAACCTCCTGCAC	305
Db	61	TGCCAGCAACATCTCCGATGGCCAGGATAATCTCACATTGCCGGGGTCACTCCTCGCAC	120
QY	306	GGGAGCATCTCCTACATCAACATCATATGCCCTCGGTGTTGGGCACCACTCTGCCCTCT	365
Db	121	AGGAGTGTCCTCTACATCAACATCATTAATGCCCTTCGGTGTGTTGATCCACTCTGTCTCT	180
QY	366	GGGATCATTCGGGAACCTCCACGGTCATCTTGGCGGTGTGAAGAAGTCCAAGCTGCACGTG	425
Db	181	GGGATCGTGGGAACCTCCACGGTCATCTTGGCTGTGTGTGAAGAAGTCCAAGCTACACTG	240
QY	426	GTCACACAACGTCCTCCCGACATCTTCATCATCAACCTCTCGTAGTAGATCTCCTCTTCT	485
Db	241	GTCAGCAACGTCCTCCCGACATCTTCATCATCAACCTCTCTGTGTGTGATCTGCTCTTCT	300
QY	486	CCTGGGATGCCCCCTCATGATCCACCAAGCTCATATGGGCAATGGGGTGTGGCACTTTGGGA	545
Db	301	GCTGGGATGCCCCCTTCATGATCCACCAAGCTCATATGGGGAACGGCGTCTGGCACTTTGGGGA	360
QY	546	GACCATGTGCACCCTCATACAGGGCATGGATGGCCAAATAGTCAGTTACACCAACCACTACAT	605
Db	361	AACCATGTGCACCCTCATACAGGGCATGGAGGCCAACAGTCAGTTACATGCAACCTACAT	420
QY	606	CCTGACCGGCATGGCCATTTGACCGGCTA CCTGGCCACTGTCCACCCCACCACTCTTCCACGAA	665
Db	421	CCTGACTGCCATGACCACTTGCACGGCTACTTGGCCACCGTCCACCCCACTCTCCTCCACCAA	480
QY	666	GTTCCGGAAGCCCTCTGTGGGCCACCTGTGTATCTGCTCTCCTGTGGGGCCCTCTCCTTCAT	725

Db	481	GTTCGGGAAGCCCTTCATGGCCACCCCTGGTGAATCTGCCTCCTGTGGGCGCTCTCCTTCAT	540
QY	726	CAGATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGTGACAGTGGG	785
Db	541	CAGATCACCCCTGTGTGGCTCTACGCCAGGGCTCATTCCTTCCAGGGGGTGTGGG	600
QY	786	CTGGCGCATACGCTTGCCCAACCCAGACACTGACCTCTACTGTTCACCCGTACCAATT	845
Db	601	CTGTGGCATCCGCTTGCCCAACCCGAGACACTGACCTCTACTGTTCACCTGTACCAATT	660
QY	846	TTTCCCTGGCCTTTGCCCTGCCTTTGTGTGTCATCACAGCCGATACGTGAGGATCCTGCA	905
Db	661	TTTCCCTGGCCTTTGCCCTTCCGTTTGTGTGTCATTACCGCCGATACGTGAATAATACACA	720
QY	906	GCGCATGACGTCTCAGTGGCCCCCGCCTCCACAGCGCAGCATCCGGCTCGGACAAGAG	965
Db	721	GCGCATGACGTCTTCCGTGGGCCCCAGCCTCCCAACGCAGCATCCGGCTTCGACAAGAG	780
QY	966	GGTGACCCCGCACAGCCCATCGCCATCTGTGTGTCCTTTGTGTGCTGGGCACCCCTACTA	1025
Db	781	GGTGACCCCGCACAGGCCATTCGCATCTGTGTGTCCTTTGTGTGCTGGGCACCCCTACTA	840
QY	1026	TGTGCTACAGCTGACCCAGTTGTCCATCAGCGCGCCGACCCCTCACCTTGTCTACTTATA	1085
Db	841	TGTGCTACAGCTGACCCAGCTGTCCATCAGCGCGCCGACCCCTCACGTTTGTCTACTTATA	900
QY	1086	CAATGCGGCCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTGTGTACTATCT	1145
Db	901	CAATGCGGCCCATCAGCTTGGGCTATGCTAACAGCTGCCTGAACCCCTTGTGTACTATAGT	960
QY	1146	GCTCTGTGAGAGCGTCCCGCAAAAGCTTGGTCTGTCTGGTGAAGCCTGCAGCCAGGGGCA	1205
Db	961	GCTCTGTGAGAGCCTTTCGAAAACGCTTGGTGTGTTCAGTGAAGCCTGCAGCCAGGGGCA	1020
QY	1206	GCTTCGGGCTGTACAGCAACGCTCAGACGGGCTGACGAGGAGAGGACGAAAGCAAAAGGAC	1265
Db	1021	GCTTCGGCAGGTCAGCAACGCTCAGACAGCTGATGAGGAGAGGACGAAAGCAAAAGGAC	1080
QY	1266	CTGA 1269	
Db	1081	CTGA 1084	

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RESULT 6
US-09-864-761-21946
; Sequence 21946, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
;

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, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00669
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00665
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00668
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00663
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00662
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00661
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00670
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: US 60/234,687
, PRIOR FILING DATE: 2000-09-21
, PRIOR APPLICATION NUMBER: US 09/608,408
, PRIOR FILING DATE: 2000-06-30
, PRIOR APPLICATION NUMBER: US 09/774,203
, PRIOR FILING DATE: 2001-01-29
, NUMBER OF SEQ ID NOS: 49117
, SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
, SEQ ID NO 21946
, LENGTH: 720
, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, OTHER INFORMATION: MAP TO 286090.10
, OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.67
, OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
, OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
, OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 0.74
, OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
, OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
, OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
, OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
, OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
, OTHER INFORMATION: SWISSPROT HIT: Q99705, EVALU0 0.00e+00
, OTHER INFORMATION: NT HIT: g111418165, EVALU0 0.00e+00
, OTHER INFORMATION: EST_HUMAN HIT: BE701073.1, EVALU0 0.00e+00
US-09-864-761-21946

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Query Match	56.7%;	Score 720;	DB 10;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 4.6e-162;		
Matches 720; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	550	ATGTGACCCCTTCATCACGGCCATGGATGCCAATAGTCAGTTTCACGACCACTTACATCCTG	609
Db	1	ATGTGCACCCCTTCATCACGGCCATGGATGCCAATAGTCAGTTTCACGACCACTTACATCCTG	60
QY	610	ACCGCCATGGCCATTTGACCGCTACCTGGCCACATGTCCACCCCATCTCTTCCACGAAGTTC	669
Db	61	ACCGCCATGGCCATTTGACCGCTACCTGGCCACATGTCCACCCCATCTCTTCCACGAAGTTC	120
QY	670	CGGAAGCCCTCTGTGGCCACCCCTGTGTATCTGCCTCTGTGGCCCTCTCCTTCATCAGC	729
Db	121	CGGAAGCCCTCTGTGGCCACCCCTGTGTATCTGCCTCTGTGGCCCTCTCCTTCATCAGC	180
QY	730	ATCACCCCTGTGTGGCTGTATGCACAGATCATCCCTTCCACGAAGGTGAGTGGGCTGC	789
Db	181	ATCACCCCTGTGTGGCTGTATGCACAGATCATCCCTTCCACGAAGGTGAGTGGGCTGC	240
QY	790	GGCATACGCCCTGGCCCAACCCAGACACTGACTCTACTGTGTACCCCTGTACCAGTTTTC	849
Db	241	GGCATACGCCCTGGCCCAACCCAGACACTGACTCTACTGTGTACCCCTGTACCAGTTTTC	300
QY	850	CTGGCCCTTGGCCCTGGCCTTTGTGTATCATCAGCCGCATACGTAGAGATCCTGCAGCGC	909
Db	301	CTGGCCCTTGGCCCTGGCCTTTGTGTATCATCAGCCGCATACGTAGAGATCCTGCAGCGC	360
QY	910	ATGACGTCCTCAGTGGCCCCCGCCTCCACGGCAGCATCCGGCTGGGACAAAGAGGGTG	969

Db	361	ATGACGTCTCAGTGGCCCCCGCCTCCACAGCGCAGCATCCGGCTGGCGACAAGAGGCTG	420
QY	970	ACCCGCACAGCCATCGCCATCTGTCTGGTCTTTCTTTGTGTGCTGGGCACCCCTACTATGTG	1029
Db	421	ACCCGCACAGCCATCGCCATCTGTCTGTCTTTCTTTGTGTGCTGGGCACCCCTACTATGTG	480
QY	1030	CTACAGCTGACCCAGTGTTCATCAGCGCGCCGACCCCTCACCTTTGTCTACTTATACAAT	1089
Db	481	CTACAGCTGACCCAGTGTTCATCAGCGCGCCGACCCCTCACCTTTGTCTACTTATACAAT	540
QY	1090	GGGGCCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTTGTGTACATCGTGCTC	1149
Db	541	GGGGCCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTTGTGTACATCGTGCTC	600
QY	1150	TGTGAGACGTTCCGCCAAACGCTGTGCTCTGTGCGGTGAAGCCTGCAGCCAGGGGCGACCTT	1209
Db	601	TGTGAGACGTTCCGCCAAACGCTGTGCTCTGTGCGGTGAAGCCTGCAGCCAGGGGCGACCTT	660
QY	1210	CGCGCTGTCAAGAACGCTCAGACGGCTGCAGGAGAGAGAGAGAGAAAGCAAAAGGCACCTGA	1269
Db	661	CGCGCTGTCAAGAACGCTCAGACGGCTGCAGGAGAGAGAGAGAGAAAGCAAAAGGCACCTGA	720

RESULT 7
US-09-895-686-25

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: Sequence 25, Application US/09895686
: Patent No. US20020106655A1
: GENERAL INFORMATION:
:   APPLICANT: Bandman, Olga
:   APPLICANT: lal, Preeti
:   APPLICANT: Tang, Y. Tom
:   APPLICANT: Baughn, Mariah R.
:   TITLE OF INVENTION: HUMAN GPCR PROTEINS
:   FILE REFERENCE: PC-0044 CIP
:   CURRENT APPLICATION NUMBER: US/09/895,686
:   CURRENT FILING DATE: 2001-06-28
:   NUMBER OF SEQ ID NOS: 74
:   SOFTWARE: PERL Program
:   SEQ ID NO 25
:   LENGTH: 519
:   TYPE: DNA
:   ORGANISM: Homo sapiens
:   FEATURE:
:   NAME/KEY: misc.feature
:   OTHER INFORMATION: Incyte ID No. US20020106655A1 SAAB00250R1
US-09-895-686-25

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Query Match	40.88;	Score 517.4;	DB 10;	length 519;
Best Local Similarity	99.88;	Pred. No. 5.4e-114;		
Matches 518;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

QY	533	GGCACTTTGGGAGACCATTGWCACCCCTCATCAGGCCATGGATGCCAATAGTCA	592
Dd	1	GGCACTTTGGGAGACCATTGTGCACCCCTCATCAGGCCATGGATGCCAATAGTCA	60
QY	593	CCAGCACCTACATTCCTGAACCGCCATGGCCATTGACCCCTAACCTGGCCACTGTCCACCCCA	652
Dd	61	CCAGCACCTACATTCCTGAACCGCCATGGCCATTGACCCCTAACCTGGCCACTGTCCACCCCA	120
QY	653	TCTCTTCCACGAAGTTCGGAAAGCCCTCTGTGGCCACCCCTGGTGATCTGCCTCTGTGGG	712
Dd	121	TCTCTTCCACGAAGTTCGGAAAGCCCTCTGTGGCCACCCCTGGTGATCTGCCTCTGTGGG	180
QY	713	CCCTCTCTCATCAGCATCACCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCAG	772
Dd	181	CCCTCTCTCATCAGCATCACCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCAG	240
QY	773	GAGGTGCAGTGGGCTGCGGATACGCGCTGCCCAACCCAGACACTGACCTCTACTGGTTCA	832
Dd	241	GAGGTGCAGTGGGCTGCGGATACGCGCTGCCCAACCCAGACACTGACCTCTACTGGTTCA	300
QY	833	CCCTGTACCAAGTTTTCTGTGGCCTTGCCCTGCCTTTTGTGTCATCACAGCCGCATACG	892

Db 301 CCTGTACCAGTTTTCCTGGCCCTTGGCCCTTGTAGTGTATCATACAGCCGATACG 360
QY 893 TGAGATCTCTGACGGCATGACGTCTCAGTGGCCCCGCCCTCCAGCGCAGCATCCGGC 952
Db 361 TGAGGATCTGACGGCATGACGTCTCAGTGGCCCCGCCCTCCAGCGCAGCATCCGGC 420
QY 953 TGGGACAAGAGGGGTGACCCGACAGCCATCGCCATCTGTGCTCTTGTGTGCT 1012
Db 421 TGGGACAAGAGGGGTGACCCGACAGCCATCGCCATCTGTGCTCTTGTGTGCT 480
QY 1013 GGGACCCCTACTATGTCTACAGCTGACCCAGTTGTCCA 1051
Db 481 GGGACCCCTACTATGTCTACAGCTGACCCAGTTGTCCA 519

RESULT 8

US-09-864-761-10236
; Sequence 10236, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10236
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO Z86090.10

; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
US-09-864-761-10236

Query Match 36.2%; Score 459; DB 10; Length 459;
Best Local Similarity 100.0%; Pred. No. 3.9e-100;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 545 AGACCATGTGCACCCCTCATCAGCGGCCATGGATGCCAATAGTCAGTTCACGACCTTACA 604
Db 1 AGACCATGTGCACCCCTCATCAGCGGCCATGGATGCCAATAGTCAGTTCACGACCTTACA 60
QY 605 TCCTGACCGCCATGGCCATTTGACCCGCTACCTGGCCACTGTGCCACCCCATCTTCCACGA 664
Db 61 TCCTGACCGCCATGGCCATTTGACCCGCTACCTGGCCACTGTGCCACCCCATCTTCCACGA 120
QY 665 AGTTCGGAAGCCCTCTGTGGCCACCCCTGTGATCTGCTCTGTGGCCCTTCTCTTCA 724
Db 121 AGTTCGGAAGCCCTCTGTGGCCACCCCTGTGATCTGCTCTGTGGCCCTTCTCTTCA 180
QY 725 TCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGAGTGG 784
Db 181 TCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGAGTGG 240
QY 785 GCTGCGCATACGCTTGGCCCAACCCAGACACTGACCTCTACTGTTTCAACCTGTACCACT 844
Db 241 GCTGCGCATACGCTTGGCCCAACCCAGACACTGACCTCTACTGTTTCAACCTGTACCACT 300
QY 845 TTTTCTGGCCCTTGGCCCTTGGCTTGTGTCATCACAGCGCATACGTGAGGATCCTGC 904
Db 301 TTTTCTGGCCCTTGGCCCTTGGCTTGTGTCATCACAGCGCATACGTGAGGATCCTGC 360
QY 905 AGCGATGACGTCCTCAATGGCCCCCGCTCCAGCGCAGATCCGGCTGCGACAAGA 964
Db 361 AGCGATGACGTCCTCAATGGCCCCCGCTCCAGCGCAGATCCGGCTGCGACAAGA 420
QY 965 GGGTGACCCGACAGCCATCGCCATCTGTGCTTCT 1003
Db 421 GGGTGACCCGACAGCCATCGCCATCTGTGCTTCT 459

RESULT 9

US-09-895-686-22
; Sequence 22, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO. US20020106655A1 1459432X12
US-09-895-686-22

Query Match 24.8%; Score 314.8; DB 10; Length 336;
Best Local Similarity 97.9%; Pred. No. 6.3e-66;
Matches 319; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 217 GAAGCCTCGCTGCTGCCACACTGGTCCCAATGCCAGACACACCTCTGATGGCCCCGATAAC 276
Db 11 GGAACCTCGCTGCTGCCACACTGGTCCCAACGCCAGACACACCTCTGATGGCCCCGATAAC 70
QY 277 CTCACCTTCAGCAGGATCACCCTCTCGCAGGGGAGCATCTCTACATCAACATCATCATG 336
Db 71 CTCACCTTCGCGAGGATCACCTCTCGCAGGGGAGCATCTCTACATCGACATCATCATG 130
QY 337 CCTTCGGTGTTCGGCACCATCTGCTCTCTGGGCATCATCGGGAATCCACGGTCACTTTC 396
Db 131 CCTTCGGTGTTCGGCACCATCTGCTCTCTGGGCATCATCGGGAATCCACGGTCACTTTC 190
QY 397 GCGGTCGTGAAGAAGTCCAAAGCTGCACCTGTGCAACAACGTCCTCCGACATCTTCATCATC 456
Db 191 GCGGTCGTGAAGAAGTCCAAAGCTGCACCTGTGCAACAACGTCCTCCGACATCTTCATCATC 250
QY 457 AACCTCTCGTAGTAGATCTCTCTTCTCTCTGGGCATGCCCTTCATGATCCACAGCTC 516
Db 251 AACCTCTCGTAGTAGATCTCTCTTCTCTCTGGGCATGCCCTTCGATGATCCACAAGCTC 310
QY 517 ATGGGCAATGGGGTGTGGCACTTTGG 542
Db 311 ATGGGCAATGGGGTGTGGCACTTTGG 336

RESULT 10
US-09-864-761-9017
; Sequence 9017, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9017
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO 286090.10
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
US-09-864-761-9017

Query Match 22.5%; Score 285.2; DB 10; Length 575;
Best Local Similarity 99.0%; Pred. No. 7.9e-59;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGTCACTGGGAGCCATGAAGAAGGAGTGGGAGGGCAGTTGGCTTGAGGCGGCAGC 60
Db 156 ATGTCACTGGGAGCCATGAAGAAGGAGTGGGAGGGCAGTTGGCTTGAGGCGGCAGC 215
QY 61 GGCTGCCAGGCTACGAGGAGGAGACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGAGCAA 120
Db 216 GGCTGCCAGGCTACGAGGAGGAGACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGAGCAA 275
QY 121 GGTGGCAGGCGCTGAGAGGCTGCCGACAGCCTGCGTGGTGGAGGGGAGCTCAGCTCGTTG 180
Db 276 GGTGGCAGGCGCTGAGAGGCTGCCGACAGCCTGCGTGGTGGAGGGGAGCTCAGCTCGTTG 335
QY 181 TGGAGCAGGCGACCGGCACTGGCTGATGAGCTGAGCCTGGAAGCCTCGCTGCCCCACTGCT 240
Db 336 TGGAGCAGGCGACCGGCACTGGCTGATGAGCTGAGCCTGGAAGCCTCGCTGCCCCACTGCT 395
QY 241 CCCAATGCCAGCAACACCTCTGATGGCCCCGATTAACCTTCACCTTCAGCAGG 290
Db 396 CCCAATGCCAGCAACACCTCTGATGGCCCCGATTAACCTTCACCTTCAGCAGG 445

RESULT 11
US-09-895-686-24/c
; Sequence 24, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 24
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020106655A1 SAAC00257R1
; NAME/KEY: unsure
; LOCATION: 14
; OTHER INFORMATION: a, t, c, g, or other
US-09-895-686-24

Query Match	21.88;	Score 276.4;	DB 10;	Length 279;
Best Local Similarity	99.38;	Pred. No. 7.8e-57;		
Matches 277; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	267	CCCCGATACCTCACTTCAAGCAGGATCACTCTCGCACGGGAGCATCTCCCTACATCAA	326
Db	279	CCCCGATACCTCACTTCCGGCAGGATCACTCTCGCACGGGAGCATCTCCCTACATCAA	220
QY	327	CATCATCATGCCCTTCGGTGTTCCGCACCATTCTGCCCTCCTGGGCATCATCGGGAAC	386
Db	219	CATCATCATGCCCTTCGGTGTTCCGCACCATTCTGCCCTCCTGGGCATCATCGGGAAC	160
QY	387	GGTCATCTTCGGGTCTGTGAAGAAGTCCAAGCTGCACCTGTTGCAACAACGTC	446
Db	159	GGTCATCTTCGGGTCTGTGAAGAAGTCCAAGCTGCACCTGTTGCAACAACGTC	100
QY	447	CTTCATCATCAACTCTCGGTAGTAGATCTCCTCTTCTTCCHGGGCATGCCCTTCA	506
Db	99	CTTCATCATCAACTCTCGGTAGTAGATCTCCTCTTCTTCCHGGGCATGCCCTTCA	40
QY	507	CCACCAAGCTCATGGGCAATGGGGTGTGGCACTTTGGGGA	545
Db	39	CCACCAAGCTCATGGGCAATGGGGTGTGGCACTTTGGGGA	1

RESULT 12
US-09-864-761-26601

```

; Sequence 26601, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:

```

```

?  APPLICANT: Penn, Sharon G.
?
?  APPLICANT: Rank, David R.
?
?  APPLICANT: Hanzel, David K.
?
?  APPLICANT: Chen, Wensheng
?
?  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
?  TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

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; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 26601

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?      LENGTH: 274
?      TYPE: DNA
?      ORGANISM: Homo sapiens
?      FEATURE:
?      OTHER INFORMATION: MAP TO 286090.10
?      OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.3
?      OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.2
?      OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
?      OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.3
?      OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
?      OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
?      OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5
?      OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
?      OTHER INFORMATION: EST_HUMAN HIT: BE312542.1, EVALUE 0.00e+00
?      OTHER INFORMATION: SWISSPROT HIT: P97639, EVALUE 1.00e-04
?      OTHER INFORMATION: NT HIT: AE004060.1, EVALUE 1.10e-02
US-09-864-761-26601

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Query Match	21.2%;	Score 269.2;	DB 10;	Length 274;
Best Local Similarity	98.9%;	Pred. No. 4e-55;		
Matches 271;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

OY	16	ATGAGAGAGGACGTGGGGAGGGCAGTGGCGCTTGAGAGCGGCACCGGCTGCCAGGCTACG	75
Dp	1	ATGAGAGAGGAGTGGGGAGGGCAGTGGCGCTTGAGAGCGGCACCGGCTGCCAGGCTACG	60
OY	76	GAGGAAGACCCCTTCCCAGACTGCGGGGCTTGCGCTCCGGACAAGGTGGCAGGCGCTGG	135
Dp	61	GAGGAAGACCCCTTCCCAGACTGCGGGGCTTGCGCTCCGGACAAGGTGGCAGGCGCTGG	120
OY	136	AGGCTGCCGCAAGCCTGCGTGGGTGAGAGGAGCACTCAGCTCGTTGTGGAGCAGGCGACC	195
Dp	121	AGGCTGCCGCAAGCCTGCGTGGGTGAGAGGAGCACTCAGCTCGTTGTGGAGCAGGCGACC	180
OY	196	GGCACCTGGCTGAGATGGAACCTGGAAGCCTGCTGTCGCCACACTGCTCCCATGCGCAGCAAC	255
Dp	181	GGCACCTGGCTGAGATGGAACCTGGAAGCCTGCTGTCGCCACACTGCTCCCATGCGCAGCAAC	240
OY	256	ACCTCTGATGGCCCCGATAACCTCACTTCAGCAG	289
Dp	241	ACCTCTGATGGCCCCGATAACCTCACTTCAGCAG	274

RESULT 13
US-09-895-686-57

; Sequence 57, Application US/09895686
; Patent No. US20020106655A1

```

; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 57
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO. US20020106655A1 701899983H11
US-09-895-57

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Query Match 20.28; Score 256; DB 10; Length 304;

Best Local Similarity 90.1%; Pred. No. 5,6e-52;
Matches 274; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 645 CCACCCCATCTCTTCCACGAGTTCCGGAAGCCCTCTGTGGCCACCCCTGGTATCTGCTT 704
|||||
Db 1 CCACCCCATCTCTTCCACGAGTTCCGGAAGCCCTCCATGGCCACCCCTGGTATCTGCTT 60
QY 705 CCTGTGGCCCTCTCTCTTCCATCAGCATCACCCCTGTGTGGCTGTATGCGACACTCATCC 764
|||||
Db 61 CCTGTGGCCCTCTCTCTTCCATCAGCATCACCCCTGTGTGGCTGTATGCGACACTCATCC 120
QY 765 CTTCACGAGGTGACGTGGGCTGGGCATACGCCCTGCCAACCACGACACTGACCTCTA 824
|||||
Db 121 CTTCACGAGGTGACGTGGGCTGGGCATACGCCCTGCCAACCACGACACTGACCTCTA 180
QY 825 CTGTTCACCTCTTACCATGTTTCTTCCCTGGCCCTTGGCCCTTGTGTGTCATCAGC 884
|||||
Db 181 CTGTTCACCTCTTACCATGTTTCTTCCCTGGCCCTTGGCCCTTGTGTGTCATCAGC 240
QY 885 CGCATACGTGAGGATCTTCGACGCCATGACGTCCATCAGTGGCCCGCCCTCCACGCGAG 944
|||||
Db 241 CGCATACGTGAGGATCTTCGACGCCATGACGTCCATCAGTGGCCCGCCCTCCACGCGAG 300
QY 945 CATC 948
|||
Db 301 CATC 304

RESULT 14
US-09-895-686-56
; Sequence 56, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 56
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020106655A1 701250242H1
US-09-895-686-56

Query Match 18.2%; Score 231; DB 10; Length 271;
Best Local Similarity 90.8%; Pred. No. 4.7e-46;
Matches 246; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 406 AAGAAGTCCAAGCTGACATGTGTGACACAACGTCGCCGACATCTTCATCAACCTCTCG 465
|||||
Db 1 AAGAATCCAAGCTGACATGTGTGACACAACGTCGCCGACATCTTCATCAACCTCTCT 60
QY 466 GTAGTAGATCTCTCTCTCTCTCTGCGCATGCCCTTCATGATCCACGACATGGCAAT 525
|||||
Db 61 GTGTGATCTCTCTCTCTCTCTGCGCATGCCCTTCATGATCCACGACATGGCAAT 120
QY 526 GGGGTGTGGCACTTGGGAGACATGTGACCCCTCATACGCGCATGGCAATAGT 585
|||||
Db 121 GGTGTGTGGCACTTGGGAGAAACATGTGACCCCTCATACGCGCATGGCAATAGT 180
QY 586 CAGTTCACGACCTACATCTGACCGCATGGCAATGACCGCTACCTGGCCACTGTC 645
|||||
Db 181 CAGTTCACGACCTACATCTGACCTGACTATGGCAATGACCGCTACTTGGCCACCGTC 240
QY 646 CACCCCATCTCTTCCACGAGTTCCGGAAGC 676

Db 241 CATCCATCTCTTCCACCAAGTTCCGGAAGC 271

RESULT 15
US-09-895-686-20
; Sequence 20, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 223
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020106655A1 1459432H1
US-09-895-686-20

Query Match 17.6%; Score 223; DB 10; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.5e-44;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 533 GGCATTTTGGGAGACCATGTGACACCCCTCATCAGCGCCATGGATGCCAATAGTCA 592
|||||
Db 1 GGCATTTTGGGAGACCATGTGACACCCCTCATCAGCGCCATGGATGCCAATAGTCA 60
QY 593 CCAGCCTTACATCTCTGACCGCCATGGCCATTTGACCGCTTACCTGGCCACTGTCCACCCA 652
|||||
Db 61 CCAGCCTTACATCTCTGACCGCCATGGCCATTTGACCGCTTACCTGGCCACTGTCCACCCA 120
QY 653 TCTCTTCCACGAGTTCCGGAAGCCCTCTGTGGCCACCCCTGGTGTATGCTGCTCTGTGG 712
|||||
Db 121 TCTCTTCCACGAGTTCCGGAAGCCCTCTGTGGCCACCCCTGGTGTATGCTGCTCTGTGG 180
QY 713 CCTCTCTTATCAGCATCACCCCTGTGTGGCTGTATGCCAG 755
|||||
Db 181 CCTCTCTTATCAGCATCACCCCTGTGTGGCTGTATGCCAG 223

Search completed: February 19, 2003, 12:08:33
Job time : 84 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 19, 2003, 08:30:46 ; Search time 3435 Seconds
(without alignments)
10751.517 Million cell updates/sec

Title: US-09-885-478-1

Perfect score: 1269
Sequence: 1 atgtcagtggagcgcacatgaa.....cagaaagcaaaagccacctga 1269

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
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33: em_htg_mus:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				Description	
No.	Score	Match	Length	DB	ID		
1	1269	100.0	1269	6	AR169785	AR169785 Sequence	
2	1267.4	99.9	2042	9	BC001736	BC001736 Homo sapi	
3	1267.4	99.9	2042	9	BC021146	BC021146 Homo sapi	
4	1264.2	99.6	1275	6	BD013168	BD013168 MCH recep	
5	1264.2	99.6	1275	9	AB063174	AB063174 Homo sapi	
6	1264.2	99.6	1275	23	BD006649	Bd006649 MCH recep	
7	1264.2	99.6	1283	6	BD013174	BD013174 MCH recep	
8	1264.2	99.6	1283	23	BD006655	Bd006655 MCH recep	
9	1237.4	97.5	1385	6	AX174768	AX174768 Sequence	
10	1115.2	87.9	1444	9	AF513988	AF513988 Macaca mu	
11	1058.8	83.4	1062	6	AX280739	AX280739 Sequence	
12	1058.8	83.4	1062	6	AX280743	AX280743 Sequence	
13	1058.8	83.4	1062	6	AX280747	AX280747 Sequence	
14	1058.8	83.4	1062	6	AX280755	AX280755 Sequence	
15	1058.8	83.4	1062	6	AX280759	AX280759 Sequence	
16	1058.8	83.4	1062	6	AX280767	AX280767 Sequence	
17	1058.8	83.4	1074	6	BD013173	BD013173 MCH recep	
18	1058.8	83.4	1074	23	BD006654	Bd006654 MCH recep	
19	1058.4	83.4	2133	6	AX280965	AX280965 Sequence	
20	1057.2	83.3	1062	6	AX280727	AX280727 Sequence	
21	1057.2	83.3	1062	6	AX280751	AX280751 Sequence	
22	1055.6	83.2	1062	6	AX280763	AX280763 Sequence	
23	1052.4	82.9	1062	6	AX280731	AX280731 Sequence	
24	1014	79.9	1062	9	AY078245	AY078245 Macaca mu	
25	999.6	78.8	1349	6	AX280735	AX280735 Sequence	
26	984.4	77.6	1877	9	HSU71092	U71092 Homo sapien	
27	984.4	77.6	3488	6	AR202509	AR202509 Sequence	
28	984.4	77.6	12257	9	HS229A8	Z86090 Human DNA s	
29	983	77.5	1316	6	AR096459	AR096459 Sequence	
30	980	77.2	980	6	AR202513	AR202513 Sequence	
31	935.6	73.7	1062	4	AY112898	AY112898 Mustela p	
32	922.8	72.7	1062	4	AY112658	AY112658 Canis fam	
33	912.8	71.9	1214	6	AR169786	AR169786 Sequence	
34	912.8	71.9	1214	10	AF008650	AF008650 Rattus no	
35	895.6	70.6	1074	6	BD013164	BD013164 MCH recep	
36	895.6	70.6	1074	23	BD006645	Bd006645 MCH recep	
37	874.8	68.9	1062	10	AF498247	AF498247 Mus muscu	
38	874.8	68.9	1062	10	AF498248	AF498248 Mus muscu	
39	842.8	66.4	128125	2	AC127953	AC127953 Rattus no	
40	820.6	64.7	5027	10	AY049011	AY049011 Mus muscu	
41	410.6	32.4	474	10	RNU77953	U77953 Rattus norv	
42	373	29.4	420	6	BD013175	BD013175 MCH recep	
43	373	29.4	420	23	BD006656	Bd006656 MCH recep	
44	333	26.2	365	4	AF273611	AF273611 Sus scrof	
45	207	16.3	775	6	AR202510	AR202510 Sequence	

ALIGNMENTS

RESULT 1
AR169785
LOCUS AR169785 1269 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6291195.
ACCESSION AR169785
VERSION AR169785.1 GI:17907693
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1269)
AUTHORS Salon,J.A., Laz,T.M., Nagorny,R. and Wilson,A.E.
TITLE DNA encoding a human melanin concentrating hormone receptor (MCH1)
and uses thereof
JOURNAL Patent: US 6291195-A 1 18-SEP-2001;

Pred. No. is the number of results predicted by chance to have a

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BASE COUNT		/organism="unknown"	
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Query Match		100.0%; Score 1269; DB 6; Length 1269;	
Best Local Similarity		100.0%; Pred. No. 8.7e-238;	
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LOCUS			
DEFINITION			
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VERSION			
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REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REMARK			
COMMENT			
Contact: MGC help desk			
Email: cgabbs-remail.nih.gov			
Tissue Procurement: ATCC			
cDNA Library Preparation: Rubin Laboratory			
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
DNA Sequencing by: Genome Sequence Centre,			
BC Cancer Agency, Vancouver, BC, Canada			
info@cgsc.bc.ca			
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,			
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,			
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo			
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven			
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline			
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stolt,			
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,			
George Yang, Scott Zuyderduyn, Marco Marra.			
Clone distribution: MGC clone distribution information can be found			
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov			
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ORIGIN

Query Match      99.9%; Score 1267.4; DB 9; Length 2042;
Best Local Similarity 99.9%; Pred. No. 1.7e-237;
Matches 1268; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATGTCAGTGGGAGCCATGAAGAAGGAGTGGGGAGGCGCAGTTGGCTTGAGGCGGCAGC 60
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QY      121  GGTGGCAGGCGCTGAGAGTCCGCGAGCCTGCGTGGGTGAGGGGAGCTCAGCTCGGTTG 180
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VERSION      BC021146.1 GI:18088973
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SOURCE      Homo sapiens.
ORGANISM      Homo sapiens.
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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JOURNAL      Strausberg,R.
REMARK      Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stolt,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 40 Row: n Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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Query Match 99.9%; Score 1267.4; DB 9; Length 2042;
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Matches 1268; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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ACCESSION BD013168.1 GI:22093357
VERSION BD013168.1
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1275)
AUTHORS Kato,K., Mori,M., Suzuki,N., Shimomura,Y., Takekawa,S. and Cho,N.
TITLE MCH receptor antagonist
JOURNAL Patent: WO 0121169-A 7 29-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD,KANEYOSHI KATO,MASAKI MORI,NOBUHIRO
SUZUKI, YUKIO SHIMOMURA,SHIRO TAKEKAWA,NOBUO CHO
COMMENT OS Homo sapiens (human)
PN WO 0121169-A/7
PD 29-MAR-2001
PF 19-SEP-2000 WO 2000JP006376

PR 20-SEP-1999 JP 99P 266278,17-JUL-2000 JP 00P 221055 PI
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,SHIRO TAKEKAWA,
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Query Match 99.68; Score 1264.2; DB 6; Length 1275;
Best Local Similarity 99.88; Pred. No. 7.5e-237;
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DEFINITION Homo sapiens SLC-1 mRNA for somatostatin receptor-like protein,
complete cds.
AB063174
AB063174.1 GI:14475646
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens cDNA to mRNA.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Shimomura,Y., Mori,M., Sugo,T., Ishibashi,Y., Abe,M., Kurokawa,T.,
Onda,H., Nishimura,O., Sumino,Y. and Fujino,M.
TITLE Isolation and identification of melanin-concentrating hormone as
the endogenous ligand of the SLC-1 receptor
JOURNAL Biochem. Biophys. Res. Commun. 261 (3), 622-626 (1999)
MEDLINE 99373129
REFERENCE 2 (bases 1 to 1275)
AUTHORS Sugo,T. and Mori,M.
TITLE Direct Submission
JOURNAL Submitted (13-JUN-2001) Tsukasa Sugo, Takeda Chemical Industries,
Ltd., Discovery Research Laboratories I, Pharmaceutical Research
Division; Wadai 10, Tsukuba, Ibaraki 300-4247, Japan
(E-mail: Sugo.Tsukasa@takeda.co.jp, Tel: 81-298-64-5010(ex.5010),
Fax: 81-298-64-5000)
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BASE COUNT 235 a 420 c 350 g 270 t
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Query Match 99.6%; Score 1264.2; DB 9; Length 1275;
Best Local Similarity 99.8%; Pred. No. 7.5e-237;
Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 901 CTGACGCGCATGACGTCCTCAGTGGCCCCCGCCCTCCAGCGCAGCATCCGGCTGGGACA 960
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QY 1261 GGCACCTGA 1269
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ID BD006649
XX AC BD006649;
XX SV BD006649.1
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DT 08-FEB-2002 (Rel. 70, Created)
DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)
DE MCH receptor antagonist.
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XX JP 03075319-T/7.
KW Homo sapiens (human)
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OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
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RA "MCH receptor antagonist";
RT Patent number JP03075319-T/7, 16-FEB-2001.
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CC PF 19-SEP-2000 JP 2000006376
CC PR 20-SEP-1999 JP 99P 266278,17-JUL-2000 JP 00P 221055
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CC PI SHIRO TAKEKAWA,
CC PI NOBUO CHO
CC PC A61K31/137,A61K31/27,A61K31/4035,A61K31/44,A61K31/445,
CC PC A61K31/4453,

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	Best Local Similarity	99.8%; Pred. No. 7.5e-237;
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QY	1	ATGTCAGTGGGAGCCATGAAGAAGGAGTGGGAGGGGAGTTGGGCTTGAGGGCGGACG 60
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QY	121	GGTGGCAGGCGCTGAGGCTGCCGACGCTGCGTGGTGGAGGGAGCTCAGCTCGGTTG 180
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QY	661	ACGAAGTTCGGGAAGCCCTCTGTGGCCACCCCTGGTGTGCTGCTGTTGGCCCTCTCC 720
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Db	847	CAGTTTTCCTGGCCCTTTGGCCCTGCCCTTTTGTGTCATCACAGCCCGCATACGTGAGGATC 906
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	VERSION	BD013174.1 GI:22093363
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	SOURCE	Homo sapiens.
	ORGANISM	Homo sapiens
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	AUTHORS	Kato,K., Mori,M., Suzuki,N., Shimomura,Y., Takekawa,S. and Cho,N.
	TITLE	MCH receptor antagonist
	JOURNAL	Patent: WO 0121169-A 13 29-MAR-2001;
		TAKEEDA CHEMICAL INDUSTRIES LTD,KANEYOSHI KATO,MASAKI MORI,NOBUHIRO
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		,SHIRO TAKEKAWA,
		PI NOBUO CHO
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Query Match	99.6%;	Score 1264.2;	DB 6;	Length 1283;
Best Local Similarity	99.8%;	Pred. No. 7.5e-237;		
Matches 1266; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

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Db	128	GGTGGCAGGCGCTGGAGGCGCTGCCGACGCTGCGTGGGTGAGGGGAGCTCAGCTCGTTG	187
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Db	368	CTCCTGGGCATCATCGGGAACCTCCACGGTCATCTTCGGGCTGTGAAGAAGTCCAAGCTG	427
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Db	968	AAGAGGGTGACCCCGCACAGCCATCGCCATCTGTGTGCTCTTGTGTGCTGGGCACCC	1027

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QY	1141	ATCGTCTCTGTGAGACGTTCCGCAAACGCTTGGTCTGTGCTGAAGCCTGCAGCCAG	1200
Db	1148	ATCGTCTCTGTGAGACGTTCCGCAAACGCTTGGTCTGTGCTGAAGCCTGCAGCCAG	1207
QY	1201	GGGCAGCTTCGGCCTGTCAAGCAACGCTCAGACGGCTGACGAGSAGAGACAGAAGAAAGCAA	1260
Db	1208	GGGCAGCTTCGGCCTGTCAAGCAACGCTCAGACGGCTGACGAGSAGAGACAGAAGAAAGCAA	1267
QY	1261	GGCACCTGA	1269
Db	1268	GGCACCTGA	1276

RESULT	8
ID	BD006655
AC	BD006655
SV	BD006655.1
DT	08-FEB-2002 (Rel. 70, Created)
DT	08-FEB-2002 (Rel. 70, Last updated, Version 1)
DE	MCH receptor antagonist.
XX	
XX	JP 03075319-T/13.
OS	Homo sapiens (human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC	Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RN	[1]
RP	1-1283
RA	Kato K., Mori M., Suzuki N., Shimomura Y., Takeka S., Cho N.;
RT	"MCH receptor antagonist";
RL	Patent number JP03075319-T/13, 16-FEB-2001.
TL	TAKEDA CHEMICAL INDUSTRIES LTD. .
CC	OS Homo sapiens (human)
CC	PN JP 03075319-T/13
CC	PD 16-FEB-2001
CC	PF 19-SEP-2000 JP 2000006376
CC	PR 20-SEP-1999 JP 99P 266278, 17-JUL-2000 JP 00P 221055
CC	PI KANEYOSHI KATO,MASAKI MORI,NOBUHIRO SUZUKI,YUKIO SHIMOMURA,
CC	PI SHIRO TAKEKAWA,
CC	PI NOBUO CHO
CC	PC A61K31/137,A61K31/27,A61K31/4035,A61K31/44,A61K31/445,
CC	PC A61K31/4453,
CC	PC A61K31/472,A61P43/00,A61P31/04,C07D211/14,C07D211/18,
CC	PC C07D211/46,C07D211/58,
CC	PC C07D211/70,C07D401/12,C07D405/12,C07D409/12,C07D417/12
CC	
CC	FH Key Location/Qualifiers
CC	FT source 1. .1283
CC	FT /db_xref="taxon:9606"
CC	FT /organism="Homo sapiens"
XX	
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Seq	Sequence 1283 BP; 238 A; 423 C; 350 G; 272 T; 0 other;

Query Match		99.6%;	Score 1264.2;	DB 23;	Length 1283;
Best Local Similarity		99.8%;	Pred. No. 7.5e-237;		
Matches 1266;		Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
QY	1	ATGTCAGTGGGAGCCATGAAGAGGAGTGGGAGGGCAGTTGGGCTTGAGGCGGCAGC	60		
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QY	61	GGCTGCCAGGCTACGGAGGAGACCCCTTCCGACTGCGGGGCTTGCGCTCCGGACAA	120		
Db	68	GGCTGCCAGGCTACGGAGGAGACCCCTTCCGACTGCGGGGCTTGCGCTCCGGACAA	127		
QY	121	GGTGCGAGGCGCTGGAGGCTGCGCGACGCTGCGTGGTGAGGGGAGCTCAGCTCGGTTG	180		
Db	128	GGTGCGAGGCGCTGGAGGCTGCGCGACGCTGCGTGGTGAGGGGAGCTCAGCTCGGTTG	187		
QY	181	TGGGAGCAGGCGACCGGCACTGGCTGGATGACCTGGAAGCCTCGCTGCTGCCACTGGT	240		
Db	188	TGGGAGCAGGCGACCGGCACTGGCTGGATGACCTGGAAGCCTCGCTGCTGCCACTGGT	247		
QY	241	CCCAATGCCAGCAACACCTCTGATGGCCCCGATACCTCACTTCAGCAGGATCACTCCT	300		
Db	248	CCCAAGCCAGCAACACCTCTGATGGCCCCGATACCTCACTTCGGCAGGATCACTCCT	307		
QY	301	CGCAGCGGGAGCATCTCTACATCAACATCATATGCTTCGGTGTTCGGCAGCATCTGC	360		
Db	308	CGCAGCGGGAGCATCTCTACATCAACATCATATGCTTCGGTGTTCGGCAGCATCTGC	367		
QY	361	CTCCTGGGCATCATCGGGAACCTCCACGGTCACTTCGCGGTGCGTGAAGAATCCAAAGCTG	420		
Db	368	CTCCTGGGCATCATCGGGAACCTCCACGGTCACTTCGCGGTGCGTGAAGAATCCAAAGCTG	427		
QY	421	CACCTGGTGCACAACGTCCTCCGACATCTTCATCATCAACCTCTCGGTAGATCTCCTC	480		
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QY	481	TTTCTCCTGGGCATGCGCTTCATGATCCACCACTCATGGGCAATGGGCTGGCACTTT	540		
Db	488	TTTCTCCTGGGCATGCGCTTCATGATCCACCACTCATGGGCAATGGGCTGGCACTTT	547		
QY	541	GGGGAGACCATGTGCACCCCTTCATCACGGGCATGGATGCCAATAGTCACTTCACCAAGCACC	600		
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QY	601	TACATCCTGACCGGCATGGGCCATGTAGCCGCTACCTGGCCACTGTCCACCCCATCTCTCC	660		
Db	608	TACATCCTGACCGGCATGGGCCATGTAGCCGCTACCTGGCCACTGTCCACCCCATCTCTCC	667		
QY	661	ACGAAGTCCGGAAGCCCTCTGTGGCCACCCTGGTATCTGCCCTCTGTGGCCCTCTCC	720		
Db	668	ACGAAGTCCGGAAGCCCTCTGTGGCCACCCTGGTATCTGCCCTCTGTGGCCCTCTCC	727		
QY	721	TTCATCAGCATACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGCA	780		
Db	728	TTCATCAGCATACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGCA	787		
QY	781	GTGGGCTGGCGCATACGCTTGCCCAACCCAGACACTGACCTCTACTGGTTCAACCTGTAC	840		
Db	788	GTGGGCTGGCGCATACGCTTGCCCAACCCAGACACTGACCTCTACTGGTTCAACCTGTAC	847		
QY	841	CAGTTTTCCTGGCCTTTGGCCCTGCTTTGTGTCATCACAGCCGCATACGTGAGATC	900		
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QY	901	CTGACGCGCATGACGTCTCAGTGGCCCCCGCCTCCAGCGCAGCATCCGGCTGCGGACA	960		
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Db	1028	TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCCGCCGACCTTCACCTTGTCTAC	1087		
QY	1081	TTATACAATGCGGCATCAGCTTGGGCTATGCCAACAAGCTGCGCTCAACCCCTTGTGTAC	1140		
Db	1088	TTATACAATGCGGCATCAGCTTGGGCTATGCCAACAAGCTGCGCTCAACCCCTTGTGTAC	1147		
QY	1141	ATCGTCTCTGTGAGACGTTCCGCAACGCTTGTCTGTGCTGCTGAGAGCCTGCAGCCCCAG	1200		
Db	1148	ATCGTCTCTGTGAGACGTTCCGCAACGCTTGTCTGTGCTGCTGAGAGCCTGCAGCCCCAG	1207		
QY	1201	GGGCAAGCTTCCGCGCTGTCAGCAACGCTTCAGACGGCTGACGAGGAGAGACAGAAAGCAAA	1260		
Db	1208	GGGCAAGCTTCCGCGCTGTCAGCAACGCTTCAGACGGCTGACGAGGAGAGACAGAAAGCAAA	1267		
QY	1261	GGCACCCTGA 1269			
Db	1268	GGCACCCTGA 1276			

RESULT 9
AX174768 1385 bp DNA linear PAT 03-JUL-2001
LOCUS AX174768
DEFINITION Sequence 1 from Patent WO0143759.
ACCESSION AX174768
VERSION AX174768.1 GI:14598289
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 1385)
AUTHORS Campbell,C.A., Haddingham,S.J., Harrison,D.C. and Hervieu,G.J.
TITLE New use
JOURNAL Patent: WO 0143759-A 1 21-JUN-2001;
SMITHKLINE BEECHAM PLC (GB)
FEATURES
location/Qualifiers
1..1385
source

BASE COUNT 255 a 471 c 371 g 288 t
ORIGIN
/db_xref="taxon:9606"
/organism="Homo sapiens"

Query Match		97.5%;	Score 1237.4;	DB 6;	Length 1385;
Best Local Similarity		99.9%;	Pred. No. 1.3e-231;		
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				Indels	0;
				Gaps	0;
QY	31	GGGAGGGGAGTTGGGCTTGGAGGGCGGACGCGCTGCCAGGCTACGAGAGAACCCCTT	90		
Db	66	GGGAGGGGAGTTGGGCTTGGAGGGCGGACGCGCTGCCAGGCTACGAGAGAACCCCTT	125		
QY	91	CCCGACTGCGGGCTTGGCGCTCCGGGACAAAGGTGGCAGGGCGCTGGAGGCTGCCAGCCT	150		
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QY	151	GCGTGGGTGGAGGGAGGCTCAGCTCGTGTGTGGAGCAGGGCAGCCGCACTGGCTGATG	210		
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QY	211	GACCTGGAAGCCTGCTGCTGCCCACTGGTCCCAATGCCAACAACACCTCTGATGGCCCC	270		
Db	246	GACCTGGAAGCCTGCTGCTGCCCACTGGTCCCAATGCCAACAACACCTCTGATGGCCCC	305		
QY	271	GATAACCTCACTTCAGCAGGATCACCTCTCGCGCAGGGGAGCATCTCTACATCAACATC	330		
Db	306	GATAACCTCACTTCAGCAGGATCACCTCTCGCGCAGGGGAGCATCTCTACATCAACATC	365		
QY	331	ATCATGCCCTTCGGTGTGGGACCATCTGCTCTGGGATCATCGGGAATCCACGGTTC	390		
Db	366	ATCATGCCCTTCGGTGTGGGACCATCTGCTCTGGGATCATCGGGAATCCACGGTTC	425		
QY	391	ATCTTGGGGTGTGAAGAAGTCCAAGCTGCTGTGCAACAACGTCGCCGACATCTTC	450		

Db	426	ATCTTCGGCGTTCGTGAAGAGTCCCAAGCTGCAC	TGGTGCAACAACGTC	CCCCGACATCTTC	485
QY	451	ATCATCAACCTCTCGG	TAGTAGATCTCTCTT	CTCTGCGCATGCCCTTCATGATCCAC	510
Db	486	ATCATCAACCTCTCGG	TAGTAGATCTCTCTT	CTCTGCGCATGCCCTTCATGATCCAC	545
QY	511	CAGCTCATGGGCAATGGGG	TGGGCAC	TTTGGGGAGACCATGTGCACCCCTCATCAGCGCC	570
Db	546	CAGCTCATGGGCAATGGGG	TGGGCAC	TTTGGGGAGACCATGTGCACCCCTCATCAGCGCC	605
QY	571	ATGGATGCCAATAGTCA	GTTCACGACGACCTACAT	CTCTGACCGCCATGGCCATTGACCGC	630
Db	606	ATGGATGCCAATAGTCA	GTTCACGACGACCTACAT	CTCTGACCGCCATGGCCATTGACCGC	665
QY	631	TACCTGGCCACTGTCC	ACCCCATCTCTTCACAGAA	GTTCGGAAAGCCCTCTGTGGCCACC	690
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QY	691	CTGGTGATCTGCC	TCCTGTGGCCCTCTCTTCATCAGCAT	CACCCCTGTGTGGCTGTAT	750
Db	726	CTGGTGATCTGCC	TCCTGTGGCCCTCTCTTCATCAGCAT	CACCCCTGTGTGGCTGTAT	785
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Db	786	GCCAGACTCATCCCT	TCCCAAGAGGTGCAGTGGGCTGCGGCAT	ATACGCTTGCCCAACCCA	845
QY	811	GACACTGACCTCTACT	GGTTACCCCTGTACCA	GTTTTTCTGCGCCTTGCCCTGCCCTTTT	870
Db	846	GACACTGACCTCTACT	GGTTACCCCTGTACCA	GTTTTTCTGCGCCTTGCCCTGCCCTTTT	905
QY	871	GTGGTCATCACAGCCG	CATACGTGAGGATCCTTCGACGCGCAT	GATGAGCTCTCAGTGGCCCCC	930
Db	906	GTGGTCATCACAGCCG	CATACGTGAGGATCCTTCGACGCGCAT	GATGAGCTCTCAGTGGCCCCC	965
QY	931	GCCTCCGAGCGCAG	CATCCGGCTGCGGACA	AAAGGGTGACCCGACAGCCATCGCCATC	990
Db	966	GCCTCCGAGCGCAG	CATCCGGCTGCGGACA	AAAGGGTGACCCGACAGCCATCGCCATC	1025
QY	991	TGCTGTGCTCTTCT	TGTGTGCTGGGACACCC	TACTATGTGCTACAGCTGACCCAGTTGTCC	1050
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QY	1051	ATCAGCCGCCGAC	CCCTGACCTTTGCTACTT	ATACAAATGCGGCCATCAGCTTGGGCTAT	1110
Db	1086	ATCAGCCGCCGAC	CCCTGACCTTTGCTACTT	ATACAAATGCGGCCATCAGCTTGGGCTAT	1145
QY	1111	GCCAACAGCTGCCT	CAACCCCTTGTGTACAT	CGTGTGTGAGACGTTCCGCAAAAGC	1170
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QY	1171	TTGGTCTCTGTGG	TGAAGCCTGACGCC	CAGGCGCAGCTTCGCGCTGTCAAGCAAGCTCAG	1230
Db	1206	TTGGTCTCTGTGG	TGAAGCCTGACGCC	CAGGCGCAGCTTCGCGCTGTCAAGCAAGCTCAG	1265
QY	1231	ACGCGTGAAGAG	GAGAGACAGAAAGCA	AAAGGACCTGA	1269
Db	1266	ACGCGTGAAGAG	GAGAGACAGAAAGCA	AAAGGACCTGA	1304
RESULT 10					
AF513988		1444 bp	mRNA	linear	PRI 10-JUN-2002
LOCUS	AF513988				
DEFINITION	Macaca mulatta melanin-concentrating hormone receptor subtype 1				
ACCESSION	AF513988				
VERSION	AF513988.1		GI:21361063		
KEYWORDS					
SOURCE	rhesus monkey.				
ORGANISM	Macaca mulatta				
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.				
REFERENCE	1 (bases 1 to 1444)				

AUTHORS	Tan,C.P., Sano,H., Iwaasa,H., Pan,J., Sailer,A., Hreniuk,D.L., Feighner,S.D., Palyha,O.C., Figueroa,D.J., Austin,C.P., Jiang,M.M., Yu,H., Ito,J., Ito,M., Ito,M., Guan,X.M., Kanatani,A., Van der ploeg,L.H.T. and Howard,A.D.				
TITLE	Melanin-Concentrating Hormone Receptor Subtypes 1 and 2: Species Specific Gene Expression				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1444)				
AUTHORS	Tan,C.P., Sano,H., Iwaasa,H., Pan,J., Sailer,A., Hreniuk,D.L., Feighner,S.D., Palyha,O.C., Figueroa,D.J., Austin,C.P., Jiang,M.M., Yu,H., Ito,J., Ito,M., Ito,M., Guan,X.M., Kanatani,A., Van der ploeg,L.H.T. and Howard,A.D.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-MAY-2002) Metabolic Disorders, Merck & Co., Box 2000 80Y-265, Rahway, NJ 07065, USA				
FEATURES	Location/Qualifiers				
source	1. 1444				
gene	/organism="Macaca mulatta"				
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	107. 1168				
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ORIGIN	RAVSNAGTADERTESKGT"				
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Best Local Similarity	97.2%;	Pred. No. 9.2e-208;			
Matches 1135;	Conservative	0;	Mismatches 33;	Indels 0;	Gaps 0;
QY	102	GGCTTGCCTCCCGGACAAGGTGGCAGCGCTGAGAGCTGCCGACGCTGCGTGGGTGA	161		
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QY	162	GGGAGCTCAGCTCGGTGTGGGACGAGCGGACCGCACTGGCTGGATGGACCTGGAAGC	221		
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QY	222	CTCGCTGCTGCCCACTGTGTCCTATGCCAGACACACCTCTGATGGCCCCGATAACCTCAC	281		
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QY	282	TTCAGCAGATCACCTCTCTCGCACGGGAGCATCTCTTACATCAACATCATCATGCTTC	341		
Db	181	CTCGGACAGATCACCTCTCTCGCTCAGGGAGCGTCTCTTACATCAACATCATCATGCTTC	240		
QY	342	GGTGTGGGACCATCTGCTCTCTGGGCATCATCGGGAACCTCCAGGTCATCTTCGCGGT	401		
Db	241	GGTGTGGGACCATCTGCTCTCTGGGCATCATCGGGAACCTCCAGGTCATCTTCGCGGT	300		
QY	402	CGTGAAGAAGTCCAAGCTGCACCTGTTGCAACAACGTCGCCGACATCTTCATCATCAACCT	461		
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QY	462	CTCGGTAGTAGATCTCTCTTCTCTCTGGGCATGCCCTTCATGATCCACAGCTCATGGG	521		
Db	361	CTCGGTAGTAGATCTCTCTTCTCTCTGGGCATGCCCTTCATGATCCACAGCTCATGGG	420		
QY	522	CAATGGGCTGTGGCATTGGGGAGACCATGTGCACCCCTCATCATCAGGCCATGGATGCCAA	581		
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Db 481 TAGTCAGTTCACGACGACCTACATCTGACCCGCGCATGGCCATTTGACCGCTACCTGGCCAC 540
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QY 702 CCTCTGTGGGCGCTCTCTCTCATCAGCATCACCCCTGTGTGCTGTATGCCAGACTCAT 761
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QY 762 CCCCCTCCAGAGGAGTGCAGTGGGCTGGGCGCATACGCTTGCCCAACCCAGACACTGACTT 821
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RESULT 11
AX280739 1062 bp DNA linear PAT 02-NOV-2001
LOCUS AX280739
DEFINITION Sequence 362 from Patent WO0177172.
ACCESSION AX280739
VERSION AX280739.1 GI:16608110
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lehmann-Bruinsma,K., Liaw,C.W. and Lin,I.L.
TITLE Non-endogenous, constitutively activated known g protein-coupled
JOURNAL Patent: WO 0177172-A 362 18-OCT-2001;
FEATURES Arena Pharmaceuticals, Inc. (US)
source Location/Qualifiers
1.1062
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 201 a 369 c 253 g 239 t
ORIGIN

Query Match 83.4%; Score 1058.8; DB 6; Length 1062;
Best Local Similarity 99.8%; Pred. No. 9,7e-197;
Matches 1060; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY	1228	CAGACGGCTGACGAGAGAGACAGAAAGCAAGGCACCTGA	1269
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RESULT 12			
LOCUS	AX280743	1062 bp	DNA
DEFINITION	Sequence 366 from Patent WO0177172.		linear
ACCESSION	AX280743		PAT 02-NOV-2001
VERSION	AX280743.1	GI:16608113	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L.		
TITLE	Non-endogenous, constitutively activated known g protein-coupled receptors		
JOURNAL	Patent: WO 0177172-A 366 18-OCT-2001; Arena Pharmaceuticals, Inc. (US)		
FEATURES	Location/Qualifiers		
source	1.1062		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
BASE COUNT	200 a	368 c	254 g 240 t
ORIGIN			
Query Match	83.4%;	Score 1058.8;	DB 6; Length 1062;
Best Local Similarity	99.8%;	Pred. No. 9.7e-197;	
Matches 1060; Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;
QY	208	ATGGACCTGGAAGCCTCGCTGCTGCCACACTGGTCCCAATGCCAGACACACCTCTGATGGC	267
Db	1	ATGGACCTGGAAGCCTCGCTGCTGCCACACTGGTCCCAATGCCAGACACACCTCTGATGGC	60
QY	268	CCCGATAACCTCACTTCACGACGATCAACCTCTCGACACGGGGAGCATCTCTACATCAAC	327
Db	61	CCCGATAACCTCACTTCGGGACGATCAACCTCTCGACACGGGGAGCATCTCTACATCAAC	120
QY	328	ATCATCATGCTTCGGTGTCTGGACCACTGCTCTCTGGCATCATCGGGAACCTCCACG	387
Db	121	ATCATCATGCTTCGGTGTCTGGACCACTGCTCTCTGGCATCATCGGGAACCTCCACG	180
QY	388	GTCATCTTCGCGGTGCTGAAGAAGTCCAAAGCTGCACCTGTGCAACAACGTCGCCGACATC	447
Db	181	GTCATCTTCGCGGTGCTGAAGAAGTCCAAAGCTGCACCTGTGCAACAACGTCGCCGACATC	240
QY	448	TTTCATCATCAACCTCTCGGTAGTAGATCTCTCTCTCTCTGGCATCGCTTTCATGATC	507
Db	241	TTTCATCATCAACCTCTCGGTAGTAGATCTCTCTCTCTCTGGCATCGCTTTCATGATC	300
QY	508	CACCAAGCTCATGGGCAATGGGGTGTGGACCTTTGGGAGAACCATGTGCACCTCATCAGC	567
Db	301	CACCAAGCTCATGGGCAATGGGGTGTGGACCTTTGGGAGAACCATGTGCACCTCATCAGC	360
QY	568	GCCATGGATGCCAATAGTCAAGTTCACGACCACTTCCATCTGACCGCCATGGCCATTGAC	627
Db	361	GCCATGGATGCCAATAGTCAAGTTCACGACCACTTCCATCTGACCGCCATGGCCATTGAC	420
QY	628	CGCTACCTGGCCACTGTCCACCCCATCTCTCCACGAAGTTCGGGAAGCCCTGTGTGGCC	687
Db	421	CGCTACCTGGCCACTGTCCACCCCATCTCTCCACGAAGTTCGGGAAGCCCTGTGTGGCC	480
QY	688	ACCTGTGATCTGCTCTCTGTGGGCCCTCTCTTCATCAGCATCAACCCCTGTGTGGCTG	747
Db	481	ACCTGTGATCTGCTCTCTGTGGGCCCTCTCTTCATCAGCATCAACCCCTGTGTGGCTG	540
QY	748	TATGCCAGACTCATCCCTTCCAGAGAGGTGCAGTGGGCTGGGCATACGCGCTGCCCAAC	807
Db	541	TATGCCAGACTCATCCCTTCCAGAGAGGTGCAGTGGGCTGGGCATACGCGCTGCCCAAC	600

QY	808	CCAGACACTGACCTCTACTGGTTACCCCTGTACCAAGTTTTCCTGGCCCTTGCCCTGCCCT	867
Db	601	CCAGACACTGACCTCTACTGGTTACCCCTGTACCAAGTTTTCCTGGCCCTTGCCCTGCCCT	660
QY	868	TTTGTGTCATACAGCCGCATACGTGAGATCCTGCAGCGCATGACGTCTCAGTGGCC	927
Db	661	TTTGTGTCATACAGCCGCATACGTGAGATCCTGCAGCGCATGACGTCTCAGTGGCC	720
QY	928	CCCGCTCCAGCGCAGCATCCGGCTGGCGACAAGAGGGTGACCCGCACAGCCATCGCC	987
Db	721	CCCGCTCCAGCGCAGCATCCGGCTGGCGACAAGAGGGTGACCCGCACAGCCATCGCC	780
QY	988	ATCTGTCTGCTCTTCTTGTGTGCTGGGACCCCTACTATGTGCTACAGCTGACCCAGTTG	1047
Db	781	ATCTGTCTGCTCTTCTTGTGTGCTGGGACCTACTATGTGCTACAGCTGACCCAGTTG	840
QY	1048	TCCATCAGCCCGCCGACCCCTCACCCTTGTCTACTTATACAATGGCGCATCAGCTTGGGC	1107
Db	841	TCCATCAGCCCGCCGACCCCTCACCCTTGTCTACTTATACAATGGCGCATCAGCTTGGGC	900
QY	1108	TATGCCAACAGCTGCTCAACCCCTTGTGTACATCGTGTCTGTGAGACGTTCGCGAAA	1167
Db	901	TATGCCAACAGCTGCTCAACCCCTTGTGTACATCGTGTCTGTGAGACGTTCGCGAAA	960
QY	1168	CGCTTGGTCTCTGCTGCTGAAGCCTGCAGCCCGGAGGAGAGCTTCGCGCTGCAGCAACGCT	1227
Db	961	CGCTTGGTCTCTGCTGCTGAAGCCTGCAGCCCGGAGGAGAGCTTCGCGCTGCAGCAACGCT	1020
QY	1228	CAGACGGCTGACGAGAGAGACAGAAAGCAAGGCACCTGA	1269
Db	1021	CAGACGGCTGACGAGAGAGACAGAAAGCAAGGCACCTGA	1062
RESULT 13			
LOCUS	AX280747	1062 bp	DNA
DEFINITION	Sequence 370 from Patent WO0177172.		
ACCESSION	AX280747		
VERSION	AX280747.1	GI:16608116	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L.		
TITLE	Non-endogenous, constitutively activated known g protein-coupled receptors		
JOURNAL	Patent: WO 0177172-A 370 18-OCT-2001;		
FEATURES	Arena Pharmaceuticals, Inc. (US)		
source	1.1062		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
BASE COUNT	200 a	370 c	253 g 239 t
ORIGIN			
Query Match 83.4%; Score 1058.8; DB 6; Length 1062;			
Best Local Similarity 99.8%; Pred. No. 9.7e-197;			
Matches 1060; Conservative 0; Mismatches 2; Indels 0; Gaps 0			
QY	208	ATGACCTGGAAGCCTCGCTGCTGCCACTGTGCCAATGCCAGACACACCTCTGATGGC	267
Db	1	ATGACCTGGAAGCCTCGCTGCTGCCACTGTGCCAATGCCAGACACACCTCTGATGGC	60
QY	268	CCCGATAACCTCACTTCAGCAGATCAACCTCTCGACAGCGGAGAGCATCTCTACATCAAC	327
Db	61	CCCGATAACCTCACTTCGCGAGATCAACCTCTCGACAGCGGAGAGCATCTCTACATCAAC	120
QY	328	ATCATCATGCTTCGGTGTCTGGACACCATCTGCTCTGGGCATCATCGGGAACCTCAGC	387
Db	121	ATCATCATGCTTCGGTGTCTGGACACCATCTGCTCTGGGCATCATCGGGAACCTCAGC	180

QY	388	GTGATCTTCGGGTCGTGAAGAAGTCCAGCTGCACCTGGTGCAACAACGTCCCGACATC	447
Db	181	GTGATCTTCGGGTCGTGAAGAAGTCCAGCTGCACCTGGTGCAACAACGTCCCGACATC	240
QY	448	TTGATCATCAACCTCTCGGAGTAGATCTCTCTTCTCCTGGGCATGCCCTTCATGATC	507
Db	241	TTGATCATCAACCTCTCGGAGTAGATCTCTCTTCTCCTGGGCATGCCCTTCATGATC	300
QY	508	CACCAAGCTCATGGGCAATGGGGTGTGGCACTTTGGGGAGAGACCATTGCAACCCATCAGC	567
Db	301	CACCAAGCTCATGGGCAATGGGGTGTGGCACTTTGGGGAGAGACCATTGCAACCCATCAGC	360
QY	568	GCCATGGATGCCAATAGTCAGTTCACCAAGCACTTACATCCTGACCGCCATGGCCATTGAC	627
Db	361	GCCATGGATGCCAATAGTCAGTTCACCAAGCACTTACATCCTGACCGCCATGGCCATTGAC	420
QY	628	CGCTACCTGGCCACTGTCCACCCCATCTCTCCACGAAGTTCGGGAAGCCCTCTGTGGCC	687
Db	421	CGCTACCTGGCCACTGTCCACCCCATCTCTCTCCACGAAGTTCGGGAAGCCCTCTGTGGCC	480
QY	688	ACCGTGGTGTCTGCTCTCTGTGGCCCTCTCTTCATCAGCATCACCCTGTGTGGCTG	747
Db	481	ACCGTGGTGTCTGCTCTCTGTGGCCCTCTCTTCATCAGCATCACCCTGTGTGGCTG	540
QY	748	TATGCCAGACTCATCCCTTCCAGAGAGTGCAGTGGGCTGGCGCATACGCTGCCCAAC	807
Db	541	TATGCCAGACTCATCCCTTCCAGAGAGTGCAGTGGGCTGGCGCATACGCTGCCCAAC	600
QY	808	CCAGACACTGACCTCTACTGTGTTACCCCTGTACCAAGTTTTCCTGGCCCTTGCCCTGCC	867
Db	601	CCAGACACTGACCTCTACTGTGTTACCCCTGTACCAAGTTTTCCTGGCCCTTGCCCTGCC	660
QY	868	TTTGTGGTATCATCAGAGCCGATACGTGAGGATCCTGCAGCGCATGAGTCTCATGTGGCC	927
Db	661	TTTGTGGTATCATCAGAGCCGATACGTGAGGATCCTGCAGCGCATGAGTCTCATGTGGCC	720
QY	928	CCCGCCTCCAGCGGAGCATCCGGCTGCGGACAAGAAGGGTGACCCGCAAGCCATCGCC	987
Db	721	CCCGCCTCCAGCGGAGCATCCGGCTGCGGACAAGAAGGGTGACCCGCAAGCCATCGCC	780
QY	988	ATCTGTCTGTCTCTTTGTGTGTGGGCAACCTACTATGTGCTACAGCTGACCCAGTTG	1047
Db	781	ATCTGTCTGTCTCTTTGTGTGTGGGCAACCTACTATGTGCTACAGCTGACCCAGTTG	840
QY	1048	TCCATCAGCCGCGGACCCCTCACCCTTTGTGTACTTATACATGCGGCCATCAGCTTGGGC	1107
Db	841	TCCATCAGCCGCGGACCCCTCACCCTTTGTGTACTTATACATGCGGCCATCAGCTTGGGC	900
QY	1108	TATGCCAACAGCTGCCCTCAACCCCTTTGTGTACTTGTGAGACGTGTCCGCAAA	1167
Db	901	TATGCCAACAGCTGCCCTCAACCCCTTTGTGTACTTGTGAGACGTGTCCGCAAA	960
QY	1168	CGCTTGGTCTGTGCGGTGAAGCTTGACGCGCCAGGGGAGAGCTTCCGCTGTGAGCAACGCT	1227
Db	961	CGCTTGGTCTGTGCGGTGAAGCTTGACGCGCCAGGGGAGAGCTTCCGCTGTGAGCAACGCT	1020
QY	1228	CAGACGGCTGACGAGGAGAGGACAGAAAGCAAGGCAACCTGA	1269
Db	1021	CAGACGGCTGACGAGGAGAGGACAGAAAGCAAGGCAACCTGA	1062

RESULT 14
AX280755 1062 bp DNA linear PAT 02-NOV-2001
LOCUS AX280755 Sequence 378 from Patent WO0177172.
DEFINITION AX280755
ACCESSION AX280755
VERSION AX280755.1 GI:16608122
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1

AUTHORS Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L.
TITLE Non-endogenous, constitutively activated known g protein-coupled
JOURNAL receptors
Patent: WO 0177172-A 378 18-OCT-2001;
Arena Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1. 1062
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 200 a 369 c 253 g 240 t
ORIGIN

Query Match 83.4%; Score 1058.8; DB 6; Length 1062;
Best Local Similarity 99.8%; Pred. No. 9.7e-197;
Matches 1060; conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	208	ATGACCTGGAAGCCCTCGCTGCTGCCACTGTGCCAATGCCAGCAACACCTCTGATGGC	267
Db	1	ATGACCTGGAAGCCCTCGCTGCTGCCACTGTGCCAATGCCAGCAACACCTCTGATGGC	60
QY	268	CCCGATACCTCACTTCAGCAGATCACTCCTCGCAGGGGAGAGCATCTCCTACATCAAC	327
Db	61	CCCGATACCTCACTTCAGCAGATCACTCCTCGCAGGGGAGAGCATCTCCTACATCAAC	120
QY	328	ATCATCATGCCCTTCGGTGTTCGGCAACCATCTGCCCTCCTGGGCATCATCGGGAACCTCCACG	387
Db	121	ATCATCATGCCCTTCGGTGTTCGGCAACCATCTGCCCTCCTGGGCATCATCGGGAACCTCCACG	180
QY	388	GTGATCTTCGGGTCGTGAAGAAGTCCAAAGCTGCACATGCTGCAACAACGTCGCCGACATC	447
Db	181	GTGATCTTCGGGTCGTGAAGAAGTCCAAAGCTGCACATGCTGCAACAACGTCGCCGACATC	240
QY	448	TTGATCATCAACCTCTCGGTAGTAGATCTCCTTTCTCTGGGCATGCCCCCTTCATGATC	507
Db	241	TTGATCATCAACCTCTCGGTAGTAGATCTCCTTTCTCTGGGCATGCCCCCTTCATGATC	300
QY	508	CACCAAGCTCAGGGCAATGGGGTGTGGCACTTTGGGGAGAACCATGTGCACCCCTCATCAGC	567
Db	301	CACCAAGCTCAGGGCAATGGGGTGTGGCACTTTGGGGAGAACCATGTGCACCCCTCATCAGC	360
QY	568	GCCATGATGCCAATAGTCAAGTCAACCAAGCAACCTACATCTGACCGCCATGGCCATTGAC	627
Db	361	GCCATGATGCCAATAGTCAAGTCAACCAAGCAACCTACATCTGACCGCCATGGCCATTGAC	420
QY	628	CGCTACCTGGCCACTGTCCACCCCATCTCTCCACGAGAGTTCGGGAAGCCCTCTGTGGCC	687
Db	421	CGCTACCTGGCCACTGTCCACCCCATCTCTCTCCACGAGAGTTCGGGAAGCCCTCTGTGGCC	480
QY	688	ACCCTGTGATCTGCCCTCTGTGGGCCCCCTCTCTTCATCAGCATCACCCCTGTGTGGCTG	747
Db	481	ACCCTGTGATCTGCCCTCTGTGGGCCCCCTCTCTTCATCAGCATCACCCCTGTGTGGCTG	540
QY	748	TATGCCAGACTCATCCCTTCCAGAGAGGTGCAGTGGGCTGGGCATACGCGCTGCCCAAC	807
Db	541	TATGCCAGACTCATCCCTTCCAGAGAGGTGCAGTGGGCTGGGCATACGCGCTGCCCAAC	600
QY	808	CCAGACACTGACCTTACTGGTTCAACCTGTACCAAGTTTTCCTGGCCCTTGCCCTGCGCT	867
Db	601	CCAGACACTGACCTTACTGGTTCAACCTGTACCAAGTTTTCCTGGCCCTTGCCCTGCGCT	660
QY	868	TTTGTGGTATCAGAGCCGCAATAGTGAAGATCTGCAAGCCGATGAGCTCTCAGTGGCC	927
Db	661	TTTGTGGTATCAGAGCCGCAATAGTGAAGATCTGCAAGCCGATGAGCTCTCAGTGGCC	720
QY	928	CCCGCTCCAGCGGAGCATCCGGCTGCGGACAAGAAGGGTGACCCGCAAGCCATCGCC	987
Db	721	CCCGCTCCAGCGGAGCATCCGGCTGCGGACAAGAAGGGTGACCCGCAAGCCATCGCC	780
QY	988	ATCTGTCTGTCTCTTTGTGTGTGGGCAACCTACTATGTGCTACAGCTGACCCAGTTG	1047
Db	781	ATCTGTCTGTCTCTTTGTGTGTGGGCAACCTACTATGTGCTACAGCTGACCCAGTTG	840
QY	1048	TCCATCAGCCGCGGACCCCTCACCCTTTGTCTACTTATACAAATGCGGCATCAGCTTGGGC	1107

PF 30-DEC-1999; 99WO-US31169.
XX
PR 31-DEC-1998; 98US-0224426.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Salon JA, Laz TM, Nagorny R, Wilson AE;
XX
DR WPI; 2000-548644/50.
P-PSDB; AAB13436.
XX
PT Novel nucleic acid encoding human melanin concentrating hormone
PT receptor useful for treating cardiovascular disorders, hypertension and
PT diabetes, whose mutant form is activated by melanin concentrating
PT hormone -
XX
PS Claim 26; Fig 1; 173pp; English.

XX
CC Neuroregulators modulate communication in the nervous system. Melanin
CC concentrating hormone 1 (MCH1) is one such neuroregulator. MCH may serve
CC as an integrative neuropeptide, involved in stress response, feeding
CC regulation and sexual activity. Also, MCH is thought to participate in
CC water balance regulation, energy metabolism, general arousal/ attention
CC state, memory and cognitive functions and psychiatric disorders. The
CC present sequence is the coding sequence of human MCH1 receptor. MCH1
CC receptor is a G-protein coupled receptor. The present sequence may be
CC used in the therapy for a variety of disorders: steroid or pituitary
CC hormone disorder, epinephrine release disorder, gastrointestinal
CC disorder, cardiovascular disorder, electrolyte balance disorder,
CC hypertension, diabetes, respiratory disorder, asthma, reproductive
CC function disorder, immune disorder, endocrine disorder, musculoskeletal
CC disorder, neuroendocrine disorder, cognitive disorder, memory disorder,
CC e.g. Alzheimer's disease, sensory modulation and transmission disorder,
CC motor coordination disorder, sensory integration disorder, dopaminergic
CC function disorder e.g. Parkinson's disease, olfaction disorder,
CC sympathetic innervation disorder, depression, stress, fluid-imbalance
CC disorder, urinary disorder e.g. urinary incontinence, seizure, pain,
CC psychotic behaviour e.g. schizophrenia, morphine tolerance, opiate
CC addiction or migraine. The present sequence is also contained in plasmid
CC pEXJ.HR-TL231 (ATCC 203197).
XX

SQ Sequence 1269 BP; 234 A; 419 C; 347 G; 269 T; 0 other;

Query Match 100.0%; Score 1269; DB 21; Length 1269;
Best Local Similarity 100.0%; Pred. No. 3.4e-285;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCAGTGGAGCCATGAAGAAGGAGTGGGGGAGTGGGCTTGGAGCGGCAGC 60
Db 1 ATGTCAGTGGAGCCATGAAGAAGGAGTGGGGGAGTGGGCTTGGAGCGGCAGC 60
QY 61 GGTGCGCAGGCTACGAGAGAACCCCTTCCGACTGCGGGGCTTGCGTCCGGACAA 120
Db 61 GGTGCGCAGGCTACGAGAGAACCCCTTCCGACTGCGGGGCTTGCGTCCGGACAA 120
QY 121 GGTGGCAGGCGCTGAGGCTGCCGAGCCTGCGTGGGTGGAGGGAGCTCAGCTCGGTTG 180
Db 121 GGTGGCAGGCGCTGAGGCTGCCGAGCCTGCGTGGGTGGAGGGAGCTCAGCTCGGTTG 180
QY 181 TGGGACAGGCGGACCGGCACTGGCTGGATGACCTGGAAGCCTCGCTGCCCACTGGT 240
Db 181 TGGGACAGGCGGACCGGCACTGGCTGGATGACCTGGAAGCCTCGCTGCCCACTGGT 240
QY 241 CCCAATGCCAGCAACACCTCTGATGGCCCCGATTAACCTCACTTCAGCAGATCACTCCT 300
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QY 301 CGCAGGGGAGCATCTCTACATCAACATCATCATGCTTGGGTGTTGGGACCATCTGC 360
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Db 361 CTCCTGGGCATCATCGGAACCTCAGGGTGCATCTTGGCGGTGCTGAAGAAGTCCAGCTG 420
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QY 1261 GGCACCTGA 1269
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Db 1261 GGCACCTGA 1269
RESULT 2
ABK14548
ID ABK14548 standard; cDNA; 1269 BP.
XX
AC ABK14548;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human cDNA encoding melanin concentrating hormone receptor, MCH1.
XX

KW Human; ss; gene; melanin concentrating hormone receptor; MCH1;
KW steroid hormone disorder; pituitary hormone disorder;
KW epinephrine release disorder; gastrointestinal disorder;
KW cardiovascular disorder; hypertension; diabetes; respiratory disorder;
KW asthma; reproductive function disorder; immune disorder;
KW musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
KW memory disorder; motor coordination disorder; obesity; eating disorder;
KW dopaminergic function disorder; pain; psychosis; opiate addiction;
KW affective disorder; migraine; transgenic.

XX Homo sapiens.

OS Key Location/Qualifiers
FH CDS 1..1269
FT /*tag= a
FT /product= "MCH1"

XX WO200202744-A2.

XX 10-JAN-2002.

XX 05-JUL-2001; 2001WO-US21350.

XX 05-JUL-2000; 2000US-0610635.

XX (SYNA-) SYNAPTIC PHARM CORP.

XX Salon JA, Laz TM, Nagorny R, Wilson AE;

XX WPI: 2002-164532/21.

XX P-PSDB; AAU75853.

PT Purified human melanin concentrating hormone receptor protein and
PT polynucleotides for screening modulator useful for treating memory
PT disorder, sensory modulation and transmission disorder, motor
PT coordination disorder

XX Claim 2; Fig 1; 524pp; English.

CC The invention relates to a purified human melanin concentrating hormone
CC (MCH1) receptor protein and its encoding nucleic acid (or mutant
CC activated by MCH or its analogue or homologue). Also included are
CC expression vectors, probes, transformed insect cells, antisense
CC oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting
CC the binding of the antibody to MCH1, a transgenic animal expressing the
CC protein, or a homologous knockout or antisense complementary to the MCH1
CC nucleic acid, ant/agonists of MCH1, and methods of isolating chemical
CC compounds which activate MCH1. The protein, nucleic acid, antibody,
CC ant/agonists and compound are useful for diagnosing and treating a
CC steroid or pituitary hormone disorder, an epinephrine release disorder, a
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder, sensory modulation and transmission disorder, motor
CC coordination disorder, sensory integration disorder, motor integration
CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder,
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC encodes human MCH1.

XX Sequence 1269 BP; 234 A; 419 C; 347 G; 269 T; 0 other;

Query Match 100.0%; Score 1269; DB 24; Length 1269;
Best Local Similarity 100.0%; Pred. No. 3.4e-285;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCAGTGGAGCCATGAAGAAGGAGTGGGAGGGCAGTTGGGCTTGAGGCGGCAGC 60
Db 1 ATGTCAGTGGAGCCATGAAGAAGGAGTGGGAGGGCAGTTGGGCTTGAGGCGGCAGC 60

QY 61 GGCTGCCAGGCTACGGAGAGAACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGACAA 120
Db 61 GCGTCCAGGCTACGGAGAGAACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGACAA 120
QY 121 GGTGGCAGGCGCTGGAGGCTGCCGAGCCTGCGTGGGTGAGAGGGAGCTCAGCTCGGTTG 180
Db 121 GGTGGCAGGCGCTGGAGGCTGCCGAGCCTGCGTGGGTGAGAGGGAGCTCAGCTCGGTTG 180
QY 181 TGGGAGCAGGCGACCGGCACTGGCTGGATGAGACCTGGAAGCCTCGCTGCGCCACTGGT 240
Db 181 TGGGAGCAGGCGACCGGCACTGGCTGGATGAGACCTGGAAGCCTCGCTGCGCCACTGGT 240
QY 241 CCCAATGCCAGCAACACACCTCTGATGGCCCCGATTAACCTCACTTCAGAGATCACCTCTC 300
Db 241 CCCAATGCCAGCAACACACCTCTGATGGCCCCGATTAACCTCACTTCAGAGATCACCTCTC 300
QY 301 CGCAGCGGAGCATCTCTCTACATCAACATCATCATGCGCTTCGGTGTTCGGCACCACTCGC 360
Db 301 CGCAGCGGAGCATCTCTCTACATCAACATCATCATGCGCTTCGGTGTTCGGCACCACTCGC 360
QY 361 CTCCTGGGCATCATCGGGAACCTCCACGGTCACTCTCGCGGTGCTGAAGAAGTCCAAGCTG 420
Db 361 CTCCTGGGCATCATCGGGAACCTCCACGGTCACTCTCGCGGTGCTGAAGAAGTCCAAGCTG 420
QY 421 CACTGGTGCAACAACAGCTCCCGGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTC 480
Db 421 CACTGGTGCAACAACAGCTCCCGGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTC 480
QY 481 TTTCTCTGGGCATGCCCTTTCATGATCCACAGCTCATGGGCAATGGGGTGTGGCACTTT 540
Db 481 TTTCTCTGGGCATGCCCTTTCATGATCCACAGCTCATGGGCAATGGGGTGTGGCACTTT 540
QY 541 GGGGAGACCATGTGCAACCTTCATCAACGGCCATGATGCAATAGTCACTTCCACAGCACC 600
Db 541 GGGGAGACCATGTGCAACCTTCATCAACGGCCATGATGCAATAGTCACTTCCACAGCACC 600
QY 601 TACATCCTGAACCGCATGGCCATGTAACCGCTACCTGGCCACTGTGCCACCCCACTCTTCC 660
Db 601 TACATCCTGAACCGCATGGCCATGTAACCGCTACCTGGCCACTGTGCCACCCCACTCTTCC 660
QY 661 ACGAAGTTCGGGAAGCCCTGTGTGGCCACCCCTGTGATCTGCTCTGCGCCCTCTCC 720
Db 661 ACGAAGTTCGGGAAGCCCTGTGTGGCCACCCCTGTGATCTGCTCTGCGCCCTCTCC 720
QY 721 TTCAATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGGTGCA 780
Db 721 TTCAATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGGTGCA 780
QY 781 GTGGGCTCGGCATACGCCCTGTGCCCAACCCAGACACTGACCTTACTGGTTACCCCTGTAC 840
Db 781 GTGGGCTCGGCATACGCCCTGTGCCCAACCCAGACACTGACCTTACTGGTTACCCCTGTAC 840
QY 841 CAGTTTTTCTGGCCTTTGGCCTGCTTTTGTGTCATCACAGCCGATACGTGAGGATC 900
Db 841 CAGTTTTTCTGGCCTTTGGCCTGCTTTTGTGTCATCACAGCCGATACGTGAGGATC 900
QY 901 CTGCAGCGCATGACGTCTCTCAGTGGCCCCCGGCTCCAGCGAGCATCCGGCTGCGGACA 960
Db 901 CTGCAGCGCATGACGTCTCTCAGTGGCCCCCGGCTCCAGCGAGCATCCGGCTGCGGACA 960
QY 961 AAGAGGCTGACCCGACAGCCATCGCCATCTGTCTGTCTTCTTGTGTGGGCAACC 1020
Db 961 AAGAGGCTGACCCGACAGCCATCGCCATCTGTCTGTCTTCTTGTGTGGGCAACC 1020
QY 1021 TACTATGTGTACAGCTGACCCAGTGTGCCATCAGCCGCGGACCCCTACCTTTGTCTAC 1080
Db 1021 TACTATGTGTACAGCTGACCCAGTGTGCCATCAGCCGCGGACCCCTACCTTTGTCTAC 1080
QY 1081 TTATACATATGCGGCCATCAGCTTGGGCTATGCGCAACAGCTGCCTCAACCCCTTTGTGTAC 1140
Db 1081 TTATACATATGCGGCCATCAGCTTGGGCTATGCGCAACAGCTGCCTCAACCCCTTTGTGTAC 1140
QY 1141 ATCGTGCTGTGTAGAGCGTTCCGCAACGCTTGGTCTGTGTGGAAGCCTGACGCCAG 1200

|||||
Db 1141 ATCGTCTGTGTAGACGTTCCGCAACCGCTGTCTGTGCGGTGAAGCCTGCAGCCAG 1200
QY 1201 GGGCAGCTTGGCGGTGTCAACAACGCTCAGACGGCTGACGAGGAGAGAGAGAAAGCAAA 1260
Db 1201 GGGCAGCTTGGCGGTGTCAACAACGCTCAGACGGCTGACGAGGAGAGAGAGAAAGCAAA 1260
QY 1261 GGCACCTGA 1269
Db 1261 GGCACCTGA 1269
RESULT 3
AADI3654
ID AADI3654 standard; cDNA; 1269 BP.
XX AADI3654;
AC
XX
DT 06-NOV-2001 (first entry)
XX
DE Human melanin-concentrating hormone receptor variant #3 cDNA.
XX
KW Human; melanin-concentrating hormone; MCH analogue; signal transduction;
KW appetite; therapy; anorexia; acquired immune deficiency syndrome; AIDS;
KW wasting; cachexia; frail elderly; weight maintenance; cancer; anorectic;
KW pain reduction; stress reduction; sexual dysfunction; variant; ss.
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1..1269
FT CDS /*tag= a
FT /product= "Human MCH receptor protein variant #3"
XX
PN WO200157070-A1.
XX
PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001WO-US03293.
XX
PR 03-FEB-2000; 2000US-0179967.
XX
PA (MERI) MERCK & CO INC.
XX
PI Bednarek M;
XX
DR MPI; 2001-483416/52.
DR P-PSDB; AAE07330.
XX
PT Novel peptide encoding a melanin-concentrating hormone analog useful
PT for increasing weight or appetite
XX
XX Disclosure; Page 33; 66pp; English.
XX
XX The present invention relates to truncated melanin-concentrating hormone
CC (MCH) analogues active at the MCH receptor. The truncated MCH analogues
CC are optionally modified peptide derivatives of mammalian MCH. The MCH
CC analogues can bind to the MCH receptor and bring about signal
CC transduction. The MCH agonists can be used to facilitate a weight gain,
CC maintenance of weight and/or an appetite increase. The MCH agonists can
CC also be used to treat disorders such as anorexia, acquired immune
CC deficiency syndrome (AIDS), wasting, cachexia and frail elderly. The MCH
CC antagonists can be used to facilitate weight loss, appetite decrease,
CC weight maintenance, cancer treatment, pain reduction, stress reduction
CC and/or treatment of sexual dysfunction. The present sequence is a human
CC MCH receptor variant cDNA.
XX
SQ Sequence 1269 BP; 234 A; 420 C; 347 G; 268 T; 0 other;

QY 1 ATGTCAAGTGGAGACCATGAAGAAGGAGTGGGAGGCAAGTTGGCTTGGAGCGCGCAGC 60
Db 1 ATGTCAAGTGGAGACCATGAAGAAGGAGTGGGAGGCAAGTTGGCTTGGAGCGCGCAGC 60
QY 61 GCGTGGCAGGCTACGGAGAGAACCCCTTCCCGACTGCGGGGCTTGGCGTCCGGGACAA 120
Db 61 GCGTGGCAGGCTACGGAGAGAACCCCTTCCCGACTGCGGGGCTTGGCGTCCGGGACAA 120
QY 121 GGTGGCAGGCGCTGGAGGCTGCCGACGCTGCGTGGGTGGAGGGAGCTCAGCTCGGTTG 180
Db 121 GGTGGCAGGCGCTGGAGGCTGCCGACGCTGCGTGGGTGGAGGGAGCTCAGCTCGGTTG 180
QY 181 TGGAGCAGCGGACCGGACCTGGCTGGATGGACCTGGAGCCTCGCTGCTGCCACTGTT 240
Db 181 TGGAGCAGCGGACCGGACCGGACCTGGCTGGATGGACCTGGAGCCTCGCTGCTGCCACTGTT 240
QY 241 CCCAATGCCAGCAACACCTGTGATGGCCCCGATAACCTCACTTCAGCAGATCAGCTCCT 300
Db 241 CCCAATGCCAGCAACACCTGTGATGGCCCCGATAACCTCACTTCAGCAGATCAGCTCCT 300
QY 301 CGCACGGGAGCATCTCCTACATCAACATCATCATGCTTGGGTGTTGGCACATCTGC 360
Db 301 CGCACGGGAGCATCTCCTACATCAACATCATCATGCTTGGGTGTTGGCACATCTGC 360
QY 361 CTCTGGGCAATCATCGGGAATCTCAAGGTATCTTGGCGGTGTTGAAGAAGTCCAAGCTG 420
Db 361 CTCTGGGCAATCATCGGGAATCTCAAGGTATCTTGGCGGTGTTGAAGAAGTCCAAGCTG 420
QY 421 CACTGGTGCAACAACAGTCCCGGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTC 480
Db 421 CACTGGTGCAACAACAGTCCCGGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTC 480
QY 481 TTTCTCTGGGCAATGCCCCCTTCATGATCCACAGCTCATGGGCAATGGGGTGTGGCACTT 540
Db 481 TTTCTCTGGGCAATGCCCCCTTCATGATCCACAGCTCATGGGCAATGGGGTGTGGCACTT 540
QY 541 GGGAGACCAATGTGCACCCCTCATCAAGGCGCATGATGCCAATAGTCAAGTTCAACGACAC 600
Db 541 GGGAGACCAATGTGCACCCCTCATCAAGGCGCATGATGCCAATAGTCAAGTTCAACGACAC 600
QY 601 TACATCCTGACCCGCCATGGCCATGACCCGCTACCTGGCCACTGTCCACCCCATCTCTCC 660
Db 601 TACATCCTGACCCGCCATGGCCATGACCCGCTACCTGGCCACTGTCCACCCCATCTCTCC 660
QY 661 ACGAAGTTCGGGAAGCCCTGTGTGGCCACCCCTGGTGTATCTGCTCTGCGCCCTCTCC 720
Db 661 ACGAAGTTCGGGAAGCCCTGTGTGGCCACCCCTGGTGTATCTGCTCTGCGCCCTCTCC 720
QY 721 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGGAGGTGCA 780
Db 721 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGGAGGTGCA 780
QY 781 GTGGCTGGCGCATAGCGCTGCGCCAAACCCAGACACTGACCTCTACTGGTTCAACCTGTAC 840
Db 781 GTGGCTGGCGCATAGCGCTGCGCCAAACCCAGACACTGACCTCTACTGGTTCAACCTGTAC 840
QY 841 CAGTTTTCCTGGCCCTTGGCCCTTTGTGTGTCATCAGAGCCGATACGTGAGGATC 900
Db 841 CAGTTTTCCTGGCCCTTGGCCCTTTGTGTGTCATCAGAGCCGATACGTGAGGATC 900
QY 901 CTGACGCGCATGACGTCTCAGTGGCCCCCGCTCCACGCGAGCATCCGGCTGGCGACA 960
Db 901 CTGACGCGCATGACGTCTCAGTGGCCCCCGCTCCACGCGAGCATCCGGCTGGCGACA 960
QY 961 AAGAGGGTGAGCCCGCACAGCCATCGCCATCTGTCTGTGTTCTTTGTGTGTGGGACCC 1020
Db 961 AAGAGGGTGAGCCCGCACAGCCATCGCCATCTGTCTGTGTTCTTTGTGTGTGGGACCC 1020
QY 1021 TACTATGTGCTACAGCTGACCCAGTTGTTCATCAGCCGCGCGGACCCCTACCTTTGTCTAC 1080
Db 1021 TACTATGTGCTACAGCTGACCCAGTTGTTCATCAGCCGCGCGGACCCCTACCTTTGTCTAC 1080

QY 1081 TTATACAATGCGGCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTGTGTAC 1140
|||||
Db 1081 TTATACAATGCGGCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTGTGTAC 1140
QY 1141 ATCGTCTCTGTGAGACGTTCCGCAACGCTTGGTCTGTGGTGAAGCCTGCAGCCAG 1200
|||||
Db 1141 ATCGTCTCTGTGAGACGTTCCGCAACGCTTGGTCTGTGGTGAAGCCTGCAGCCAG 1200
QY 1201 GGGCAGCTTCGCGCTGTACAGACGCTCAGACGGCTGACGAGAGAGACAGAAAGCAAA 1260
|||||
Db 1201 GGGCAGCTTCGCGCTGTACAGACGCTCAGACGGCTGACGAGAGAGACAGAAAGCAAA 1260
QY 1261 GGCACCTGA 1269
|||||
Db 1261 GGCACCTGA 1269

RESULT 4
AAA91189
ID AAA91189 standard; DNA; 1269 BP.

XX AAA91189;
XX 08-MAY-2001 (first entry)
XX Human MCH-R3 coding sequence.
DE
XX
XX Human; melanin-concentrating hormone receptor; MCH-R1; MCH-R2; MCH-R3;
KW weight loss; weight gain; cancer; pain; diabetes; stress; therapy;
KW sexual dysfunction; ds.
XX
XX Homo sapiens.
OS

Key Location/Qualifiers
FT CDS 1..1269
FT /*tag= a
FT /product= "MCH-R3"

WO200105947-A1.

PD 25-JAN-2001.
XX
XX 10-JUL-2000; 2000WO-US18733.
PF
XX 14-JUL-1999; 99US-0143706.
PR
XX (MERI) MERCK & CO INC.
XX
PI Howard AD;
XX
XX WPI: 2001-159528/16.
DR P-PSDB; AAY97670.
XX

PT Melanin-concentrating hormone receptor polypeptides for increasing or
PT decreasing appetite, reducing stress and to screen for compounds that
PT bind to the receptor -

XX Claim 7; Page 22; 43pp; English.

CC This sequence encodes a melanin-concentrating hormone (MCH) receptor
CC protein of the invention, designated MCH-R3. MCH receptor fragments and
CC polypeptides are useful in assays to screen for compounds that bind to
CC the MCH receptor and modulate the activity of the receptor. MCH Receptor
CC activity is modulated to achieve weight loss, weight gain, to treat
CC cancer (e.g. colon or breast), reduce pain, treat diabetes, reduce stress
CC or treat sexual dysfunction. Nucleic acid coding for the MCH receptor can
CC be used to cause an increase in appetite and to create a test system
CC (e.g. a transgenic animal) for screening for compounds affecting MCH
CC receptor expression. Inhibition of MCH receptor nucleic acid activity is
CC useful to inhibit appetite or stress.

XX Sequence 1269 BP; 234 A; 420 C; 347 G; 268 T; 0 other;

Query Match 99.6%; Score 1264.2; DB 22; Length 1269;
Best Local Similarity 99.8%; Pred. No. 4.4e-284;
Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGTACAGTGGAGCCATGAAGAAGGAGTGGGAGGCGAGTTGGGCTTGGAGCGGCAGC 60
|||||
Db 1 ATGTACAGTGGAGCCATGAAGAAGGAGTGGGAGGCGAGTTGGGCTTGGAGCGGCAGC 60
QY 61 GGCTGCCAGGCTACGGAGGAAGACCCCTTCCCGACTGCGGGGCTTGGCTCCGGACAA 120
|||||
Db 61 GGCTGCCAGGCTACGGAGGAAGACCCCTTCCCAACTGCGGGGCTTGGCTCCGGACAA 120
QY 121 GGTGGCAGGCGCTGGAAGGCTCCCGCAGCCTGCGTGGGTGAGGGGAGCTCAGCTCGGTTG 180
|||||
Db 121 GGTGGCAGGCGCTGGAAGGCTCCCGCAGCCTGCGTGGGTGAGGGGAGCTCAGCTCGGTTG 180
QY 181 TGGGAGCAGGCGGACCGGCACTGGCTGGATGGAACCTGGAAGCCTGCTGCTGCCACTGGT 240
|||||
Db 181 TGGGAGCAGGCGGACCGGCACTGGCTGGATGGAACCTGGAAGCCTGCTGCTGCCACTGGT 240
QY 241 CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCATTGACAGGATCACCTTCCT 300
|||||
Db 241 CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCATTGACAGGATCACCTTCCT 300
QY 301 CGCAGCGGAGCATCTCCTACATCAACATCATCATGCTTCGGTGTGGCACCATCTGC 360
|||||
Db 301 CGCAGCGGAGCATCTCCTACATCAACATCATCATGCTTCGGTGTGGCACCATCTGC 360
QY 361 CTCCTGGGCATCATCGGGAAGCTCCAGGTCATCTTCGGCGTGTGAAGAAGTCCAAGCTG 420
|||||
Db 361 CTCCTGGGCATCATCGGGAAGCTCCAGGTCATCTTCGGCGTGTGAAGAAGTCCAAGCTG 420
QY 421 CACTGTGCAACAACAGCTCCCGGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTC 480
|||||
Db 421 CACTGTGCAACAACAGCTCCCGGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTC 480
QY 481 TTTCTCTGGGCATGCCCCCTTCATGATCCACAGCTCATGGGCAATGGGGTGTGGCACTTT 540
|||||
Db 481 TTTCTCTGGGCATGCCCCCTTCATGATCCACAGCTCATGGGCAATGGGGTGTGGCACTTT 540
QY 541 GGGAGACCATGTGCACCCCTCATGACGGCCATGGATGCCAATGTCAGTTCAACAGCACC 600
|||||
Db 541 GGGAGACCATGTGCACCCCTCATGACGGCCATGGATGCCAATGTCAGTTCAACAGCACC 600
QY 601 TACATCCTGACCGGCATGGCCATTGACCGGTACCTGGCCACTGTGCCAACCCTCTTCC 660
|||||
Db 601 TACATCCTGACCGGCATGGCCATTGACCGGTACCTGGCCACTGTGCCAACCCTCTTCC 660
QY 661 ACGAGTTCCGGGAAGCCCTGTGAGCCACCCCTGGTATGTGCCCTGTGGCCCTCTCC 720
|||||
Db 661 ACGAGTTCCGGGAAGCCCTGTGAGCCACCCCTGGTATGTGCCCTGTGGCCCTCTCC 720
QY 721 TTTCATCAGCATCACCCCTGTGTGCTGTATGCCAGACTCATCCCTTCCAGAGAGGTGA 780
|||||
Db 721 TTTCATCAGCATCACCCCTGTGTGCTGTATGCCAGACTCATCCCTTCCAGAGAGGTGA 780
QY 781 GTGGGCTGGGCATACGCGCTGCCCCAACCCAGACACTGACCTCTACTGTTCAACCCTGTAC 840
|||||
Db 781 GTGGGCTGGGCATACGCGCTGCCCCAACCCAGACACTGACCTCTACTGTTCAACCCTGTAC 840
QY 841 CAGTTTTTCTGCGCTTGGCCTTGCCCTTTTGTGTGTCATCAGACCCGATACGTGAGATC 900
|||||
Db 841 CAGTTTTTCTGCGCTTGGCCTTGCCCTTTTGTGTGTCATCAGACCCGATACGTGAGATC 900
QY 901 CTGCAGCGCATGACGTCTCTAGTGGCCCCCGCCTCCCAAGCGAGCATCCGGCTGCGGACA 960
|||||
Db 901 CTGCAGCGCATGACGTCTCTAGTGGCCCCCGCCTCCCAAGCGAGCATCCGGCTGCGGACA 960
QY 961 AAGAGGGTGACCCGACAGCCATCGCCATCTGTCTGTGTTCTTTGTGTGCTGGGACCC 1020
|||||
Db 961 AAGAGGGTGACCCGACAGCCATCGCCATCTGTCTGTGTTCTTTTGTGTGCTGGGACCC 1020
QY 1021 TACTATGTGCTACAGCTGACCAGTTGTCCATCAGCCGCGGACCCCTCACCCTTTGTCTAC 1080

|||||
Db 1021 TACTATGTGCTACAGCTGACCCAGTGTTCATCAGCCGCCGACCCCTCACCCTTGTCTAC 1080
OY 1081 TTATACAAATGCGGCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTGTGTAC 1140
Db 1081 TTATACAAATGCGGCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTGTGTAC 1140
OY 1141 ATGTGCTCTGTGAGACGTTCCGCAACGCTTGGTCTGCTGGTGAAAGCCTGACGCCAG 1200
Db 1141 ATGTGCTCTGTGAGACGTTCCGCAACGCTTGGTCTGCTGGTGAAAGCCTGACGCCAG 1200
OY 1201 GGGCAGCTTCGCGCTGTACAGCAAGCTCAGACGGCTGACGAGGAGAGACAGAAAGCAAA 1260
Db 1201 GGGCAGCTTCGCGCTGTACAGCAAGCTCAGACGGCTGACGAGGAGAGACAGAAAGCAAA 1260
OY 1261 GGCACCTGA 1269
Db 1261 GGCACCTGA 1269

RESULT 5
AAH47297 standard; cDNA; 1269 BP.
ID AAH47297 standard; cDNA; 1269 BP.
XX AAH47297;
AC
XX 30-NOV-2001 (first entry)
DT
XX Human long form MCH1R cDNA.
DE
XX Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion;
KW fluorescent polypeptide; orexigenic; anabolic; food intake; MCH1R; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 1..1269
FT /*tag= a
XX WO200168706-A1.
PN 20-SEP-2001.
PD
XX 14-MAR-2001; 2001WO-US08071.
PF
XX 15-MAR-2000; 2000US-0189698.
PR
XX (MERI) MERCK & CO INC.
PA
XX Marsh DJ;
PI
XX WPI; 2001-565791/63.
DR P-PSDB; AAB85894.
DR
XX Fusion proteins comprising melanin concentrating hormone receptor
PT peptides and fluorescent proteins, useful for identifying appetite
PT stimulants -
PS Example 1; Page 17-18; 71pp; English.
XX
CC The invention provides melanin concentrating hormone (MCH) receptor
CC (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise
CC MCHR polypeptide regions from different species. The MCHR fusion protein
CC comprise MCHR polypeptide region and a fluorescent polypeptide region
CC joined directly, or via a linker, to the carboxy side of the MCHR
CC polypeptide region. The MCHR fusion proteins can be expressed by standard
CC recombinant methodology. MCH action promotes feeding (orexigenic) and up
CC regulation of MCH activity stimulates food intake. The present sequence
CC represents a human long form MCH1R cDNA.
XX
SQ Sequence 1269 BP; 234 A; 420 C; 347 G; 268 T; 0 other;

Query Match 99.6%; Score 1264.2; DB 22; Length 1269;

Best Local Similarity 99.8%; Pred. No. 4.4e-284;
Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 ATGTACAGTGGAGCCATGAAGAGGAGTGGGAGGGCAGTTGGCTTGGAGCGGAGC 60
Db 1 ATGTACAGTGGAGCCATGAAGAGGAGTGGGAGGGCAGTTGGCTTGGAGCGGAGC 60
OY 61 GGCTGCCAGGCTACGGAGGAAGACCCCTTCCGACTGCCGGGCTTGGCTCCGGAGCAA 120
Db 61 GGCTGCCAGGCTACGGAGGAAGACCCCTTCCGACTGCCGGGCTTGGCTCCGGAGCAA 120
OY 121 GGTGGCAGGCGCTGAGAGGCTGCGCAGCCTGCGTGGGTGAGAGGAGAGCTCAGCTCGTTG 180
Db 121 GGTGGCAGGCGCTGAGAGGCTGCGCAGCCTGCGTGGGTGAGAGGAGAGCTCAGCTCGTTG 180
OY 181 TGGAGCAGGCGACCGGCACCTGGCTGGATGACCTGGAAGCCTGCTGCTGCCACTGGT 240
Db 181 TGGAGCAGGCGACCGGCACCTGGCTGGATGACCTGGAAGCCTGCTGCTGCCACTGGT 240
OY 241 CCCAATGCCAGCAACACCTCTGATGGCCCGGATTAACCTCACTTCAGCAGATCACCTCCT 300
Db 241 CCCAATGCCAGCAACACCTCTGATGGCCCGGATTAACCTCACTTCAGCAGATCACCTCCT 300
OY 301 CGCAGCGGGAGCATCTCTACATCAACATCATCATGCTTCGGTGTTCGGCACCATTGC 360
Db 301 CGCAGCGGGAGCATCTCTACATCAACATCATCATGCTTCGGTGTTCGGCACCATTGC 360
OY 361 CTCCTGGGCATATCGGGAACCTCCACGGTCACTTCGCGGTCGTGAAGAAGTCCAAAGCTG 420
Db 361 CTCCTGGGCATATCGGGAACCTCCACGGTCACTTCGCGGTCGTGAAGAAGTCCAAAGCTG 420
OY 421 CACTGTGCAACACGTCGCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTC 480
Db 421 CACTGTGCAACACGTCGCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTC 480
OY 481 TTTCTCTGGGCATGCCCTTCATGATGACCAAGCTCATGAGGCAATGGGTGTGGCACTTT 540
Db 481 TTTCTCTGGGCATGCCCTTCATGATGACCAAGCTCATGAGGCAATGGGTGTGGCACTTT 540
OY 541 GGGAGACCAATGCAACCCCTCATCAGCGCCATGATGCCAATAGTCAAGTTCACCAGACAC 600
Db 541 GGGAGACCAATGCAACCCCTCATCAGCGCCATGATGCCAATAGTCAAGTTCACCAGACAC 600
OY 601 TACATCCTGACCGCCATGCGCATTTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC 660
Db 601 TACATCCTGACCGCCATGCGCATTTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC 660
OY 661 ACGAAGTTCGGGAAGCCCTCTGTGGCCACCCCTGGTATCTGCTCTGTGGCCCTCTCC 720
Db 661 ACGAAGTTCGGGAAGCCCTCTGTGGCCACCCCTGGTATCTGCTCTGTGGCCCTCTCC 720
OY 721 TTCATCAGCATCAACCCCTGTGTGGCTGTATGCCAGACTCATGCCCTTCCAGAGGTGCA 780
Db 721 TTCATCAGCATCAACCCCTGTGTGGCTGTATGCCAGACTCATGCCCTTCCAGAGGTGCA 780
OY 781 GTGGGCTGGGCATACGCTTGCCCAACCCAGACACTGACCTCTACTGTTCAACCTGTAC 840
Db 781 GTGGGCTGGGCATACGCTTGCCCAACCCAGACACTGACCTCTACTGTTCAACCTGTAC 840
OY 841 CAGTTTTTCTGGCCTTGGCCCTGCTTGTGTGTCATCACAGCGCATACGTGAGGATC 900
Db 841 CAGTTTTTCTGGCCTTGGCCCTGCTTGTGTGTCATCACAGCGCATACGTGAGGATC 900
OY 901 CTGACGCGATGAGCTCTCAGTGGCCCGGCTCCAGCGCAGCAATCCGGCTGCGGACA 960
Db 901 CTGACGCGATGAGCTCTCAGTGGCCCGGCTCCAGCGCAGCAATCCGGCTGCGGACA 960
OY 961 AAGAGGTGACCCGACACAGCCATCGCCATCTGTCTTGTGTGTGCTGGCACCC 1020
Db 961 AAGAGGTGACCCGACACAGCCATCGCCATCTGTCTTGTGTGTGCTGGCACCC 1020
OY 1021 TACTATGTGCTACAGCTGACCCAGTTGTTCATCAGCCGCCGACCCCTCACCCTTGTCTAC 1080
Db 1021 TACTATGTGCTACAGCTGACCCAGTTGTTCATCAGCCGCCGACCCCTCACCCTTGTCTAC 1080

Db 1021 TACTATGTGCTACAGCTGACCCAGTGTGTCATCAGCCGCCGACCCTCACCTTTGTCTAC 1080
QY 1081 TTATACATGCGGCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTTGTGTAC 1140
Db 1081 TTATACATGCGGCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTTGTGTAC 1140
QY 1141 ATCGTCTCTGTGAGAGCTTCCGCAACGCTTGGTCTGTGCGTGAAGCCTGCAGCCAG 1200
Db 1141 ATCGTCTCTGTGAGAGCTTCCGCAACGCTTGGTCTGTGCGTGAAGCCTGCAGCCAG 1200
QY 1201 GGGCAGCTTGGGCTGTCAACAACGCTCAGACGGCTGACGAGAGAGAGACAGAAAGCAA 1260
Db 1201 GGGCAGCTTGGGCTGTCAACAACGCTCAGACGGCTGACGAGAGAGAGAGACAGAAAGCAA 1260
QY 1261 GGCACCTGA 1269
Db 1261 GGCACCTGA 1269

RESULT 6
AAA72918
ID AAA72918 standard; cDNA; 1275 BP.

AC AAA72918;
XX
DT 22-NOV-2000 (first entry)
XX

DE Human SLC-1 cDNA sequence SEQ ID NO:10.
XX

KW SLC-1; MHC; melanin concentrating hormone; screening; eating;
KW appetite stimulator; appetite regulator; period pain; atonic bleeding;
KW caesarean section; milk congestion; antibiotic agent; drug;
KW foetal asphyxia; cervical rupture; premature birth; uterine rupture;
KW Prader-Willi syndrome; anorectic; gynaecological; abortifaciant;
KW antoanaemia; anabolic; orphan G protein-couple receptor protein; ss.
XX

OS Homo sapiens.
XX

PN WO200040725-A1.
XX

PD 13-JUL-2000.
XX

XX 27-DEC-1999; 99WO-JP07336.
PF

XX 28-DEC-1998; 98JP-0374454.
PR

PR 28-APR-1999; 99JP-0122688.
PR

PR 02-SEP-1999; 99JP-0249300.
PR

XX (TAKE) TAKEDA CHEM IND LTD.
PA

XX Mori M, Shimomura Y, Takekawa S, Sugo T, Ishibashi Y, Kitada C;
PI Suzuki N;
PI

XX WPI: 2000-475832/41.
DR P-PSDB; AAB12779.
DR

XX Screening methods for compounds as SLC-1 (ant)agonists useful in the
PT treatment of eating disorders and as preventives and remedies for e.g.
PT atonic bleeding and Prader-Willi syndrome -
PT

XX Example 8; Page 110-111; 123pp; Japanese.
PS

XX The present invention describes a method for screening components (I) or
CC their salts that can alter the binding properties of melanin-
CC concentrating hormone (MCH) or its derivative or salt to SLC-1 or its
CC salt. Compounds identified by (I) are useful as SLC-1 (ant)agonists in
CC eating disorders and as preventives and remedies for e.g. period pains,
CC uterine recovery failure, caesarean section, artificial interruption of
CC pregnancy, galactostosis, tonic uterine contraction, foetal asphyxia,
CC rupture of uterus, cervical rupture, premature birth and Prader-Willi
CC syndrome. The present sequence represents the human SLC-1 cDNA sequence,
CC which is used in an example from the present invention.
XX

SQ Sequence 1275 BP; 235 A; 420 C; 350 G; 270 T; 0 other;

Query Match 99.6%; Score 1264.2; DB 21; Length 1275;
Best Local Similarity 99.8%; Pred. No. 4.4e-284;
Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGTCAGTGGAGCCATGAGAAGGAGTGGGAGGCGAGTGGGCTTGGAGCGGACG 60
Db 7 ATGTCAGTGGAGCCATGAGAAGGAGTGGGAGGCGAGTGGGCTTGGAGCGGACG 66
QY 61 GGCTGCCAGGCTACGGAAGAGAACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGACAA 120
Db 67 GGCTGCCAGGCTACGGAAGAGAACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGACAA 126
QY 121 GGTGGCAGGCGCTGGAGGCTGCCGACAGCCTGCGTGGGTGAGAGGGAGCTCAGCTCGGTTG 180
Db 127 GGTGGCAGGCGCTGGAGGCTGCCGACAGCCTGCGTGGGTGAGAGGGAGCTCAGCTCGGTTG 186
QY 181 TGGGAGCAGGCGGACCGGCACTGGCTGGATGGACCTGGAAGCCTGCTGCTGCCACTGGT 240
Db 187 TGGGAGCAGGCGGACCGGCACTGGCTGGATGGACCTGGAAGCCTGCTGCTGCCACTGGT 246
QY 241 CCCAATGCCAGCAACACCTCTGATGGCCCCGATTAACCTCACTTCAAGAGATCAGCTCCT 300
Db 247 CCCAAGCCAGCAACACCTCTGATGGCCCCGATTAACCTCACTTCAAGAGATCAGCTCCT 306
QY 301 CGCACGGGAGCATCTCTACATCAACATCATCATGCTTCCGTTGTTCCGACCATCTGC 360
Db 307 CGCACGGGAGCATCTCTACATCAACATCATCATGCTTCCGTTGTTCCGACCATCTGC 366
QY 361 CTCTGGGATCATCGGGAAGTCCACGGTCACTCTTCCGGTCTGGAAGAAGTCCAAGCTG 420
Db 367 CTCTGGGATCATCGGGAAGTCCACGGTCACTCTTCCGGTCTGGAAGAAGTCCAAGCTG 426
QY 421 CACTGTGCAACAACGTTCCCGACATCTTCAATCATCAACCTCTCGGTAGTAGATCTCTC 480
Db 427 CACTGTGCAACAACGTTCCCGACATCTTCAATCATCAACCTCTCGGTAGTAGATCTCTC 486
QY 481 TTCTCTGGGATGCTTCAATGATCCACAGCTCAATGGGCAATGGGTTGGCACTTT 540
Db 487 TTCTCTGGGATGCTTCAATGATCCACAGCTCAATGGGCAATGGGTTGGCACTTT 546
QY 541 GGGAGAACCATGTGCACCCCTCATCAGCGGCATGGATGCCAATAGTCAAGTTCACAGACCC 600
Db 547 GGGAGAACCATGTGCACCCCTCATCAGCGGCATGGATGCCAATAGTCAAGTTCACAGACCC 606
QY 601 TACATCCTGACCGCCATGGCCATTGACCGGCTACCTGGCCACTGTCCACCCCATCTTCC 660
Db 607 TACATCCTGACCGCCATGGCCATTGACCGGCTACCTGGCCACTGTCCACCCCATCTTCC 666
QY 661 ACGAAGTTCGGGAAGCCCTGTGTGGCCACCCCTGTGATGTGCTCTGTGGGCCCTTCC 720
Db 667 ACGAAGTTCGGGAAGCCCTGTGTGGCCACCCCTGTGATGTGCTCTGTGGGCCCTTCC 726
QY 721 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGTGCA 780
Db 727 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGTGCA 786
QY 781 GTGGGCTGCGGATACGCTGCTGCCCAACCCAGACACTGACTTACTGTTACCCCTGTAC 840
Db 787 GTGGGCTGCGGATACGCTGCTGCCCAACCCAGACACTGACTTACTGTTACCCCTGTAC 846
QY 841 CAGTTTTCCTGGCCTTGGCCCTGCTTTGTGTATCATCAGCCGATACGTAGAGATC 900
Db 847 CAGTTTTCCTGGCCTTGGCCCTGCTTTGTGTATCATCAGCCGATACGTAGAGATC 906
QY 901 CTGACAGGATGAGTCTCTAGTGGCCCCCGCTCCAGGCGACATCCGGCTGCGGACA 960
Db 907 CTGACAGGATGAGTCTCTAGTGGCCCCCGCTCCAGGCGACATCCGGCTGCGGACA 966
QY 961 AAGAGGGTACCCGACACAGCATGCGCATCTGTCTGTCTTTGTGTGCTGGGACCC 1020
Db 967 AAGAGGGTACCCGACACAGCATGCGCATCTGTCTGTCTTTGTGTGCTGGGACCC 1026

QY	1021	TACTATGTGCTACAGCTGACCACAGTTGTGCCATCAGCCGCCGACCCCTCACCTTGTCTAC	1080
Dd	1027	TACTATGTGCTACAGCTGACCACAGTTGTGCCATCAGCCGCCGACCCCTCACCTTGTCTAC	1086
QY	1081	TTATACAATGGCGGCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTGTGTAC	1140
Dd	1087	TTATACAATGGCGGCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTGTGTAC	1146
QY	1141	ATCGTCTCTGTGAGAGCTTCGCCAAACGCTTGTGCTGTGCGTGAAGCCGTGAGCCCAG	1200
Dd	1147	ATCGTCTCTGTGAGAGCTTCGCCAAACGCTTGTGCTGTGCGTGAAGCCGTGAGCCCAG	1206
QY	1201	GGGAGCTTCGGCGTGTCAAGCAACGCTCAGACGGCTGACGAGGAGAGACAGAACAATA	1260
Dd	1207	GGGAGCTTCGGCGTGTCAAGCAACGCTCAGACGGCTGACGAGGAGAGACAGAACAATA	1266
QY	1261	GGCACCCTGA	1269
Dd	1267	GGCACCCTGA	1275

RESULT	7
AAAF86229	
ID	AAAF86229 standard; cDNA; 1275 BP.
XX	
AC	AAAF86229;
XX	
DT	05-JUL-2001 (first entry)

Human melanin concentrating hormone receptor (SLC-1) cDNA.

KW Melanin concentrating hormone; MCH; antagonist; diamine compound;
 KW anorectic; antidiabetic; ophthalmological; neuroprotective; nephrotropic;
 KW antiarteriosclerotic; antiarthritic; obesity; diabetes; arteriosclerosis;
 KW arthritis; melanin concentrating hormone receptor; SLC-1; human; ss.

OS Homo sapiens.

FH	Key	Location/Qualifiers
FT	CDS	7..1275

```
FT      /*tag= a
FT      /product= "SLC-1"
FT      /note= "Melanin concentrating hormone receptor"
```

PN WO200121169-A1.

PD 29-MAR-2001.

PF 19-SEP-2000; 2000WO-JP06376.

PR 20-SEP-1999; 99JP-0266278.

PR 17-JUL-2000; 2000JP-0221055.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Kato K, Mori M, Suzuki N, Shimomura Y, Takekawa S, Choh N;

DR WPI; 2001-328055/34.

XX

PT diamine compounds for treating obesity -

PS Examples; Page 271-273; 284pp; Japanese.

CC This invention relates to melanin concentrating hormone (MCH)

Use of the MCH antagonists can result in anorectic, antidiabetic,

CC and antiarthritic activity. Melanin concentrating hormone (MCH)

hypophyseal adiposity, hypothalamic obesity and hyperphagia) and

associated disorders such as diabetes, diabetic complications (such as diabetic retinopathy, diabetic neuropathy and diabetic nephropathy), arteriosclerosis and arthritis in the knees. The present sequence represents human cDNA encoding melanin concentrating hormone receptor (SLC-1). The SLC-1 cDNA is used in examples to demonstrate the use of the antagonists of the invention.

Sequence 1275 BP; 235 A; 420 C; 350 G; 270 T; 0 other;

Query Match	99.6%;	Score 1264.2;	DB 22;	Length 1275;
Best Local Similarity	99.8%;	Pred. No. 4.4e-284;		
Matches 1266; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

0y 1 ATGTCAGTGGGAGCCATGAGAGAGGAGTGGGGAGGGCAGTTGGGCTTGGAGGCGGCACC 60
 |||||
 Db 7 ATGTCAGTGGGAGCCATGAGAGAGGAGTGGGGAGGGCAGTTGGGCTTGGAGGCGGCACC 66

61 GGCTGCCAGGCTACGGAGGAAGACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGACAA 120
 67 GGCTGCCAGGCTACGGAGGAAGACCCCTTCCCAACTGCGGGGCTTGCGCTCCGGACAA 126

121 GGTGGCAGCGCTGGAGGCTGCCCAAGCTTGCCTGGGTGGAGGGGAGCTCAGCTTCGGTTG 180
 |||||
 127 GGTGGCAGCGCTGGAGGCTGCCCAAGCTTGCCTGGGTGGAGGGGAGCTCAGCTTCGGTTG 186
 Db

QY 181 TGGAGCAGGCGACCGGCACTGGCTGGATGGACCTGGAAGCCTCGCTGCTGCCCACTGGT 240
|||||
Db 187 TGGGAGCAGGCGACCGGCACTGGCTGGATGGACCTGGAAGCCTCGCTGCTGCCCACTGGT 246
|||||

QY 241 CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACTCTACTTCAGCAGGATCACTCCT 300
|||||
Db 247 CCCAAGCGCAGCAACACCTCTGATGGCCCCGATAACTCTACTTCGGCAGGATCACTCCT 306
|||||

QY 301 CGCACGGGAGCATCTCCTACATCAACATCATCATGCGCTTCGGTGTTCGGCACCATCTGC 360
|||||
Db 307 CGCACGGGAGCATCTCCTACATCAACATCATCATGCGCTTCGGTGTTCGGCACCATCTGC 366
|||||

QY 361 CTCCTGGGCATCATCGGGAACTCCACGGTCATCTTCGGCGTCTGAAGAACTCCAAGCTG 420
|||||
db 367 CTCCTGGGCATCATCGGGAACTCCACGGTCATCTTCGGCGTCTGAAGAACTCCAAGCTG 426
|||||

QY 421 CACTGTGCAACACAGTCCCGACATCTTCATCATCAACCTCTGGTAGTAGATCTCCTC 480
|||||
db 427 CACTGTGCAACACAGTCCCGACATCTTCATCATCAACCTCTGGTAGTAGATCTCCTC 486
|||||

481 TTTTCTGGGCGATGCCCTTCATGATCCACCAGCTCATGGGCAATTGGGTGTGCACCTTT 540
 |||||
 487 ATTTCATCCTCCCCCATTCCTCTCTTGAATGACACCAATCCCTGATCCCTGCTCTCTTT 546

OY 541 GGGAGACCATGTGCACCCTCATTCACGGCCATGATGCCAATAGTCA GTTCACCA GCACC 600
|||||
E47 |||||

601 TACATCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCACCCCATCTCTCC 660
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699 |||||
700 |||||

661 ACGAGTTCGGAGAGCCCTCTGTGGCCACCCCTGTGATCTGCTCTGTGGCCCTCTCC 720

721 TTCATCAGCATCACCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCACGAGGTGCA 780

781 GTGGGCTGGGGCATACGGCTGGCCCAACCCAGACACTGACCTCTACTGGTTACACCTGTAC 840

841 CAGTTTTCTGGCCCTTGGCCCTTTGTGTGTCATCACAGCCGATACGTAGGATC 900

QY	901	CTGCAGCGCATGACGTCTCTCAGTGGCCCCCGCTCTCCAGCGCAGCATCCGGCTGGGACA	960
Db	907	CTGCAGCGCATGACGTCTCTCAGTGGCCCCCGCTCTCCAGCGCAGCATCCGGCTGGGACA	966
QY	961	AAGAGGGTGACCCCGCACAGCCATCGCCATCTGTCTGTCTTTGTGTGTGGCAACC	1020
Db	967	AAGAGGGTGACCCCGCACAGCCATCGCCATCTGTCTGTCTTTGTGTGTGGCAACC	1026
QY	1021	TACTATGTGTACAGCTGACCCAGTTGTTCATCAGCCGCCGACCCCTACCTTGTCTAC	1080
Db	1027	TACTATGTGTACAGCTGACCCAGTTGTTCATCAGCCGCCGACCCCTACCTTGTCTAC	1086
QY	1081	TTATACAATGCGGCCATCAGCTTGGGTATGCCAACAGCTGCCTCAACCCCTTGTGTAC	1140
Db	1087	TTATACAATGCGGCCATCAGCTTGGGTATGCCAACAGCTGCCTCAACCCCTTGTGTAC	1146
QY	1141	ATCGTCTCTGTGAGACGTTCCGCCAAACGCTTGTGTCTGTGGTGAAGCCTGCAGCCCAG	1200
Db	1147	ATCGTCTCTGTGAGACGTTCCGCCAAACGCTTGTGTCTGTGGTGAAGCCTGCAGCCCAG	1206
QY	1201	GCGCAGCTTCGCGCTGTCAAGCAACGCTCAGACGCGCTGACGAGGAGAGACAGAAGCAA	1260
Db	1207	GCGCAGCTTCGCGCTGTCAAGCAACGCTCAGACGCGCTGACGAGGAGAGACAGAAGCAA	1266
QY	1261	GGCACCCTGA	1269
Db	1267	GGCACCCTGA	1275

RESULT 8	
AAAF86975	
ID	AAAF86975 standard; cDNA; 1275 BP.
XX	
AC	AAAF86975;
XX	
DT	06-JUL-2001 (first entry)
XX	
DE	Human SLC-1 coding sequence #1.
XX	
KW	Rat; human; SLC-1; MCH receptor; melanin-concentrating hormone;
KW	obesity; diabetes; hypertension; arteriosclerosis; hyperphagia;
KW	emotional disorder; reproductive disorder; memory disorder;
KW	dementia; hormonal disorder; gonitis; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	7..1275
FT	/*tag= a
FT	/product= "SLC-1"
XX	
PN	WO200121577-A2.
XX	
PD	29-MAR-2001.
XX	
PF	19-SEP-2000; 2000WO-JP06375.
XX	
PR	20-SEP-1999; 99JP-0266298.
PR	16-DEC-1999; 99JP-0357889.
PR	20-APR-2000; 2000JP-0126272.
XX	
PA	(TAKE) TAKEDA CHEM IND LTD.
XX	
PI	Kato K, Terauchi J, Mori M, Suzuki N, Shimomura Y, Takekawa S;
PI	Ishihara Y;
XX	
DR	WPI; 2001-354775/37.
DR	P-PSDB; AAB96871.
XX	
PT	New aromatic compounds are melanin concentrating hormone antagonists,
PT	useful as anorectic agents, for treating or preventing obesity, also
PT	memory or hormonal disorders or diabetes -
XX	

PS Examples; Page 357-358; 363pp; English.

XX

CC The present invention describes aromatic compounds capable of acting as

CC melanin-concentrating hormone (MCH) antagonists. Melanin-concentrating

CC hormone is an appetite control factor and antagonists were expected to be

CC useful as anti-obesity agents. They can be used in the treatment of

CC obesity, including malignant mastocytosis, exogenous, hyperinsular,

CC hypoplasmic, hypothyroid, hypothalamic, symptomatic, infantile, upper

CC body, alimentary, hypogonadal, simple and central obesity, systemic

CC mastocytosis and hypophyseal adiposity, hypertension, arteriosclerosis,

CC hyperphagia, emotional disorders, reproductive function disorders, memory

CC disorders, dementia, hormonal disorders, diabetes and gonitis. MCH binds

CC to the SLC-1 receptor. The present sequence is a version of the human

CC SLC-1 coding sequence given in the specification.

XX

SQ Sequence 1275 BP; 235 A; 420 C; 350 G; 270 T; 0 other;

Query Match	99.68;	Score 1264.2;	DB 22;	length 1275;
Best Local Similarity	99.88;	Pred. No. 4.4e-284;		
Matches 1266; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

QY	1	ATGTCAGTGGGAGCCATGAAGAAGGAGTGGGGAGGGCAGTTGGGCTTGAGAGCGGCACAGC	60
Db	7	ATGTCACTGGGAGCCATGAAGAAGGAGTGGGGAGGGCAGTTGGGCTTGAGAGCGGCACAGC	66
QY	61	GCGTGCACGAGCTACGGAGGAAGACCCTTCCGACTGCGGGGCTTCGCCCTCCGGACAA	120
Db	67	GCGTGCACGAGCTACGGAGGAAGACCCTTCCGACTGCGGGGCTTCGCCCTCCGGACAA	126
QY	121	GGTGGCAGGCGCTGGAGGCTGCCGACGCTGCGTGGGTGGAGGGAGCTCAGCTCGGTTG	180
Db	127	GGTGGCAGGCGCTGGAGGCTGCCGACGCTGCGTGGGTGGAGGGAGCTCAGCTCGGTTG	186
QY	181	TGGGAGCAGGCGCACCGGCACTGGCTGGATGGACCTGGAGGCTCGCTGCTGCCACTGGT	240
Db	187	TGGGAGCAGGCGCACCGGCACTGGCTGGATGGACCTGGAGGCTCGCTGCTGCCACTGGT	246
QY	241	CCCATTGCCAGCAACACCTCTGATGGCCCCGATTAACCTCACTTCAGCAGATCAACCTCCT	300
Db	247	CCCATTGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTCGCGCAGGATCAACCTCCT	306
QY	301	CGCACGGGGAGCATCTCCTACATCAACATCATCATGCTTCGGTGGTGGGACCATCTTGC	360
Db	307	CGCACGGGGAGCATCTCCTACATCAACATCATCATGCTTCGGTGGTGGGACCATCTTGC	366
QY	361	CTCCTGGGCATCATCGGGAACCTCCAGGTCATCTTCGCGGTGCTGAAGAAGTCCAAGCTG	420
Db	367	CTCCTGGGCATCATCGGGAACCTCCAGGTCATCTTCGCGGTGCTGAAGAAGTCCAAGCTG	426
QY	421	CAC TGGTGCAACAACAGTCCCCGACATCTTCATCATCATCAACCTCTCGTAGTAGATCTCCTC	480
Db	427	CAC TGGTGCAACAACAGTCCCCGACATCTTCATCATCATCAACCTCTCGTAGTAGATCTCCTC	486
QY	481	TTTTCTCTGGGCATGCCCTTCATGATTCACCAAGCTCATGCGCAATGGGGTGTGGCACTTT	540
Db	487	TTTTCTCTGGGCATGCCCTTCATGATTCACCAAGCTCATGCGCAATGGGGTGTGGCACTTT	546
QY	541	GGGGAGACCATGTGCACCCCTCATCAAGGCGCATGGATGCCAATAGTCAGTTCAACGACACC	600
Db	547	GGGGAGACCATGTGCACCCCTCATCAAGGCGCATGGATGCCAATAGTCAGTTCAACGACACC	606
QY	601	TACATCCTGACCGCCATGGGCATTCGACCGCTAACCTGGCCACTGTCCACCCCATCTCTTCC	660
Db	607	TACATCCTGACCGCCATGGGCATTCGACCGCTAACCTGGCCACTGTCCACCCCATCTCTTCC	666
QY	661	ACGAAGTCCGGGAAGCCCTCTGTGGGCCACCCCTGTGATCTGCTCTGTGGGCCCTCTCC	720
Db	667	ACGAAGTCCGGGAAGCCCTCTGTGGGCCACCCCTGTGATCTGCTCTGTGGGCCCTCTCC	726
QY	721	TTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGGAGGTGCA	780
Db	727	TTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGGAGGTGCA	786

QY	781	GTGGGCTGCGGCATACGCGCTTGCCCAACCCAGACACTGACCTCTACTGGTTCACCCCTGTAC	840
Db	787	GTGGGCTGCGGCATACGCGCTTGCCCAACCCAGACACTGACCTCTACTGGTTCACCCCTGTAC	846
QY	841	CAGTTTTCCTGGCCCTTTGCCCTGCCCTTTTGTGGTCATCAGACCCGCATACGTGAGGATC	900
Db	847	CAGTTTTCCTGGCCCTTTGCCCTGCCCTTTTGTGGTCATCAGACCCGCATACGTGAGGATC	906
QY	901	CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCCTCCAGCGCAGCATCCGGCTGCGGACA	960
Db	907	CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCCTCCAGCGCAGCATCCGGCTGCGGACA	966
QY	961	AAGAGGGTGACCCCGCACAGCCATCGCCATCTGTCTGTCTTCTTGTGTGCTGGGCACCC	1020
Db	967	AAGAGGGTGACCCCGCACAGCCATCGCCATCTGTCTGTCTTCTTGTGTGCTGGGCACCC	1026
QY	1021	TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGACCCCTCACCTTTGTCTAC	1080
Db	1027	TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGACCCCTCACCTTTGTCTAC	1086
QY	1081	TTATACATAGCGGCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTTGTGTAC	1140
Db	1087	TTATACATAGCGGCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTTGTGTAC	1146
QY	1141	ATCGTGCTCTGTGAGACGTTCCGCCAAACGCTTGGTCTCTGTGGTGAAGCCCTGCAGCCAG	1200
Db	1147	ATCGTGCTCTGTGAGACGTTCCGCCAAACGCTTGGTCTCTGTGGTGAAGCCCTGCAGCCAG	1206
QY	1201	GGGCAGCTTGGCGCTGTGAGCAACGCTCAGACCGGCTGACGAGGAGAGACAGAAAGCAAA	1260
Db	1207	GGGCAGCTTGGCGCTGTGAGCAACGCTCAGACCGGCTGACGAGGAGAGACAGAAAGCAAA	1266
QY	1261	GGCACCTGA 1269	
Db	1267	GGCACCTGA 1275	

RESULT 9	
ABK10854	
ID	ABK10854 standard; DNA; 1275 BP.
XX	
AC	ABK10854;
XX	
DT	05-JUN-2002 (first entry)
XX	
DE	DNA encoding human melanin concentrating hormone receptor, SLC-1.
XX	
KW	G protein-coupled orphan; receptor; SLT; melanin-concentrating hormone;
KW	MCH; appetite-stimulating agent; obesity; malignant mastocytosis;
KW	exogenous obesity; hyperinsulinar obesity; sexual function disorder;
KW	overpowering intermittent pain; still born; uterus rupture;
KW	premature birth; Prader-Willi syndrome; SLC-1; human; gene; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	7..1275
FT	/*tag= a
FT	/product= "SLC-1"
FT	/note= "Melanin concentrating hormone receptor"
XX	
PN	WO200203070-A1.
XX	
PD	10-JAN-2002.
XX	
PF	04-JUL-2001; 2001WO-JP05809.
XX	
PR	05-JUL-2000; 2000JP-0208254.
XX	
PA	(TAKE) TAKEDA CHEM IND LTD.
XX	
PI	Mori M, Shimomura Y, Harada M, Sugo T, Shintani Y;
XX	

DR WPI, 2002-164552/21.
DR P-PSDB; AAU77541.
XX
XX Screening for compounds or salts which alter affinity of
PT melanin-concentrating hormone with its receptor to provide agonists as
PT appetite-stimulating agents and its antagonist for preventing or
PT treating obesity, uses a protein or hormone -
XX
XX
PS Disclosure; Page 106-107; 112pp; Japanese.
XX
XX The invention describes a method of screening for compounds or their
CC salts that can change affinity of melanin-concentrating hormone (MCH)
CC with its G protein-coupled orphan receptor protein, SLC. The screened
CC MCH receptor agonists are useful as appetite-stimulating agents and its
CC antagonist for preventing or treating obesity e.g. malignant
CC mastocytosis, exogenous obesity and hyperinsular obesity, and also
CC for treating sexual function disorders, overpowering intermittent pains,
CC still borns, uterus rupture, premature birth and Prader-Willi syndrome.
CC This sequence encodes the human melanin concentrating hormone SLC-1,
CC described in the invention.
XX
XX
SQ Sequence 1275 BP; 235 A; 420 C; 350 G; 270 T; 0 other;

Query Match	99.6%;	Score 1264.2;	DB 24;	Length 1275;
Best Local Similarity	99.8%;	Pred. No. 4.4e-284;		
Matches 1266;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;
QY 1	ATGTCAGTGGGAGCCATGAAGAAGGAGTGGGAGGGCAGTTGGGCTTGAGGGCGGACG	60		
Db 7	ATGTCAGTGGGAGCCATGAAGAAGGAGTGGGAGGGCAGTTGGGCTTGAGGGCGGACG	66		
QY 61	GGCTGCCAGGCTACGAGGAAGACCCCTTCCGACTGCGGGCTTGGCGTCCGGACAA	120		
Db 67	GGCTGCCAGGCTACGAGGAAGACCCCTTCCGACTGCGGGCTTGGCGTCCGGACAA	126		
QY 121	GGTGGCAGGGCGCTGAGAGCTGCCGACGCTGCGTGGGTGAGGGGAGCTCAGCTCGTTG	180		
Db 127	GGTGGCAGGGCGCTGAGAGCTGCCGACGCTGCGTGGGTGAGGGGAGCTCAGCTCGTTG	186		
QY 181	TGGGAGCAGGCGACCGGCACTGGCTGGATGGACCTGGAAAGCTTCGCTGCCCCACTGGT	240		
Db 187	TGGGAGCAGGCGACCGGCACTGGCTGGATGGACCTGGAAAGCTTCGCTGCCCCACTGGT	246		
QY 241	CCCAATGCCAGCAACACCTCTGTATGGCCCCGATTAACCTCACTTCAGCAGGATCACCTCCT	300		
Db 247	CCCAACGCCAGCAACACCTCTGTATGGCCCCGATTAACCTCACTTCGCGCAGGATCACCTCCT	306		
QY 301	CGCACGGGGAGCATCTCCTACATCAACATCATCATGCGCTTCGGTGTGGCACCATCTGC	360		
Db 307	CGCACGGGGAGCATCTCCTACATCAACATCATCATGCGCTTCGGTGTGGCACCATCTGC	366		
QY 361	CTCCTGGGCATCATGGGGAACGCCAGGTCATCTTCGCGGTCTGGAAGAAGTCCAAAGCTG	420		
Db 367	CTCCTGGGCATCATGGGGAACGCCAGGTCATCTTCGCGGTCTGGAAGAAGTCCAAAGCTG	426		
QY 421	CACCTGGTGCAACAACGTCGCCGACATCTTCATCATCAACCTTCGGTAGTAGATCTCCTC	480		
Db 427	CACCTGGTGCAACAACGTCGCCGACATCTTCATCATCAACCTTCGGTAGTAGATCTCCTC	486		
QY 481	TTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTT	540		
Db 487	TTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTT	546		
QY 541	GGGGAGACCATGTGCACCCCTCATCAGGGCCATGGATGCCAATAGTCAGTTCACAGCACC	600		
Db 547	GGGGAGACCATGTGCACCCCTCATCAGGGCCATGGATGCCAATAGTCAGTTCACAGCACC	606		
QY 601	TACATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCC	660		
Db 607	TACATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCC	666		
QY 661	ACGAAGTTCGGAAGCCCTCTGTGGCCACCCCTGGTGTGATCTGCCCTCTGTGGGCCCTCTCC	720		

Db	667	ACGAAGTTCGGGAAGCCCTCTGTGGCCACCCTGGTGAATCTGCCCTCCTGTGGGCCCTCTCC	726
QY	721	TTTCATCAGCATCACCCCTGTGTGGCTGTATGCGCAGACTCATCCCCCTTCCAGAGGTGCA	780
Db	727	TTTCATCAGCATCACCCCTGTGTGGCTGTATGCGCAGACTCATCCCCCTTCCAGAGGTGCA	786
QY	781	GTGGGCTGCGGCATACGCTTGCCCAACCAGACACTGACCTTACTGTGTTCAACCTGTAC	840
Db	787	GTGGGCTGCGGCATACGCTTGCCCAACCAGACACTGACCTTACTGTGTTCAACCTGTAC	846
QY	841	CAGTTTTTCCCTGGCCCTTTGCCCTTGCCCTTTTGTGTGTCATCACAGCCGCATACGTGAGATC	900
Db	847	CAGTTTTTCCCTGGCCCTTTGCCCTTGCCCTTTTGTGTGTCATCACAGCCGCATACGTGAGATC	906
QY	901	CTGCAGCGCATGACGTCCCTCAGTGGCCCCCGCCCTCCACGGCAGCATCCGGCTGGGACA	960
Db	907	CTGCAGCGCATGACGTCCCTCAGTGGCCCCCGCCCTCCACGGCAGCATCCGGCTGGGACA	966
QY	961	AAGAGGGTGACCCCGCACAGCCATCGCCATCTGTCTGTCTTCTTGTGTGCTGGGCACCC	1020
Db	967	AAGAGGGTGACCCCGCACAGCCATCGCCATCTGTCTGTCTTCTTGTGTGCTGGGCACCC	1026
QY	1021	TACTATGTGCTACAGCTGACCCAGTGTGTCATCAGCGCCCGACCCCTCACCCTTTGTCTAC	1080
Db	1027	TACTATGTGCTACAGCTGACCCAGTGTGTCATCAGCGCCCGACCCCTCACCCTTTGTCTAC	1086
QY	1081	TTATACAATGCGGCCCATCAGCTTGGGCTATGCGCAACAGCTGCCTCAACCCCTTTGTCTAC	1140
Db	1087	TTATACAATGCGGCCCATCAGCTTGGGCTATGCGCAACAGCTGCCTCAACCCCTTTGTCTAC	1146
QY	1141	ATCGTGCTCTGTGAGAGCTTCCGCAACGCTTGTCTCTGTCGGTGAAGCCTGCAGCCAG	1200
Db	1147	ATCGTGCTCTGTGAGAGCTTCCGCAACGCTTGTCTCTGTCGGTGAAGCCTGCAGCCAG	1206
QY	1201	GGGCAGCTTCGGCGTTCAGCAACGCTCAGACCGGCTGACGAGGAGAGACAGAAAGCAAA	1260
Db	1207	GGGCAGCTTCGGCGTTCAGCAACGCTCAGACCGGCTGACGAGGAGAGACAGAAAGCAAA	1266
QY	1261	GGCACCCTGA 1269	
Db	1267	GGCACCCTGA 1275	

RESULT 10	
ABA92411	
ID	ABA92411 standard; cDNA; 1275 BP.
XX	
AC	ABA92411;
XX	
DT	14-MAR-2002 (first entry)
XX	
DE	Human SLC-1 encoding cDNA SEQ ID NO:8.
XX	
KW	Human; SLC-1; melanin concentrating hormone antagonist; obesity;
KW	anorectic; antidiabetic; hypotensive; antiarteriosclerotic;
KW	diabetes; hypertension; arteriosclerosis; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	
FT	Location/Qualifiers
FT	7..1275
FT	/*tag= a
FT	/product= "SLC-1"
XX	
PN	WO200182925-A1.
XX	
PD	08-NOV-2001.
XX	
PF	26-APR-2001; 2001WO-JP03614.
XX	
PR	28-APR-2000; 2000JP-0134295.
PR	13-DEC-2000; 2000JP-0384897.
XX	

(TAKE) TAKEDA CHEM IND LTD.
Ishihara Y, Suzuki N, Takekawa S;
WPI; 2002-075131/10.
P-PSDB; ABB04941.
Melanin aggregating hormone antagonist for treating obesity -
Example; Page 209-210; 223pp; Japanese.
The present invention describes a melanin aggregating hormone antagonist (I). (I) has anorectic, antidiabetic, antiarteriosclerotic and hypotensive. (I) can be used in the treatment and prevention of obesity. It may be combined with treatments for diabetes, hypertension or arteriosclerosis. The present sequence encodes human SLC-1, which is used the exemplification of the present invention.
Sequence 1275 BP; 235 A; 420 C; 350 G; 270 T; 0 other;
Query Match 99.6%; Score 1264.2; DB 24; Length 1275;
Best Local Similarity 99.8%; Pred. No. 4.4e-284;
Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ATGTCAGTGGGAGCCATGAAGAAGGAGTGGGGAGGGCAGTTGGGCTTGGAGGCGGCAGC	60
Db	7	ATGTCAGTGGGAGCCATGAAGAAGGAGTGGGGAGGGCAGTTGGGCTTGGAGGCGGCAGC	66
QY	61	GGCTGCCAGGCTACGGAGGAAGACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGGACAA	120
Db	67	GGCTGCCAGGCTACGGAGGAAGACCCCTTCCCAACTGCGGGGCTTGCGCTCCGGGACAA	126
QY	121	GGTGGCAGGCGCTGGAGGCTGCCGAGCCTGCGTGGGTGGAGGGAGCTCAGCTCGGTTG	180
Db	127	GGTGGCAGGCGCTGGAGGCTGCCGAGCCTGCGTGGGTGGAGGGAGCTCAGCTCGGTTG	186
QY	181	TGGGAGCAGGCGGACCGGCACTGGCTGGATGGACCTGGAAGCCTCGCTGCCCCACTGGT	240
Db	187	TGGGAGCAGGCGGACCGGCACTGGCTGGATGGACCTGGAAGCCTCGCTGCCCCACTGGT	246
QY	241	CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTACAGCAGATCACTCCT	300
Db	247	CCCAACGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTCCGGCAGATCACTCCT	306
QY	301	CGCACGGGGAGCATCTCCTACATCAACATCATCATGCGCTCGGTGTTGGCACCATCTGC	360
Db	307	CGCACGGGGAGCATCTCCTACATCAACATCATCATGCGCTCGGTGTTGGCACCATCTGC	366
QY	361	CTCCTGGGCATCATCGGGAATCCACGGTCATCTTGCGGTGTGAAGAAGTCCAAAGCTG	420
Db	367	CTCCTGGGCATCATCGGGAATCCACGGTCATCTTGCGGTGTGAAGAAGTCCAAAGCTG	426
QY	421	CACTGGTGCAACAACGTCGCCCGACATCTTCATCATCAACCTCTCGGTAGATCTCTCCTC	480
Db	427	CACTGGTGCAACAACGTCGCCCGACATCTTCATCATCAACCTCTCGGTAGATCTCTCCTC	486
QY	481	TTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTT	540
Db	487	TTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTT	546
QY	541	GGGGAGACCATGTGCACCCCTCATCAACGGCCATGGATGCCAATAGTCAAGTTCACCAAGACC	600
Db	547	GGGGAGACCATGTGCACCCCTCATCAACGGCCATGGATGCCAATAGTCAAGTTCACCAAGACC	606
QY	601	TACATCTCTGACCGCCCATGGCCATGACCGCTAACCTGGCCACTGTCCACCCCATCTCTCC	660
Db	607	TACATCTCTGACCGCCCATGGCCATGACCGCTAACCTGGCCACTGTCCACCCCATCTCTCC	666
QY	661	ACGAAGTTCGGAAGCCCTCTGTGGCCACCCCTGGTGTCTGCGCTCTGTGGGCCCTCTCC	720
Db	667	ACGAAGTTCGGAAGCCCTCTGTGGCCACCCCTGGTGTCTGCGCTCTGTGGGCCCTCTCC	726
QY	721	TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCACGAGAGGTGCA	780

Db 727 TTTCATCAGCATACCCCTGTGTGGCTATGCGAGACTCATCCCTTCCAGAGAGTGCA 786
QY 781 GTGGCTGGGCATACGCTGCCAACCCAGACACTGACCTTACTGTGTTCACCCGTAC 840
Db 787 GTGGCTGGGCATACGCTGCCAACCCAGACACTGACCTTACTGTGTTCACCCGTAC 846
QY 841 CAGTTTTCCTGGCCTTTGCCCTGCCCTTTGTGTGTCATCACAGCCGCATACGTAGAGATC 900
Db 847 CAGTTTTCCTGGCCTTTGCCCTGCCCTTTGTGTGTCATCACAGCCGCATACGTAGAGATC 906
QY 901 CTGCAGCCGATGACGTCCTCAGTGGCCCCGCCCTCCAGCGCAGCATCCGGCTGGGACA 960
Db 907 CTGCAGCCGATGACGTCCTCAGTGGCCCCGCCCTCCAGCGCAGCATCCGGCTGGGACA 966
QY 961 AAGAGGTGACCCGCACAGCCATCCCATCTGTCTGCTTTGTGTGCTGGGACCC 1020
Db 967 AAGAGGTGACCCGCACAGCCATCCCATCTGTCTGCTTTGTGTGCTGGGACCC 1026
QY 1021 TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCGCCACCTTGTGTAC 1080
Db 1027 TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCGCCACCTTGTGTAC 1086
QY 1081 TTATACAATGGGCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTGTGTAC 1140
Db 1087 TTATACAATGGGCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTGTGTAC 1146
QY 1141 ATCGTGTCTGTGAGAGCTTCCGCAACGCTTGGTCCGTGCGTGAAGCCTGCAGCCAG 1200
Db 1147 ATCGTGTCTGTGAGAGCTTCCGCAACGCTTGGTCCGTGCGTGAAGCCTGCAGCCAG 1206
QY 1201 GGGCAGCTTGGCGCTGTACGCAACGCTCAGACGGCTGACGAGAGAGAGAAAGCAA 1260
Db 1207 GGGCAGCTTGGCGCTGTACGCAACGCTCAGACGGCTGACGAGAGAGAGAAAGCAA 1266
QY 1261 GGCACCTGA 1269
Db 1267 GGCACCTGA 1275

RESULT 11
AAI69442
ID AAI69442 standard; DNA; 1275 BP.
XX AAI69442;
AC AAI69442;
XX
DT 28-FEB-2002 (first entry)
XX
DE Human SLC-1 cDNA.
XX
KW SLC-1; melanin-concentrating hormone antagonist; anorectic; depression;
KW antidiabetic; hypotensive; antiarteriosclerotic; antilipaeamic; obesity;
KW antiarthritic; antidepressant; tranquiliser; malignant mastocytosis;
KW hypophyseal adiposity; hypothyroid obesity; hyperphagia; diabetes;
KW hypertension; arteriosclerosis; hyperlipidaemia; arthritis; anxiety;
KW human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..1275
FT /*tag= a
FT /product= "SLC-1"
XX
XX WO200187834-A1.
PN
PD 22-NOV-2001.
XX
XX 15-MAY-2001; 2001WO-JP04015.
PF
XX 16-MAY-2000; 2000JP-0148674.
PR 13-APR-2001; 2001JP-0116219.
XX

PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Ishihara Y, Terauchi J, Suzuki N, Takekawa S, Aso K;
XX
DR WPI, 2002-055668/07.
DR P-PSDB; AAG80611.
XX
PT Use of new and known amine derivatives as melanin concentrating hormone
PT antagonists for treating e.g. obesity, diabetes, hypertension and
PT arteriosclerosis
XX
PS Disclosure; Page 251-252; 283pp; Japanese.
XX
CC This invention describes a novel use of an amine derivative (I) as a
CC melanin concentrating hormone antagonist which has anorectic,
CC antidiabetic, hypotensive, antiarteriosclerotic, antilipaeamic,
CC antiarthritic, antidepressant and tranquiliser activity. The products of
CC the invention can be used as melanin concentrating hormone antagonists
CC for treating and preventing obesity (including malignant mastocytosis,
CC hypophyseal adiposity, hypothyroid obesity, infantile obesity and
CC hyperphagia), diabetes, hypertension and arteriosclerosis as well as
CC diabetic complications, hyperlipidaemia, arthritis, depression and
CC anxiety. This sequence encodes the human melanin-concentrating hormone
CC SLC-1 gene described in the method of the invention.
XX
SQ Sequence 1275 BP; 235 A; 420 C; 350 G; 270 T; 0 other;
Query Match 99.6%; Score 1264.2; DB 24; Length 1275;
Best Local Similarity 99.8%; Pred. No. 4.4e-284;
Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGTACGTGGAGCGCATGAAGAAGGAGTGGGAGGGGAGTGGGCTTGGAGCGGACG 60
Db 7 ATGTACGTGGAGCGCATGAAGAAGGAGTGGGAGGGGAGTGGGCTTGGAGCGGACG 66
QY 61 GCGTCCAGGCTACGAGGAGGAAGACCCCTTCCGACTGCGGGGCTTGGCGGACAA 120
Db 67 GCGTCCAGGCTACGAGGAGGAAGACCCCTTCCGACTGCGGGGCTTGGCGGACAA 126
QY 121 GGTGGCAGGCGCTGAGGCTGCCGACGCTGCGTGGTGAGGGGAGCTCAGCTCGTTG 180
Db 127 GGTGGCAGGCGCTGAGGCTGCCGACGCTGCGTGGTGAGGGGAGCTCAGCTCGTTG 186
QY 181 TGGGAGCAGCGCGGCACTGGCTGATGAGCCTGGAAGCCTCGCTGCCACTGGT 240
Db 187 TGGGAGCAGCGCGGCACTGGCTGATGAGCCTGGAAGCCTCGCTGCCACTGGT 246
QY 241 CCCAATGCCAGCAACCTCTGATGGGCCCGATTAACCTCACTTCAAGAGATCACTCCT 300
Db 247 CCCAATGCCAGCAACCTCTGATGGGCCCGATTAACCTCACTTCCGGCAGATCACTCCT 306
QY 301 GCGACGGGAGCATCTCTACATCAACATCATATGCTTGGGTGGGACCATCTGC 360
Db 307 GCGACGGGAGCATCTCTACATCAACATCATATGCTTGGGTGGGACCATCTGC 366
QY 361 CTCCTGGGCATCATGGGAACCTCCACGGTCACTTGGCGGTGGAAGAAGTCCAAGCTG 420
Db 367 CTCCTGGGCATCATGGGAACCTCCACGGTCACTTGGCGGTGGAAGAAGTCCAAGCTG 426
QY 421 CACTGTGCAACAACGTCCCGACATCTTCATCATCAACCTCTCGGTAGATCTCTC 480
Db 427 CACTGTGCAACAACGTCCCGACATCTTCATCATCAACCTCTCGGTAGATCTCTC 486
QY 481 TTTCTCCTGGGCATGCCCTTCATGATCCACAGCTCATGGGCAATGGGGTGTGGCACTTT 540
Db 487 TTTCTCCTGGGCATGCCCTTCATGATCCACAGCTCATGGGCAATGGGGTGTGGCACTTT 546
QY 541 GGGAGACCATGTGACCCCTCATCAGCGGCATGGATGCCAATAGTCACTCAGCAGACC 600
Db 547 GGGAGACCATGTGACCCCTCATCAGCGGCATGGATGCCAATAGTCACTCAGCAGACC 606
QY 601 TACATCCTGACCGCATGCGCATTGAACGGTACCTGGCCACTGTCCACCCCATCTCTTCC 660

Db	607	TACATCCTGACCGGCATGGCCATTGACCGGCTACCTGGCCACTGTCCACCCCATCTCTCC	666
QY	661	ACGAAGTTCGGGAAGCCCTCTGTGGCCACCCTGTGTATGCTCCTCTGTGGCCCTCTCC	720
Db	667	ACGAAGTTCGGGAAGCCCTCTGTGGCCACCCTGTGTATGCTCCTCTGTGGCCCTCTCC	726
QY	721	TTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTTCATCCCTTCCAGAGGTGCA	780
Db	727	TTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTTCATCCCTTCCAGAGGTGCA	786
QY	781	GTGGGCTGCGGCATACGCGTGTGCCCCAACCCAGACACTGACTCTACTGGTTCACCCCTGAC	840
Db	787	GTGGGCTGCGGCATACGCGTGTGCCCCAACCCAGACACTGACTCTACTGGTTCACCCCTGAC	846
QY	841	CAGTTTTCCTGGCCCTTGGCCCTGCCCCTTTTGTGTGTCATCACAGCCGCATACGTGAGATC	900
Db	847	CAGTTTTCCTGGCCCTTGGCCCTGCCCCTTTTGTGTGTCATCACAGCCGCATACGTGAGATC	906
QY	901	CTGCAGCGCATGACGCTCTCAGTGGCCCCCGCCTCCACGCGACATCCGGCTGGCGACA	960
Db	907	CTGCAGCGCATGACGCTCTCAGTGGCCCCCGCCTCCACGCGACATCCGGCTGGCGACA	966
QY	961	AAGAGGGTGACCCCGCACAGCCATCGCCATCTGTGTGCTTCTTTGTGTGCTGGCAACC	1020
Db	967	AAGAGGGTGACCCCGCACAGCCATCGCCATCTGTGTGCTTCTTTGTGTGCTGGCAACC	1026
QY	1021	TACTATGTGTACAGCTGACCCCAAGTTGTCCATCAGCCCGCCGACCCTCACCCTTGTCTAC	1080
Db	1027	TACTATGTGTACAGCTGACCCCAAGTTGTCCATCAGCCCGCCGACCCTCACCCTTGTCTAC	1086
QY	1081	TTATACATGCGGCGCATCAGCTTGGGCTATGCCCCAACAGCTGCCCTCAACCCCTTGTGTAC	1140
Db	1087	TTATACATGCGGCGCATCAGCTTGGGCTATGCCCCAACAGCTGCCCTCAACCCCTTGTGTAC	1146
QY	1141	ATCGTGCTCTGTGAGAGCGTTCCGCAAAAGCCTTGGTCTGTGCGGTGAAGCCTGCAGCCAG	1200
Db	1147	ATCGTGCTCTGTGAGAGCGTTCCGCAAAAGCCTTGGTCTGTGCGGTGAAGCCTGCAGCCAG	1206
QY	1201	GGGCAGCTTCGCGCTGTCTCAGCAACGCTCAGACGCGCTGACGAGAGAGACAGAAAGCAAA	1260
Db	1207	GGGCAGCTTCGCGCTGTCTCAGCAACGCTCAGACGCGCTGACGAGAGAGACAGAAAGCAAA	1266
QY	1261	GGCACCTGA 1269	
Db	1267	GGCACCTGA 1275	
RESULT 12			
AAA72924			
ID	AAA72924 standard; cDNA; 1283 BP.		
XX	AAA72924;		
AC			
XX	22-NOV-2000 (first entry)		
DT			
XX	Human SLC-1 (L) cDNA sequence SEQ ID NO:17.		
DE			
XX	SLC-1; MHC; melanin concentrating hormone; screening; eating;		
KW	appetite stimulator; appetite regulator; period pain; atonic bleeding;		
KW	caesarean section; milk congestion; antibiotic agent; drug;		
KW	foetal asphyxia; cervical rupture; premature birth; uterine rupture;		
KW	Prader-Willi syndrome; anorectic; gynaecological; abortifaciant;		
KW	autoanaemia; anabolic; orphan G protein-couple receptor protein; ss.		
OS	Homo sapiens.		
XX	WO200040725-A1.		
PN	13-JUL-2000.		
XX	27-DEC-1999; 99WO-JP07336.		
PF	28-DEC-1998; 98JP-0374454.		
XX			
PR			

PR	28-APR-1999;	99JP-0122688.
PR	02-SEP-1999;	99JP-0249300.
PA	(TAKE) TAKEDA CHEM IND LTD.	
XX		
PI	Mori M, Shimomura Y, Takekawa S, Sugo T, Ishibashi Y, Kitada C;	
PI	Suzuki N;	
XX		
DR	WPI; 2000-475832/41.	
PT	Screening methods for compounds as SLC-1 (ant)agonists useful in the	
PT	treatment of eating disorders and as preventives and remedies for e.g.	
PT	atonic bleeding and Prader-Willi syndrome -	
XX		
PS	Example 11; Page 115-116; 123pp; Japanese.	
CC	The present invention describes a method for screening components (I) or	
CC	their salts that can alter the binding properties of melanin-	
CC	concentrating hormone (MCH) or its derivative or salt to SLC-1 or its	
CC	salt. Compounds identified by (I) are useful as SLC-1 (ant)agonists in	
CC	eating disorders and as preventives and remedies for e.g. period pains,	
CC	uterine recovery failure, caesarean section, artificial interruption of	
CC	pregnancy, galactostosis, tonic uterine contraction, foetal asphyxia,	
CC	rupture of uterus, cervical rupture, premature birth and Prader-Willi	
CC	syndrome. The present sequence represents a human SLC-1 cDNA sequence,	
CC	which is used in an example from the present invention.	
XX		
SQ	Sequence 1283 BP; 238 A; 423 C; 350 G; 272 T; 0 other;	
	Query Match	99.6%; Score 1264.2; DB 21; Length 1283;
	Best Local Similarity	99.8%; Pred. No. 4.4e-284;
	Matches 1266; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1 ATGTCAGTGGGAGGCCATGAAGAAGGAGTGGGAGGGGCAGTTGGCTTGAGGGCGCAGC	60
Db	8 ATGTCAGTGGGAGCCATGAAGAAGGAGTGGGAGGGGCAGTTGGCTTGAGGGCGCAGC	67
QY	61 GGCTGCCAGGCTACGAGGAGAACCCCCCTTCCCAGACTGGCGGGCTTGCGCTCCGGACAA	120
Db	68 GGCTGCCAGGCTACGAGGAGAACCCCCCTTCCAACATGGCGGGCTTGCGCTCCGGACAA	127
QY	121 GGTGGCAGGCGCTGAGGCTGCCGACGCTGCGTGGGTGAGGGGAGCTCAGCTCGGTTG	180
Db	128 GGTGGCAGGCGCTGAGGCTGCCGACGCTGCGTGGGTGAGGGGAGCTCAGCTCGGTTG	187
QY	181 TGGGAGCAGGCGCGGCACTGGCTGGATGACCCTGGAAGCCTCGCTGCGCCACTGGT	240
Db	188 TGGGAGCAGGCGCGGCACTGGCTGGATGACCCTGGAAGCCTCGCTGCGCCACTGGT	247
QY	241 CCCAATGCCAGCAACACTCTGATGGCCCCGATAACCTTCACTTCAGCAGGATCACCTCT	300
Db	248 CCCAAGCCAGCAACACTCTGATGGCCCCGATAACCTTCACTTCGCGAGATCACCTCT	307
QY	301 CGCAGCGGGAGCATCTCTTACATCAACATCATCATGCTTGGGTGTCGGCACCATTCGC	360
Db	308 CGCAGCGGGAGCATCTCTTACATCAACATCATCATGCTTGGGTGTCGGCACCATTCGC	367
QY	361 CTCCTGGGCATCATGGGAACCTCCACGGTCACTTTCGGGGTGTGAAGAAGTCCAAGCTG	420
Db	368 CTCCTGGGCATCATGGGAACCTCCACGGTCACTTTCGGGGTGTGAAGAAGTCCAAGCTG	427
QY	421 CACTGGTGCAACAACGTCGCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTC	480
Db	428 CACTGGTGCAACAACGTCGCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTC	487
QY	481 TTCTCTCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTT	540
Db	488 TTCTCTCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTT	547
QY	541 GGGAGACCATGTGACCCCTCATCACGGCCATGGATGCCAATAGTCAGTTACCCAGCACC	600
Db	548 GGGAGACCATGTGACCCCTCATCACGGCCATGGATGCCAATAGTCAGTTACCCAGCACC	607

QY	601	TACATCCTGACCCGCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC	660
Db	608	TACATCCTGACCCGCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC	667
QY	661	ACGAAGTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCCTCTGTGGGCCCTCTCC	720
Db	668	ACGAAGTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCCTCTGTGGGCCCTCTCC	727
QY	721	TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGCA	780
Db	728	TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGCA	787
QY	781	GTGGGCTCGGCATACGCCCTGCCCCAACCCAGACACTGACCTCTACTGGTTCACCCCTGTAC	840
Db	788	GTGGGCTCGGCATACGCCCTGCCCCAACCCAGACACTGACCTCTACTGGTTCACCCCTGTAC	847
QY	841	CAGTTTTCCTGGCCTTTGGCCCTGCCCTTTGTGTCAATCACAGCCGATACGTGAGATC	900
Db	848	CAGTTTTCCTGGCCTTTGGCCCTGCCCTTTGTGTCAATCACAGCCGATACGTGAGATC	907
QY	901	CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTCCAGCGCAGCATCCGGCTGGCGACA	960
Db	908	CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTCCAGCGCAGCATCCGGCTGGCGACA	967
QY	961	AAGAGGTGACCCCGCACAGCCATCGCCATCTGTCTGTCCTTTGTGTGCTGGGCAACC	1020
Db	968	AAGAGGTGACCCCGCACAGCCATCGCCATCTGTCTGTCCTTTGTGTGCTGGGCAACC	1027
QY	1021	TACTATGTGCTACAGCTGACCCCAAGTTGTCCATCAGCGCCCGCAACCCCTACCTTTGTCTAC	1080
Db	1028	TACTATGTGCTACAGCTGACCCCAAGTTGTCCATCAGCGCCCGCAACCCCTACCTTTGTCTAC	1087
QY	1081	TTATACAATGCGGCCCATCAGCTTGCGCTATGCCAACAGCTGCCCTCAACCCCTTTGTGTAC	1140
Db	1088	TTATACAATGCGGCCCATCAGCTTGCGCTATGCCAACAGCTGCCCTCAACCCCTTTGTGTAC	1147
QY	1141	ATCGTGCTCTGTGAGACGCTCCGCCAAACGCTTGTCCTGTCGGGTGAAGCCTGCAGCCACG	1200
Db	1148	ATCGTGCTCTGTGAGACGCTCCGCCAAACGCTTGTCCTGTCGGGTGAAGCCTGCAGCCACG	1207
QY	1201	GGGCAGCTTCGGCGTGTCAACAACGCTCAGACGGCTGACAGAGAGAGACAGAAAGCAAA	1260
Db	1208	GGGCAGCTTCGGCGTGTCAACAACGCTCAGACGGCTGACAGAGAGAGACAGAAAGCAAA	1267
QY	1261	GGCACCTGA 1269	
Db	1268	GGCACCTGA 1276	

RESULT	13
AAAF86235	
ID	AAAF86235 standard; cDNA; 1283 BP.
XX	
AC	AAAF86235;
XX	
DT	
XX	05-JUL-2001 (first entry)
DE	Human melanin concentrating hormone receptor (L) (SLC-1 L) related cDNA.
XX	
KW	Melanin concentrating hormone; MCH; antagonist; diamine compound;
KW	anorectic; antidiabetic; ophthalmological; neuroprotective; nephrotropic;;
KW	antiarteriosclerotic; antiarthritic; obesity; diabetes; arteriosclerosis;;
KW	arthritis; melanin concentrating hormone receptor; SLC-1; human; ss.
XX	
OS	Homo sapiens.
XX	
PN	WC200121169-A1.
XX	
PD	29-MAR-2001.
XX	
PF	19-SEP-2000; 2000WO-JP06376.
XX	
PR	20-SEP-1999; 99JP-0266278.

PR 17-JUL-2000; 2000JP-0221055.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
PA
XX
XX Kato K, Mori M, Suzuki N, Shimomura Y, Takekawa S, Choh N;
PI
XX
XX WPI; 2001-328055/34.
DR
XX
XX Melanin concentrating hormone antagonists comprise new and known
PT
PT diamine compounds for treating obesity -
XX
XX
PS Examples; Page 275-276; 284pp; Japanese.

CC This invention relates to melanin concentrating hormone (MCH)
CC antagonists, comprising a diamine compound or its prodrug and/or salt.
CC Use of the MCH antagonists can result in anorectic, anti-diabetic,
CC ophthalmological, neuroprotective, nephrotropic, antiarteriosclerotic,
CC and antiarthritic activity. Melanin concentrating hormone (MCH)
CC antagonists can be used for treating obesity (e.g. exogenous obesity,
CC hypophyseal adiposity, hypothalamic obesity and hyperphagia) and
CC associated disorders such as diabetes, diabetic complications (such as
CC diabetic retinopathy, diabetic neuropathy and diabetic nephropathy),
CC arteriosclerosis and arthritis in the knees. The present sequence
CC represents cDNA related to human melanin concentrating hormone receptor
CC (SIC-1). The sequence is used in examples demonstrating the use of the
CC antagonists of the invention.

Sequence 1283 BP; 238 A; 423 C; 350 G; 272 T; 0 other;

Query match	99.68;	Score 1264.2;	DB 22;	Length 1283;
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Best Local Similarity	99.8%;	Pred. No. 4.4e-284;
Matches 1266;	Conservative	0;
	Mismatches	3;
	Indels	0;
	Gaps	0;

QY 1 ATGTCAGTGGAGCCATGAAGAAGGAGCTGGCGCTTGAGAGCGGCACG 60
|||||
8 ATGTCAGTGGAGCCATGAAGAAGGAGCTGGCGCTTGAGAGCGGCACG 67

Db

QY 61 GGCTGCAGGCTACGGAGGAGACCCCTTCCGACTGCGGGGCTTGGGCTCCGGACAA 120
|||||
Db 68 GGCTGCAGGCTACGGAGGAGACCCCTTCCCAACTGCGGGGCTTGGGCTCCGGACAA 127

QY 121 GGTGGCAGCGCTGGAGGCTGCCGACCTGCCTGGGTGGAGGGAGCTCAGCTCGGTTG 180
 128 GGTGGCAGCGCTGGAGGCTGCCGACCTGCCTGGGTGGAGGGAGCTCAGCTCGGTTG 187

QY 181 TGGAGCAGGCGACCGGCACTGGCTGGATGGAACCTGGGAAGCCTCGCTGCCTGCCCACTGGT 240
|||||
188 TGGGAGCAGGCGACCGGCACTGGCTGGATGGAACCTGGGAAGCCTCGCTGCCTGCCCACTGGT 247

[illegible]

QY 301 CGCACGGGAGCATCTCTACATCAACATCATCATGCGCTTCGGGTGTTGGCACCACATCTGC 366
|||||
Db 308 CGCACGGGAGCATCTCTACATCAACATCATCATGCGCTTCGGGTGTTGGCACCACATCTGC 367

QY 361 CTCCTGGCATCATCGGGAACTCCACGTCATCTTGGGTCGTGAAGAAGTCCAAGCTG 420
|||||
Db 368 CTCCTGGGCATCATCGGGAACTCCACGTCATCTTGGGTCGTGAAGAAGTCCAAGCTG 427

	QY	421	CAC TGGTGCACAACGTC	CCCCGACATCTT	CATCATCAACCCTCTCGGTAGTAGATCTCCTC	480
	Db	428	CAC TGGTGCACAACGTC	CCCCGACATCTT	CATCATCAACCCTCTCGGTAGTAGATCTCCTC	487

OY	481	TTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGCAATGGGGTGTCGACATT	540
Db	488	TTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGCAATGGGGTGTCGACATT	547

QY 541 GGGGAGCCATGTGCACCCCTCATCAGGGCCATGGATGCCATAGTCACTTCACCAGCACC 6000

Dh 548 GGGGAGCCATGTGCACCCCTCATCAGGGCCATGGATGCCAATAGTCACTTCACCAGCACC 6070

QY	601	TACATCCTGACCCGCCCATGGCCATTGACCGGCTACCTGGCCACTGTCCACCCCATCTCTCC	660
Db	608	TACATCCTGACCCGCCCATGGCCATTGACCGGCTACCTGGCCACTGTCCACCCCATCTCTCC	667
QY	661	ACGAAGTCCGGAAAGCCCTCTGTGGCCACCCTGTGTGATCTGCTCCTCTGTGGCCCTTCC	720
Db	668	ACGAAGTCCGGAAAGCCCTCTGTGGCCACCCTGTGTGATCTGCTCCTCTGTGGCCCTTCC	727
QY	721	TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATFCCCCTTCCCAGAGGTGCA	780
Db	728	TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATFCCCCTTCCCAGAGGTGCA	787
QY	781	GTGGGCTCGGGCATACGCCCTGGCCCAACCCAGACACTGACCTCTACTGGTCAACCTGTAC	840
Db	788	GTGGGCTCGGGCATACGCCCTGGCCCAACCCAGACACTGACCTCTACTGGTCAACCTGTAC	847
QY	841	CAGTTTTCCTGGCCCTTTGGCCCTGCCCTTTTGTGTGTCATCACAGCCGCATACGTAGGATC	900
Db	848	CAGTTTTCCTGGCCCTTTGGCCCTGCCCTTTTGTGTGTCATCACAGCCGCATACGTAGGATC	907
QY	901	CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTCCAGCGCAGCATCCGGCTGGGAGCA	960
Db	908	CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTCCAGCGCAGCATCCGGCTGGGAGCA	967
QY	961	AAGAGGGTGACCCCGCACAGCCATCGCCATCTGTCTGTCCTTTTGTGTGGGCAACC	1020
Db	968	AAGAGGGTGACCCCGCACAGCCATCGCCATCTGTCTGTCCTTTTGTGTGGGCAACC	1027
QY	1021	TACTATGTGCTACAGCTGACCCAGTGTGCCATCAGCCCCGACCCCTACCTTTGTCTAC	1080
Db	1028	TACTATGTGCTACAGCTGACCCAGTGTGCCATCAGCCCCGACCCCTACCTTTGTCTAC	1087
QY	1081	TTATACAATGCGGCCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTTGTGTAC	1140
Db	1088	TTATACAATGCGGCCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTTGTGTAC	1147
QY	1141	ATCGTGCTCTGTGAGAGCTTCCGCAAAAGCTTGTCTCTGTGGTGAAGCCTGCAGCCAG	1200
Db	1148	ATCGTGCTCTGTGAGAGCTTCCGCAAAAGCTTGTCTCTGTGGTGAAGCCTGCAGCCAG	1207
QY	1201	GGGCAGCTTCGGCGTCTCAGCAACGCTCAGACGGGTGACGAGGAGGACAGAAAGCAAA	1260
Db	1208	GGGCAGCTTCGGCGTCTCAGCAACGCTCAGACGGGTGACGAGGAGGACAGAAAGCAAA	1267
QY	1261	GGCACCCTGA 1269	
Db	1268	GGCACCCTGA 1276	

RESULT 14	
AAAF86981	
ID	AAAF86981 standard; cDNA; 1283 BP.
XX	
AC	AAAF86981;
XX	
DT	06-JUL-2001 (first entry)
XX	
DE	Human SLC-1 coding sequence #3.
XX	
KW	Rat; human; SLC-1; MCH receptor; melanin-concentrating hormone;
KW	obesity; diabetes; hypertension; arteriosclerosis; hyperphagia;
KW	emotional disorder; reproductive disorder; memory disorder;
KW	dementia; hormonal disorder; gonitis; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200121577-A2.
XX	
PD	29-MAR-2001.
XX	
PF	19-SEP-2000; 2000WO-JP06375.
XX	
PR	20-SEP-1999; 99JP-0266298.

16-DEC-1999; 99JP-0357889.
20-APR-2000; 2000JP-0126272.
(TAKE) TAKEDA CHEM IND LTD.
Kato K, Terauchi J, Mori M, Suzuki N, Shimomura Y, Takekawa S;
Ishihara Y;
WPI; 2001-354775/37.
New aromatic compounds are melanin concentrating hormone antagonists,
useful as anorectic agents, for treating or preventing obesity, also
memory or hormonal disorders or diabetes -
Examples; Page 362-363; 363pp; English.
The present invention describes aromatic compounds capable of acting as
melanin-concentrating hormone (MCH) antagonists. Melanin-concentrating
hormone is an appetite control factor and antagonists were expected to be
useful as anti-obesity agents. They can be used in the treatment of
obesity, including malignant mastocytosis, exogenous, hyperinsular,
hypoplasmic, hypothyroid, hypothalamic, symptomatic, infantile, upper
body, alimentary, hypogonadal, simple and central obesity, systemic
mastocytosis and hypophyseal adiposity, hypertension, arteriosclerosis,
hyperphagia, emotional disorders, reproductive function disorders, memory
disorders, dementia, hormonal disorders, diabetes and gonitis. MCH binds
to the SLC-1 receptor. The present sequence is a version of the human
SLC-1 coding sequence given in the specification.

Q	Sequence	1283 BP;	238 A;	423 C;	350 G;	272 T;	0 other;
	Query Match	99.6%;	Score 1264.2;	DB 22;	Length 1283;		
	Best Local Similarity	99.8%;	Pred. No. 4.4e-284;				
	Matches 1266;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;		

QY	1	ATGTCAGTGGGAGCCATTGAAGAAGGGAGTGGGGAGGGCAGTTGGCTTGAGAGCGGCACG	60
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QY	61	GGCTGCCAGGCTTACGGAGAACCCCCCTTCCCGACTGCGGGCTTGCGCTCCGGGACAA	120
Dd	68	GGCTGCCAGGCTTACGGAGAACCCCCCTTCCCAACTGCGGGCTTGCGCTCCGGGACAA	127
QY	121	GGTGGCAGGCGCTGGAGGCTGCCCGACGCTGCGTGGGTGAGGGGAGCTCAGCTCGTTG	180
Dd	128	GGTGGCAGGCGCTGGAGGCTGCCCGACGCTGCGTGGGTGAGGGGAGCTCAGCTCGTTG	187
QY	181	TGGAGCAGGCCACCGGCACCTGGCTGGATGGACCTGGAAAGCCTTGCTGCCCACCTGT	240
Dd	188	TGGAGCAGGCCACCGGCACCTGGCTGGATGGACCTGGAAAGCCTTGCTGCCCACCTGT	247
QY	241	CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTGACGAGGATCACCTCT	300
Dd	248	CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTGCGGAGATCACCTCT	307
QY	301	CGCAGCGGGAGCATCTCCTACATCAACAATCATCATGCGCTTGCGTGTGCGCACCACATCTGC	360
Dd	308	CGCAGCGGGAGCATCTCCTACATCAACAATCATCATGCGCTTGCGTGTGCGCACCACATCTGC	367
QY	361	CTCCTGGGCATCATCGGGAACTCCACGGTCATCTTCCGGGTCTGGAAGAAGTCCAAGCTG	420
Dd	368	CTCCTGGGCATCATCGGGAACTCCACGGTCATCTTCCGGGTCTGGAAGAAGTCCAAGCTG	427
QY	421	CACCTGGTGCACAACGTCCTCCCGACATCTTCATCATCAACCTCTTCGGTAGTAGATCTCTTC	480
Dd	428	CACCTGGTGCACAACGTCCTCCCGACATCTTCATCATCAACCTCTTCGGTAGTAGATCTCTTC	487
QY	481	TTTTCTCTGGGCATGCCCTTCATGATCCACGACTCATGGGCAATGGGGTGTGGCACTTT	540
Dd	488	TTTTCTCTGGGCATGCCCTTCATGATCCACGACTCATGGGCAATGGGGTGTGGCACTTT	547
QY	541	GGGAGACCATGTGCACCTCATCAGGGCATGATGCCAATAGTCAGTTCACCAGCACCC	600

Db	548	GGGGAGACCATGTGCACCCCTCATCAAGGCCATGGATGCCAATAGTCAAGTTCCACCAGACC	607
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Db	608	TACATCCTGACCGCCCATGGCCATTGACCGGCTACCTGGCCACTGTCCACCCCATCTCTCC	667
QY	661	ACGAAGTCCGGAAAGCCCTCTGTGGCCACCCTGGTGTATGCTCCCTCTGTGGCCCTTCC	720
Db	668	ACGAAGTCCGGAAAGCCCTCTGTGGCCACCCTGGTGTATGCTCCCTCTGTGGCCCTTCC	727
QY	721	TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGCA	780
Db	728	TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGCA	787
QY	781	GTGGGCTGGGCATACGCCCTGCTCCCAACCCAGACACTGACCTCTACTGGTCAACCTGTAC	840
Db	788	GTGGGCTGGGCATACGCCCTGCTCCCAACCCAGACACTGACCTCTACTGGTCAACCTGTAC	847
QY	841	CAGTTTTCCTGGCCTTGGCCCTGCCTTTTGTGTATACAGCCGCATACGTAGAGATC	900
Db	848	CAGTTTTCCTGGCCTTGGCCCTGCCTTTTGTGTATACAGCCGCATACGTAGAGATC	907
QY	901	CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTCCACAGCGCATCCGGCTGGCGACA	960
Db	908	CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTCCACAGCGCATCCGGCTGGCGACA	967
QY	961	AAGAGGGTGACCCCGCACAGCCATCGCCATCTGTCTGTCTTTGTGTGCTGGGCACC	1020
Db	968	AAGAGGGTGACCCCGCACAGCCATCGCCATCTGTCTGTCTTTGTGTGCTGGGCACC	1027
QY	1021	TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGAACCCCTCACCTTTGTAC	1080
Db	1028	TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGAACCCCTCACCTTTGTAC	1087
QY	1081	TTATACATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTGTGTAC	1140
Db	1088	TTATACATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTGTGTAC	1147
QY	1141	ATCGTGCTCTGTAGAGCGTTCGGCAAAAGCCTTGGTCTCTGTGGTGAAGCCTGCAGCCAG	1200
Db	1148	ATCGTGCTCTGTAGAGCGTTCGGCAAAAGCCTTGGTCTCTGTGGTGAAGCCTGCAGCCAG	1207
QY	1201	GGGCAGCTTCGGCCTGTACCAACAGCTCAGACGGCTGACGAGGAGAGAGAGAAAGCAA	1260
Db	1208	GGGCAGCTTCGGCCTGTACCAACAGCTCAGACGGCCTGACGAGGAGAGAGAGAAAGCAA	1267
QY	1261	GGCACCTGA 1269	
Db	1268	GGCACCTGA 1276	

```

RESULT 15
ID ABA92417 standard; cDNA; 1283 BP.
XX
AC ABA92417;
XX
DT 14-MAR-2002 (first entry)
XX
DE Human SLC-1 (L) nucleotide sequence SEQ ID NO:15.
XX
KW Human; SLC-1; melanin concentrating hormone antagonist; obesity;
KW anorectic; antidiabetic; hypotensive; antiarteriosclerotic;
KW diabetes; hypertension; arteriosclerosis; ss.
XX
OS Homo sapiens.
XX
PN WO200182925-A1.
XX
PD 08-NOV-2001.
XX
PF 26-APR-2001; 2001WO-JP03614.
XX

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PR 28-APR-2000; 2000JP-0134295.
PR 13-DEC-2000; 2000JP-0384897.
XX
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
XX Ishihara Y, Suzuki N, Takekawa S;
XX
DR WPI; 2002-075131/10.
XX
PT Melanin aggregating hormone antagonist for treating obesity -
PS Example; Page 214-215; 223pp; Japanese.
XX
CC The present invention describes a melanin aggregating hormone antagonist
CC (I). (I) has anorectic, antidiabetic, antiarteriosclerotic and
CC hypotensive. (I) can be used in the treatment and prevention of obesity.
CC It may be combined with treatments for diabetes, hypertension or
CC arteriosclerosis. The present sequence represents a human SLC-1 (L) cDNA
CC sequence, which is used in the exemplification of the present invention.
XX
SQ Sequence 1283 BP; 238 A; 423 C; 350 G; 272 T; 0 other;

Query Match	99.6%;	Score 1264.2;	DB 24;	Length 1283;
Best Local Similarity	99.8%;	Pred. No. 4.4e-284;		
Matches 1266;	Conservative	0;	Mismatches 3;	Indels 0;
Gaps	0;			
QY	1	ATGTCACTGGGAGCCATGAAGAAGGAGTGGGGAGGGCAGTTGGCTTGAGCGCGCAGC	60	
Db	8	ATGTCACTGGGAGCCATGAAGAAGGAGTGGGGAGGGCAGTTGGCTTGAGCGCGCAGC	67	
QY	61	GGCTGCCAGGCTACGGAGGAGACCCCTTCCCGACTGCGGGGCTTGGCTCCGGACAA	120	
Db	68	GGCTGCCAGGCTACGGAGGAGACCCCTTCCCAACTGCGGGGCTTGGCTCCGGACAA	127	
QY	121	GGTGGCAGGCGCTGGAGGCTGCCGACCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTTG	180	
Db	128	GGTGGCAGGCGCTGGAGGCTGCCGACCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTTG	187	
QY	181	TGGGAGCAGGGCGACCGGCACCTGGATGGAGCTGGAAAGCCTGCTGTGCCACTGGT	240	
Db	188	TGGGAGCAGGGCGACCGGCACCTGGATGGAGCTGGAAAGCCTGCTGTGCCACTGGT	247	
QY	241	CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCAGCTTCAGGAGATCACCTCTCT	300	
Db	248	CCCAACGCCAGCAACACCTCTGATGGCCCCGATAACCTCAGCTTCGGCAGAGATCACCTCTCT	307	
QY	301	CGCACGGGGAGCATCTCCTACATCAACATCATCATGCTTCGGTGTGGCACCATCTGCG	360	
Db	308	CGCACGGGGAGCATCTCCTACATCAACATCATCATGCTTCGGTGTGGCACCATCTGCG	367	
QY	361	CTCCTGGGCATCATCGGGAAGCTCCACGGTCATCTTCGGGGTGGTGAAGAAGTCCAAAGCTG	420	
Db	368	CTCCTGGGCATCATCGGGAAGCTCCACGGTCATCTTCGGGGTGGTGAAGAAGTCCAAAGCTG	427	
QY	421	CACGTGTGCAACAACGTCGCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTC	480	
Db	428	CACGTGTGCAACAACGTCGCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTC	487	
QY	481	TTTTCTCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTT	540	
Db	488	TTTTCTCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTT	547	
QY	541	GGGAGAACCATGTGCACCCCTCATACGGCCATGGATGCCAATAGTCAATTCAACGACACC	600	
Db	548	GGGAGAACCATGTGCACCCCTCATACGGCCATGGATGCCAATAGTCAATTCAACGACACC	607	
QY	601	TACATCTGACCGCCATGGCCATGACCGCTACCTGGCCACTGTCCACCCCATCTCTTC	660	
Db	608	TACATCTGACCGCCATGGCCATGACCGCTACCTGGCCACTGTTCACCCCATCTCTCTTC	667	
QY	661	ACGAAGTCCCGAAGCCCTCTGTGGCCACCCCTGGTATCTGCTCTCTGTGGGCCCTCTCC	720	
Db	668	ACGAAGTCCCGAAGCCCTCTGTGGCCACCCCTGGTATCTGCTCTCTGTGGGCCCTCTCC	727	

QY 721 TTCATCAGCATCACCCTGTGTGGCTGTATGCCAGACTCATCCCCCTTCCAGAGGTGCA 780
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Db 788 GTGGGCTGCGGCATACGCCCTGCCCCAACCCAGACACTGACCTCTACTGGTTCACCCCTGTAC 847
QY 841 CAGTTTTCCTGGCCCTTGCCCTGCCTTTTGTGTGTCATCACAGCCGATACGTAGGATC 900
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Db 848 CAGTTTTCCTGGCCCTTGCCCTGCCTTTTGTGTGTCATCACAGCCGATACGTAGGATC 907
QY 901 CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTCCAGCGCATCCGGCTGCGGACA 960
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Db 908 CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTCCAGCGCATCCGGCTGCGGACA 967
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Db 968 AAGAGGCGTGAACCGGACAGCCATCGCCATCTGTGCTCTTCTTGTGTGCTGGGACCC 1027
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Search completed: February 19, 2003, 09:33:07
Job time : 299 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 19, 2003, 09:23:11 ; Search time 2090 Seconds
(without alignments)
9833.528 Million cell updates/sec

Title: US-09-885-478-1
Perfect score: 1269
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Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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BM805549
BM805549.1 GI:19122372
EST.
SOURCE
human.
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 1114)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM12725 row: m column: 24
High quality sequence start: 52
High quality sequence stop: 684.

FEATURES

Location/Qualifiers

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/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
(destroyed); Site_2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

BASE COUNT      198 a      375 c      299 g      241 t      1 others
ORIGIN

Query Match      76.7%; Score 973.8; DB 14; Length 1114;
Best Local Similarity 95.7%; Pred. No. 1.3e-208;
Matches 1043; Conservative 0; Mismatches 43; Indels 4; Gaps 4;

QY 29 TGGGAGGGCAGTTGGGCTTGAGGCGGGCAGCGGCTGCCAGGCTACGGAGGAAGACCC 88
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Db 83 TTCCCGACTGCGGGGCTTGCGCTCCGGGACAAGGTGGCAGGCGCTGGAGGCTGCCGAGC 142

QY 149 CTGCGTGGTGAGGGGAGCTCAGCTCGGTTGTGGAGCAGGCGGCGGACCTGCTGGA 208
Db 143 CTGCGTGGTGAGGGGAGCTCAGCTCGGTTGTGGAGCAGGCGGCGGACCTGCTGGA 202

QY 209 TGGACCTGGAAGCCTCGCTGCTGCCCACTGTGCCAATGCCAGACAACACTCTGATGCC 268
Db 203 TGGACCTGGAAGCCTCGCTGCTGCCCACTGTGCCAATGCCAGACAACACTCTGATGCC 262

QY 269 CCGATAACCTCACTTCAGCAGGATCACTCTCGCAGCGGGAGCATCTCTACATCAACA 328
Db 263 CCGATAACCTCACTTCGGCAGGATCACTCTCGCAGCGGGAGCATCTCTACATCAACA 322

QY 329 TCATCATGCCCTTCGGTGTTCGGGCACCACTCTCCTCGGGCATCATCGGAACTCCAGG 388
Db 323 TCATCATGCCCTTCGGTGTTCGGGCACCACTCTCCTCGGGCATCATCGGAACTCCAGG 382

QY 389 TCATCTTGGGGTCTGGAAGAGTCCAAAGCTGCACGTGTGCAACAACGTCCCGACATCT 448
Db 383 TCATCTTGGGGTCTGGAAGAGTCCAAAGCTGCACGTGTGCAACAACGTCCCGACATCT 442

QY 449 TCATCATCAACCTCTCGGTAGATCTCCTTTCTCCTGGCATGCCCTTCATGATCC 508
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QY 509 ACCAGCTCATGGGCAATGGGGTGTGGCACTTTGGGAGAGCAATGTGCACCCCTCATACGG 568
Db 503 ACCAGCTCATGGGCAATGGGGTGTGGCACTTTGGGAGAGCAATGTGCACCCCTCATACGG 562

QY 569 CCATGGATGCCAATAGTCAGTTCACAGCACCTACATCCTGACCGCCATGGCCATTGACC 628
Db 563 CCATGGATGCCAATAGTCAGTTCACAGCACCTACATCCTGACCGCCATGGCCATTGACC 622

QY 629 GCTACCTGGCCACTGTCCACCCCACTCTTCCACGAGAAGTCCGGAAGCCCTGTGTGCCA 688
Db 623 GCTACCTGGCCACTGTCCACCCCACTCTTCCACGAGAAGTCCGGAAGCCCTGTGTGCCA 682

QY 689 CCCTGGTATCTGCCCTCTGTGGGCCCTCTCTTCATCAGCATCACCCCTGTGTGGCTGT 748
Db 683 CCCTGGTATCTGCCCTCTGTGGGCCCTCTCTTCATCAGCATCACCCCTGTGTGGCTGT 742

QY 749 ATGCCAGACTCATCCCTTCCAGAGGTGACGTGGGCTCGGCATACGCTGCCCAACC 808
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QY 809 CAGACACTGACCTCTACTGCTTCACCCCTGTACCAAGTTTTCCTGGCCCTTGCCCTGCCTT 868
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QY 869 TTGTGTCATCACAGCCGCATACGTGAGGATCTGCAGCGCATGACGTCCTCAGTGCGCC 928
Db 862 TTGTGTCATCACAGCCGCATACGTGAGGATCTGCACAACGCATGACGTCCTCAGTGCGCC 921

QY 929 CCGCCTCCAGCGCAGCATCCGGCTGCGGACAAGAGGCTGACCCCGACAGCATCGCCA 988
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QY 989 TCTGTCTGTCTT-CTTTGTGTGCTGGGCACACCTACTATGTGCTACAGCTGACCCAGTTG 1047
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QY 1048 TCCATCAGCC-GCCCGACCCCTCACCTTTGTCTACTTATACAATGCCGCCATCAGCTTGG 1106
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QY 1107 CTATGCCAAC 1116
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RESULT 2
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LOCUS      958 bp      mRNA      linear      EST 25-SEP-2001
DEFINITION 603025173F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5195443 5',
            mRNA sequence.
ACCESSION  BI754621
VERSION    BI754621.1 GI:15746199
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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REFERENCE  1 (bases 1 to 958)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.lnl.gov
            Plate: L1AM11489 row: b column: 20
            High quality sequence stop: 862.
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
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BASE COUNT      168 a      329 c      256 g      205 t
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Query Match      69.9%; Score 886.4; DB 13; Length 958;
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Matches 941; Conservative 0; Mismatches 16; Indels 5; Gaps 4;			
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Db	1	AGCGGCTGCCAGGCTTACGAGAGAACCCCTTCCCGACTGCGGGGCTTGGCTCCGGGA	60
QY	118	CAAGGTGGCAGGCGCTTGAGGCTGCCGACCTGCGTGGGTGAGGGGAGCTCAGCTCGG	177
Db	61	CAAGGTGGCAGGCGCTTGAGGCTGCCGACCTGCGTGGGTGAGGGGAGCTCAGCTCGG	120
QY	178	TTGTGGAGCAGGGCGACCGGCACTGGCTGGATGACCTGGAAGCCTGCTGCTGCCACT	237
Db	121	TTGTGGAGCAGGGCGACCGGCACTGGCTGGATGACCTGGAAGCCTGCTGCTGCCACT	180
QY	238	GGTCCCAATGCCAGCAACACCTGTGATGGCCCCGATAACCTCAGTTGACAGGATCACCT	297
Db	181	GGTCCCAATGCCAGCAACACCTGTGATGGCCCCGATAACCTCAGTTGCGCAGGATCACCT	240
QY	298	CCTGCGACGGGGAGCATCTCCTACATCAACATCATCATGCCCTTGGTGTCCGACCATC	357
Db	241	CCTGCGACGGGGAGCATCTCCTACATCAACATCATCATGCCCTTGGTGTCCGACCATC	300
QY	358	TGCTCTCTGGGCATCATCGGGAATCCACGGTCATCTCGCGGTGTAAGAAGTCCAAG	417
Db	301	TGCTCTCTGGGCATCATCGGGAATCCACGGTCATCTCGCGGTGTAAGAAGTCCAAG	360
QY	418	CTGCATGCTGCAACAACAGTCCCCGACATCTTCATCATCAACCTCTCGGTAGATCTC	477
Db	361	CTGCATGCTGCAACAACAGTCCCCGACATCTTCATCATCAACCTCTCGGTAGATCTC	420
QY	478	CTCTTCTCTCTGGGCATGCCCTTTCATGATCCACAGCTCATGGGCAATGGGTGTGGCAC	537
Db	421	CTCTTCTCTCTGGGCATGCCCTTTCATGATCCACAGCTCATGGGCAATGGGTGTGGCAC	480
QY	538	TTTGGGAGACCATGTGCACCCCTCATACGGCCATGGATGCCAATAGTCAGTTCAACAGC	597
Db	481	TTTGGGAGACCATGTGCACCCCTCATACGGCCATGGATGCCAATAGTCAGTTCAACAGC	540
QY	598	ACCTACATCTTGACCGGCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCT	657
Db	541	ACCTACATCTTGACCGGCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCT	600
QY	658	TCCAGGAAGTTCGGGAAGCCCTGTGTGGCCACCCCTGTGATGTGCCCTCTGTGGCCCTC	717
Db	601	TCCAGGAAGTTCGGGAAGCCCTGTGTGGCCACCCCTGTGATGTGCCCTCTGTGGCCCTC	660
QY	718	TCCCTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGGAGGT	777
Db	661	TCCCTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGGAGGT	720
QY	778	GCAGTGGGCTGGGCATACGCCCTGCCCC-AAACCAGACACTGACCTCTACTGGTTACCCCT	836
Db	721	GCAGTGGGCTGGGCATACGCCCTGCCCCAAACCAGACACTGACCTCTACTGGTTACCCCT	780
QY	837	GTAACAGTTTTCCTGGCCCTTGGCCCTGCTTTGTGGTCAATCAAGCCGACATACGTAG	896
Db	781	GTAACAGTTTTCCTGGCCCTTGGCCCTGCTTTGTGGTCAATCAAG-CGCATACGTAG	839
QY	897	GATCCTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTGCCAGCGCAGCATCCGGCTGC	956
Db	840	GATCCTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTGCCAGCGCAGCATCCGGCTGC	899
QY	957	GACAAAGAGGGTGACCCGACAGCCATCGCCATCTGTGTGTCTTCTTTGTGTGTGGGC	1016
Db	900	GACAAAGAGGGTGACCCG-6CAGGCATCGCCATCTG--CTGGCTTCTTTGTGTGTGGGC	956
QY	1017	AC 1018	
Db	957	CC 958	

RESULT 3

BI757659			
LOCUS	BI757659	872 bp	mRNA linear EST 25-SEP-2001
DEFINITION	603027991F1 NIH_MGC_114	Homo sapiens	cdna clone IMAGE:5198231 5',
ACCESSION	BI757659		mRNA sequence.
VERSION	BI757659.1	GI:15749237	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 872)		
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/.	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-r@mail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	CDNA Library Preparation: Life Technologies, Inc.		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LLAM11496	row: f	column: 24
	High quality sequence stop: 829.		
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/lab_host="DH10B"			
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Site_2: EcoRV (destroyed); RNA source anonymous pool of 6			
male brains, age range 23-27 yo. Library is oligo-dT			
primed and directionally cloned (EcoRV site is destroyed			
upon cloning). Average insert size 1.5 kb, insert size			
range 1-3 kb. Library is normalized and enriched for			
full-length clones and was constructed by C. Gruber			
(Invitrogen). Research Genetics tracking code 019. Note:			
this is a NIH_MGC Library."			
BASE COUNT			
ORIGIN			
156 a 306 c 208 g 202 t			
Query Match			
Best Local Similarity 98.7%; Pred. No. 3.2e-172;			
Matches 860; Conservative 0; Mismatches 7; Indels 4; Gaps 4;			
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Db	1	CGACCGGCACTGGCTGATGACCTGGAAGCCTCGCTGCTGCCCACTGTCACCATGCCA	60
QY	251	GCAACACTCTGATGGCCCCGATTAACCTCACTTCAGCAGATCACCTCTCGCAGGGGA	310
Db	61	GCAACACTCTGATGGCCCCGATTAACCTCACTTCGGCAGATCACCTCTCGCAGGGGA	120
QY	311	GCATTCCTACATCAACATCATATGCTTGGGTGTGGGCACCATCTGCCCTGGGCA	370
Db	121	GCATTCCTACATCAACATCATATGCTTGGGTGTGGGCACCATCTGCCCTGGGCA	180
QY	371	TCATCG-GGAACCTCAGGTCATCTTCGGGTCGTGAAGAAGTCCAAGCTGCACCTGGTC	429
Db	181	TCATCGGGAAGTCCACGGTCATCTTCGGGTCGTGAAGAAGTCCAAGCTGCACCTGGTC	240
QY	430	AACAAGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTTCTCTCTG	489
Db	241	AACAAGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTTCTCTCTG	300
QY	490	GGCATGCCCTTCATGATTCACCAAGCTGAGGGCAATGGGGTGTGGCACTTTGGGAGACC	549
Db	301	GGCATGCCCTTCATGATTCACCAAGCTGAGGGCAATGGGGTGTGGCACTTTGGGAGACC	360

QY 550 ATGTGACCCCTCATCAGGGCCATGGATGCCAATAGTCACTCACCAGCACCATCATCTCG 609
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Db 361 ATGTGACCCCTCATCAGGGCCATGGATGCCAATAGTCACTCACCAGCACCATCATCTCG 420
QY 610 ACCGCCATGGCCATTGACCGCTACCTGGCCACTGTGCCACCCCATCTCTTCACGAACTTC 669
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Db 421 ACCGCCATGGCCATTGACCGCTACCTGGCCACTGTGCCACCCCATCTCTTCACGAACTTC 480
QY 670 CGAAGCCCTCTGTGGCCACCCTGGTGTATCTGCTCTCTGGGCCCTCTCTCTTCATCAGC 729
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Db 481 CGAAGCCCTCTGTGGCCACCCTGGTGTATCTGCTCTCTGGGCCCTCTCTCTTCATCAGC 540
QY 730 ATCACCCTGTGTGGCTGTATGCCAGACTCATCCCCCTTCCAGAGAGGTGCAGTGGGCTGC 789
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Db 541 ATCACCCTGTGTGGCTGTATGCCAGACTCATCCCCCTTCCAGAGAGGTGCAGTGGGCTGC 600
QY 790 GGCATACGGCTGCCCAACCCAGACACTGACCTCTACTGCTTCAACCCCTGTACCAGTTTTC 849
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Db 780 ACCCGACAGCCATCGCCATCTGTCTGTCTTCTTGTGTGGGACCCCTACTATGTG 1029
QY 970 ACCCGACAGCCATCGCCATCTGTCTGTCTTCTTGTGTGGGACCCCTACTATGTG 1029
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Db 780 ACCCGTACAG-CATCGCCATCTGTCTGTCTTCTTGTGTGGGAC-CCTACTATGTG 837
QY 1030 CTACAGCTGACCCAGTGTGTCCATCAGCGGCC 1060
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Db 838 CTACAGTGTGACCCAGTGTGTCCATCAGCGGCC 868

RESULT 4

LOCUS BG913631 921 bp mRNA linear EST 05-JUN-2001
DEFINITION 602811509F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4943498
5', mRNA sequence.

ACCESSION BG913631
VERSION BG913631.1 GI:14294107
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 921)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10887 row: a column: 03
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Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Best Local Similarity 93.8%; Pred. No. 1.4e-163;
Matches 860; Conservative 0; Mismatches 51; Indels 6; Gaps 5;

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QY 115 GGACAAGGTGGCAGGCGCTGGAGGCTGCCGACGCTGCGTGGTGGAGGGAGCTCAGCT 174
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Db 61 GGACAAGGTGGCAGGCGCTGGAGGCTGCCGACGCTGCGTGGTGGAGGGAGCTCAGCT 120
QY 175 CGGTTGTGGAGCAGCGCAGCCGACCTGGATGGACCTGGAAGCCTCGCTGCTGCC 234
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Db 121 CGGTTGTGGAGCAGCGCAGCCGACCTGGATGGACCTGGAAGCCTCGCTGCTGCC 180
QY 235 ACTGTCCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTCACAGAGATCA 294
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Db 181 ACTGTCCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTCGCAAGATCA 240
QY 295 CCTCCTCGCAGCGGAGCATCTCCTACATCAACATCATCATGCTTCCGTTGCTCGCAC 354
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Db 241 CCTCCTCGCAGCGGAGCATCTCCTACATCAACATCATCATGCTTCCGTTGCTCGCAC 300
QY 355 ATCTGCCCTCCTGGGCATCATCGGGAACCTCCACGGTCACTCTTCCGGTGTGAAGAAGTCC 414
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Db 301 ATCTGCCCTCCTGGGCATCATCGGGAACCTCCACGGTCACTCTTCCGGTGTGAAGAAGTCC 360
QY 415 AAGCTGCACTGTGCAACAACAGTCCCGACATCTTCATCATCAACCTCTCGGTAGTAGAT 474
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Db 361 AAGCTGCACTGTGCAACAACAGTCCCGACATCTTCATCATCAACCTCTCGGTAGTAGAT 420
QY 475 CTCCCTCTTCTCCGCGCATGCCCCCTTCATGATCCACCAGCTCATGGGCAATGGGTTGG 534
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Db 421 CTCCCTCTTCTCCGCGCATGCCCCCTTCATGATCCACCAGCTCATGGGCAATGGGTTGG 480
QY 535 CACTTTGGGAGACCATGTGCACCCCTCATGCAGCGCCATGATGCCAATAGTCAAGTTACCC 594
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Db 481 CACTTTGGGAGACCATGTGCACCCCTCATGCAGCGCCATGATGCCAATAGTCAAGTTACCC 540
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Db      899 CCGAGAAAGATGGGAG 915

RESULT 5
BI818742
LOCUS
DEFINITION      BI818742          797 bp      mRNA      linear      EST 04-OCT-2001
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                  mRNA sequence.
ACCESSION      BI818742
VERSION        BI818742.1  GI:15930292
KEYWORDS
SOURCE
ORGANISM      human.
                  Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL        National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT        Unpublished (1999)
                  Contact: Robert Strausberg, Ph.D.
                  Email: cgabs-remail.nih.gov
                  Tissue Procurement: Life Technologies, Inc.
                  cDNA Library Preparation: Life Technologies, Inc.
                  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                  DNA Sequencing by: Incyte Genomics, Inc.
                  Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LLNL at:
                  http://image.llnl.gov
                  Plate: LLAM11445 row: 0 column: 17
                  High quality sequence stop: 774.
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            oligo-dT primed and directionally cloned (EcoRV site is
            destroyed upon cloning). Average insert size 1.8 kb,
            insert size range 1-3 kb. Library is normalized and
            enriched for full-length clones and was constructed by C.
            Gruber (Invitrogen). Research Genetics tracking code
            021. Note: this is a NIH_MGC Library."
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Best Local Similarity 99.5%; Pred. No. 8.8e-163;
Matches 793; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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OY      77 AGGAAGACCCCTTCCGACTGCGGGCTTCGCTCCGGGACAAGGTGGCAGGCGCTGA 136
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Db      61 AGGAAGACCCCTTCCGACTGCGGGCTTCGCTCCGGGACAAGGTGGCAGGCGCTGA 120

OY      137 GGCTGCCGACGCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTGTGGAGCAGGGCAGCCG 196
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Db      121 GGCTGCCGACGCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTGTGGAGCAGGGCAGCCG 180

OY      197 GCACTGGCTGATGAGACCTGGAAGCCTCGCTGCTGCCACTGTGCCAATGCCAGCAACA 256
        |||||||
Db      181 GCACTGGCTGATGAGACCTGGAAGCCTCGCTGCTGCCACTGTGCCAATGCCAGCAACA 240

OY      257 CCTCTGATGGCCCGATAACCTCACTTACGACAGATCACCTCTCGCACGGGAGCATCT 316
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OY      497 CCTTCATGATCCACAGCTCATGCGCAATGGGGTGTGGCACTTTGGGGAGACCATGTGCA 556
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OY      617 TGGCCATTGACCGCTACCTGGCCACCTGTCCACCCCATCTCTTCCAGAAATTCCGGAAGC 676
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Db      601 TGGCCATTGACCGCTACCTGGCCACCTGTCCACCCCATCTCTTCCAGAAATTCCGGAAGC 660

OY      677 CCTCTGTGGCCACCCCTGTGATCTGCTCTGTGGGCCCTCTCCTTCATCAGCATCACCC 736
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Db      661 CCTCTGTGGCCACCCCTGTGATCTGCTCTGTGGGCCCTCTCCTTCATCAGCATCA-CC 719

OY      737 CTGTGTGCTGTATGCCAGACTCATCCCTTCCACAGAGGTGA-GTGGGCTGGCGCATTA 795
        |||||||
Db      720 CTGTGTGCTGTATGCCAGACTCATCCCTTCCACAGAGGTGCAATGTGGCTGGCGCATTA 779

OY      796 CGCCTGCCCAACCCAGA 812
        |||||||
Db      780 CGCCTGCCCAAGCCAGA 796

RESULT 6
BF342364
LOCUS
DEFINITION      BF342364          834 bp      mRNA      linear      EST 22-NOV-2000
                  602013155F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4148940
                  5', mRNA sequence.
ACCESSION      BF342364
VERSION        BF342364.1  GI:11289365
KEYWORDS
SOURCE
ORGANISM      human.
                  Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL        National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT        Unpublished (1999)
                  Contact: Robert Strausberg, Ph.D.
                  Email: cgabs-remail.nih.gov
                  Tissue Procurement: David N. Louis, M.D.
                  cDNA Library Preparation: Life Technologies, Inc.
                  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                  DNA Sequencing by: Incyte Genomics, Inc.
                  Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LLNL at:
                  http://image.llnl.gov
                  Plate: LLAM9409 row: n column: 13
                  High quality sequence start: 20
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		/lab_host="DH10B (T1 phage-resistant)"	
		/note="Organ: brain; Vector: pCMV-SpOR6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.57 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP Library."	
BASE COUNT	142 a	271 c	232 g 188 t 1 others
ORIGIN			
Query Match	49.3%;	Score 625.2;	DB 12; Length 834;
Best Local Similarity	95.1%;	Pred. No. 2.9e-130;	
Matches 720; Conservative	0;	Mismatches 29;	Indels 8; Gaps 7;
OY	67	CAGGCTACGGAGGAAGACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGGACAGAAGTGGC	126
Db	29	CAGGCTACGGAGGATGACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGGACAGAAGTGGC	88
OY	127	AGCGGCTGAGGCTGCCGAGCCTGCGTGGGTGGAGGGAGCTCAGCTGGTGTGGGAG	186
Db	89	AGCGGCTGAGGCTGCCGAGCCTGCGTGGGTGGAGGGAGCTCAGCTGGTGTGGGAG	148
OY	187	CAGGCGACCGGCACTGGCTGATGGACCTGGAAGCCTGCTGCTGCCACTGGTCCCAAT	246
Db	149	CAGGCGA-CGGCACTGGCTGATGGACCTGGAAGCCTGCTGCTGCCACTGGTCCCAAG	207
OY	247	GCCAGCAA-CACCTTGATGGCCCCGATAACCTCACTTCAGCAGGATCACCTCCTCGCAC	305
Db	208	GCCAGCAAGCACCTTGATGGCCCCGATAACCTCACTTCGGCAGGATCACCTCCTCGCAC	267
OY	306	GGGAGCATCTCTACATCAACATCATATGCTGCTGGTGTGGCACCATCTGCTCCT	365
Db	268	GGGAGCATCTCTCTACATCAACATCATATGCTGCTGGTGTGGCACCATCTGCTCCT	327
OY	366	GGGATCATCGGGAACCTCCAGGTCATCTTGGCGGTGTAAGAAGTCCAAGCTGCAC	425
Db	328	GGGATCATCGGGAACCTCCAGGTCATCTTGGCGGTGTAAGAAGTCCAAGCTGCAC	387
OY	426	GTCAACAACGTCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTCTTCT	485
Db	388	GTCAACAACGTCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTCTTCT	447
OY	486	CCTGGGATGCCCTTCATGATCCACCAAGCTCATGGGCAATGGGGTGTGGCATTGGGGA	545
Db	448	CCTGGGATGCCCTTCATGATCCACCAAGCTCATGGGCAATGGGGTGTGGCATTGGGGA	507
OY	546	GACCATGTGACCCCTCATCAGGCGCATGGATGCCAATAGTCAGTTCAACGACACTACAT	605
Db	508	GACCATGTGACCCCTCATCAGGCGCATGGATGCCAATAGTCAGTTCAACGACACTACAT	567
OY	606	CCTGACCGCCATGGCCATTGACCGGTACCTGGCAGCTGTCCACCCCATCTCTTCCAGAA	665
Db	568	CCTGNACG-CATGGCCATTGACCG--TACCTGGCCAGCTGTCCACCCCATCTCTTCCAGAA	625
OY	666	GTTCCGGAAGCCCTCTGTGGCAACCCCTGGTATCTGCCCTCTGTGGGCCCTCTCTTCAT	725
Db	626	GTTCCGGAAGCCCTCTGTGG--CACCCCTGGTATCTGTCTCTGTGGGCCCTCTCTTCAT	684
OY	726	CAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGG-TGCAGTGG	784
Db	685	CAGCATCACCCCTGTGTGG--TGTTCAGAGACTCATCCCTTCCAGAGAGTGCAGTGG	742
OY	785	GCTGGGATACGCTGCCCAACCCAGACACTGACCT	821
Db	743	GCTGGGATACGCTGCCCAACCCAGATGACTCTACT	779
RESULT 7			
LOCUS	BF966511	845 bp	mRNA linear EST 23-JAN-2001
DEFINITION	602286863F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4375863 5', mRNA sequence.		
ACCESSION	BF966511		
VERSION	BF966511.1 GI:12333726		
KEYWORDS	EST.		

SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 845)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10041 row: m column: 16 High quality sequence stop: 661.				
FEATURES	Location/Qualifiers				
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	/clone_lib="NIH_MGC_95"				
	/tissue_type="hippocampus"				
	/lab_host="DH10B"				
	/note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."				
BASE COUNT	137 a	279 c	246 g	183 t	
ORIGIN					
Query Match	48.0%;	Score 609.4;	DB 12;	Length 845;	
Best Local Similarity	92.8%;	Pred. No. 1e-126;			
Matches	706;	Conservative	0;	Mismatches 46;	Indels 9;
					Gaps 6;
OY	34	AGGCGAGTTGGGCTTGAGAGCGCGGAGGCTGCCAGGCTACGGAGGAAGACCCCTTCCC	93		
Db	1	AGCGGAGGTGGGCTTGAGAGCGCGGAGGCTGCCAGGCTACGGAGGAAGACCCCATTTCC	60		
OY	94	GACTGGGGGCTTGCGCTCCGGGACAAAGTGGCAGGGCTGTGAGGCTGCCGACGCTGGC	153		
Db	61	AACTGGGGGCTTGCGCTCCGGGACAAAGTGGCAGGGCTGTGAGGCTGCCGACGCTGGC	120		
OY	154	TGGGTGAGGGAGGCTCAGCTCGGTGTGGGAGCAGGGCAGCCGGCATGGCTGGATGGAC	213		
Db	121	TGGGTGAGGGAGGCTCAGCTCGGTGTGGGAGCAGGGCAGCCGGCATGGCTGGATGGAC	180		
OY	214	CTGGAAGCCTCGCTGCTGCCCACTGTGCCAATGCCAGCAACACCTCTGATGGCCCGAT	273		
Db	181	CTGGAGCCTCGCTGCTGCCCACTGTGCCAAGCCAGCAACACCTCTGATGGCCCGAT	240		
OY	274	AACCTCACTTACGAGGATCACCTCTCGGACGGGGAGCATCTCTACATCAACATCATC	333		
Db	241	AACCTCACTTACGAGGATCACCTCTCGGACGGGGAGCATCTCTACATCAACATCATC	300		
OY	334	ATGCCTTGGGTGTTCGGCACCATCTGCCCTTGGGCATCATCGGGAAGTCCACGGTCAATC	393		
Db	301	ATGCCTTGGGTGTTCGGCACCATCTGCCCTTGGGCATCATCGGGAAGTCCACGGTCAATC	360		
OY	394	TTGCGGGTGTGAAGAAGTCCAAGCTGCACCTGTGCAACAACAGTCCCGGACATTTCAATC	453		
Db	361	TTGCGGGTGTGAAGAAGTCCAAGCTGCACCTGTGCAACAACAGTCCCGGACATTTCAATC	420		
OY	454	ATCAACCTCTCGGTAGTAGATCTCTCTTCTCTGGGCATGCCCTTCATGATCCACCAG	513		

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Db 421 ATCAACCTCTCGTAGTAGATCTCTCTTCTCTCTGGCATGCCCTTCATGATCCACAG 480
QY 514 CTCATGGCAATGGGGTGTGGCACTTTGGGGAGAGACCATGTGCACCCCTCATCAGGGCATG 573
Db 481 CTCATGGCAATGGGGTGTGGCACTTTGGGGAGAGACCATGTGCACCCCTCATCAGG-CATG 539
QY 574 GATGCCAATAGTCACTTCACAGCACCCTACATCCTGACCGCCCATGGCCATGACCGCTAC 633
Db 540 GATGCCAATAGTCACTTCACAGCACCCTACATCCTGACG-CATGGGCATTGACCGCTAC 598
QY 634 CTGG-CCACTGTCCACCCCATCTCTTCCACGAAGT--CCGGAAGCCCTCTGTGGCCAC 689
Db 599 CTGGCCCACTGTCCACCCCATCTCTTCCACGAAGTCCCGGAAGCCCTCTGTGGGCC 658
QY 690 CCTGTGATCTGCTCTCTGTG-GGCCCTCTCTCTTCATCAGCATCACCCCTGTGTGGCT-- 746
Db 659 CTGTTGATCTTGTCTCTCTGTGTGGCCCTCTCTTCATTCAGTTTACCCCTGTGTGGTTG 718
QY 747 GTATGCCAGACTATCCCCCTTCCCAGAGGTGCAGTGGGCT 787
Db 719 GTTTCCAATTCATCTCTCCGAGGGGCTGGGCTGGGT 759

RESULT 8
LOCUS BG519797 869 bp mRNA linear EST 02-APR-2001
DEFINITION 602578956F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503484 5',
mRNA sequence.
ACCESSION BG519797
VERSION BG519797.1 GI:13515559
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 869)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM176 row: P column: 13
High quality sequence stop: 780.
Location/Qualifiers

FEATURES
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/clone="IMAGE:3503484"
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/issue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; site_1: XhoI; site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 175 a 259 c 258 g 177 t
ORIGIN

Query Match 46.5%; Score 590.2; DB 12; Length 869;
Best Local Similarity 98.5%; Pred. No. 2.2e-122;
Matches 606; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 ATGTCACTGGGAGCCATGAAGAGGAGTGGGAGGCGAGTTGGCTTGAAGCGGCAGC 60
Db 215 ATGTCACTGGGAGCCATGAAGAGGAGTGGGAGGCGAGTTGGCTTGAAGCGGCAGC 274
QY 61 GGCTGCCAGGCTACGGAGGAAGACCCCTTCCGACTGCGGGGCTTGGCTCCGGGACAA 120
Db 275 GGCTGCCAGGCTACGGAGGAAGACCCCTTCCGACTGCGGGGCTTGGCTCCGGGACAA 334
QY 121 GGTGGCAGGCGCTGGAGGCTGGCCGACGCTGCGTGGGTGGAGGGAGGAGCTCAGCTGGTTG 180
Db 335 GGTGGCAGGCGCTGGAGGCTGGCCGACGCTGCGTGGGTGGAGGGAGGAGCTCAGCTGGTTG 394
QY 181 TGGAGCAGGCGCAGCCGCGACTGCTGATGACCTGGAAGCCTCGCTGCCACTGGT 240
Db 395 TGGAGCAGGCGCAGCCGCGACTGCTGATGACCTGGAAGCCTCGCTGCCACTGGT 454
QY 241 CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTCAGCAGATCACCTCCT 300
Db 455 CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTCAGCAGATCACCTCCT 514
QY 301 CGCAGCGGAGCATCTCTACATCAACATCATCATGCTTGGGTGTGGCAACCATCTGC 360
Db 515 CGCAGCGGAGCATCTCTACATCAACATCATCATGCTTGGGTGTGGCAACCATCTGC 574
QY 361 CTCCTGGGCATCATCGGGAACCTCCAGCTCATCTTCCGGCTCGTGAAGAATCCAACTG 420
Db 575 CTCCTGGGCATCATCGGGAACCTCCAGCTCATCTTCCGGCTCGTGAAGAATCCAACTG 634
QY 421 C-ACTGTGCAACAACAGTCCCGGACATCTTCATCATCAACCTCTCGGTAGTATCTCCT 479
Db 635 CAACTGTGCAACAACAGTCCCGGACATCTTCATCATCAACCTCTCGGTAGTATCTCCT 694
QY 480 CTTTCTCTGGGCATGCCCCCTTCATGATCCACAGCTCATGAGGCAATGGGGTGGCAGCTT 539
Db 695 CTTTCTCTGGGCATGCCCCCTTCATGATCCACAGCTCATGAGGCAATGGGGTGGCAGCTA 754
QY 540 TGGGAGACCATGTGCACCCCTCATTCAGCGGCATGATGCCAATAGTCAGTTTCAACGAC 599
Db 755 TGGGAGACCATGTGCACCCCTCATTCAGCGGCATGATGCCAATAGTCAGTTTCAACGAG 814
QY 600 CTACATCTGACCGC 614
Db 815 CTACATCTGACCGC 829

RESULT 9
LOCUS BI818110 685 bp mRNA linear EST 04-OCT-2001
DEFINITION 603032324F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173852 5',
mRNA sequence.
ACCESSION BI818110
VERSION BI818110.1 GI:15928318
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 685)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11432 row: O column: 05
High quality sequence stop: 679.
Location/Qualifiers

FEATURES

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		/lab_host="DH10B"			
		/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."			
BASE COUNT	132 a	205 c	212 g	136 t	
ORIGIN					
Query Match 44.6%; Score 566.2; DB 13; Length 685;					
Best Local Similarity 99.5%; Pred. No. 5.1e-117;					
Matches 568; Conservative 0; Mismatches 3; Indels 0; Gaps 0;					
QY	1	ATGTCAGTGGAGCCATGAGAAGGAGGTGGAGGCGAGTTGGCTTGAGCGCGCAGC	60		
Db	115	ATGTCAGTGGAGCCATGAGAAGGAGTGGGAGGCGAGTTGGCTTGAGGCGGCAGC	174		
QY	61	GGCTGCCAGGCTACGAGAGAACCCCTTCCGACTGCGGGGCTTGCGCTCCGGAGCAA	120		
Db	175	GGCTGCCAGGCTACGAGAGAACCCCTTCCGACTGCGGGGCTTGCGCTCCGGAGCAA	234		
QY	121	GGTGGAGGCGCTGAGAGCTGCCGACGCTGCGTGGTGGAGGGAGCTCAGCTCGGTTG	180		
Db	235	GGTGGAGGCGCTGAGAGCTGCCGACGCTGCGTGGTGGAGGGAGCTCAGCTCGGTTG	294		
QY	181	TGGGACGAGGCGGACCGGCACTGGCTGGATGACCTGGAAGCCTCGCTGCCACTGGT	240		
Db	295	TGGGACGAGGCGGACCGGCACTGGCTGGATGAGCCTGGAAGCCTCGCTGCCACTGGT	354		
QY	241	CCCAATGCCACACACACCTCTGATGGCCCCGATAACCTCACTTCAGCAGATCACTCT	300		
Db	355	CCCAATGCCACACACACCTCTGATGGCCCCGATAACCTCACTTCGGCAGATCACTCT	414		
QY	301	CGCAGCGGAGCATCTCTACATCAACATCATCATGCTTGGCTGTCGGCAACCATCTGC	360		
Db	415	CGCAGCGGAGCATCTCTACATCAACATCATCATGCTTGGCTGTCGGCAACCATCTGC	474		
QY	361	CTCCTGGGCATCATGGGAACCTCCAGGTCATCTTCCGGTCTGAAGAGTCCAAGCTG	420		
Db	475	CTCCTGGGCATCATGGGAACCTCCAGGTCATCTTCCGGTCTGAAGAGTCCAAGCTG	534		
QY	421	CACGTGTGCAACAACGTCCCGACATCTTCATCATCAACCTCTCGTAGATCTCTC	480		
Db	535	CACGTGTGCAACAACGTCCCGACATCTTCATCATCAACCTCTCGTAGATCTCTC	594		
QY	481	TTTCTCTGGGCATGCCCCCTTCATGATCCACCAGCTCATGGGCAATGGGTGTGGCACTT	540		
Db	595	TTTCTCTGGGCATGCCCCCTTCATGATCCACCAGCTCATGGGCAATGGGTGTGGCACTT	654		
QY	541	GGGAGACCATGTGCACCCCTCATCAGGGCCA	571		
Db	655	GGGAGACCATGTGCACCCCTCATCAGGGACA	685		
RESULT 10					
LOCUS	BE312747	859 bp	mRNA	linear	EST 26-OCT-2000
DEFINITION	601150756f1 NIH_MGC_19	Homo sapiens	cdna	clone	IMAGE:3503484 5',
mRNA sequence.					
ACCESSION	BE312747				
VERSION	BE312747.1	GI:9131846			
KEYWORDS	EST.				
SOURCE	human.				

ORGANISM		Homo sapiens			
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.			
REFERENCE		1 (bases 1 to 859)			
AUTHORS		NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL		unpublished (1999)			
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov Tissue Procurement: ATCC cdna Library Preparation: Ling Hong/Rubin Laboratory cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM176 row: p column: 13 High quality sequence start: 3 High quality sequence stop: 733.			
FEATURES		Location/Qualifiers			
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		/tissue_type="neuroblastoma"			
		/lab_host="DH10B (phage-resistant)"			
		/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cdna made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."			
BASE COUNT	151 a	267 c	254 g	186 t	1 others
ORIGIN					
Query Match 38.5%; Score 489; DB 10; Length 859;					
Best Local Similarity 94.0%; Pred. No. 1.2e-99;					
Matches 553; Conservative 0; Mismatches 26; Indels 9; Gaps 4;					
QY	1	ATGTCAGTGGAGCCATGAGAAGGAGTGGGAGGGCAGTTGGCTTGAGCGCGCAGC	60		
Db	194	ATGTCAGTGGAGCCATGAGAAGGAGTGGGAGGGCAGTTGGCTTGAGCGCGCAGC	253		
QY	61	GGCTGCCAGGCTACGAGAGAACCCCTTCCGACTGCGGGGCTTGCGCTCCGGAGCAA	120		
Db	254	GGCTGCCAGGCTACGAGAGAACCCCTTCCGACTGCGGGGCTTGCGCTCCGGAGCAA	313		
QY	121	GGTGGAGGCGCTGAGAGCTGCCGACGCTGCGTGGTGGAGGGGAGCTCAGCTCGGTTG	180		
Db	314	GGTGGAGGCGCTGAGAGCTGCCGACGCTGCGTGGTGGAGGGGAGCTCAGCTCGGTTG	373		
QY	181	TGGGAGCAGGCGGACCGGCACTGGCTGGATGACCTGGAAGCCTCGCTGCCACT--G	238		
Db	374	TGGGAGCAGGCGGACCGGCACTGGCTGGATGACCTGGAAGCCTCGCTGCCACTTGG	433		
QY	239	GTCCCAATGCCACACAACCTCTGATGGCCCCGATAACCTCACTTCAGCAGATCACTC	298		
Db	434	TTCCCAATGCCACACAACCTCTGATGGCCCCGATAACCTCACTTCGGCAGATCACTC	493		
QY	299	CTGCACGGGAGCATCTCTACATCAACATCATGCTTCCGTTGGGACACATCT	358		
Db	494	CTGCACGGGAGCATCTCTACATCAACATCATGCTTCCGTTGGGACACATCT	553		
QY	359	GCCTCCTGGGCATTCGGAACCTCCACGGTCATCTTCCGGTGTGAAGAGTCCAAGC	418		
Db	554	GCCTCCTGGGCATTCGGAACCTCCACGGTCATCTTCCGGTGTGAAGAGTCCAAGC	613		
QY	419	TGCACGTGTGCAACAAGTCCCGACATC--TTCATCATCAACCTCTCGGTAG----TAG	472		
Db	614	TGCACGTGTGCAACAAGTCCCGACATCTTTCATCATCAACCTCTCGGTAGGTAGATCT	673		


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QY 473 ATCTCCTCTTTCCTCTGGGACATGCCCTTCATGATCCACCAGCTTCATGGGCAATGGGGTGT 532
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Db 674 CCTTCTTCTCTGTGGCATTCGNCCTTCATGATCCACCAGCTTCATGGGCAATGGGGTGT 733
QY 533 GGCAC-TTTGGGGAGACCATGTGCACCCCTCATCAGCGCCATGATGCC 579
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Db 734 GGCACTTTTGGGGAGACCCTGTGGCCCTCATCATCAGCATGGGTGGC 781

RESULT 11
BE312542 600 bp mRNA linear EST 26-OCT-2000
LOCUS 601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5',
DEFINITION mRNA sequence.
ACCESSION BE312542
VERSION BE312542
KEYWORDS EST.
SOURCE BE312542.1 GI:9131383
ORGANISM human.
          Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 600)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: ATCC
          CDNA Library Preparation: Ling Hong/Rubin Laboratory
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
          Plate: L1CM175 row: m column: 05
          High quality sequence start: 7
          High quality sequence stop: 574.

FEATURES
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            /clone_lib="NIH_MGC_19"
            /tissue_type="neuroblastoma"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
            EcoRI; cDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5'
            adaptor: GGCACGAG(G). Library constructed by Ling Hong
            in the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: this is a NIH_MGC library."

BASE COUNT 113 a 174 c 197 g 116 t

Query Match 30.4%; Score 386.4; DB 10; Length 600;
Best Local Similarity 99.5%; Pred. No. 1.3e-76;
Matches 398; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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RESULT 12
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LOCUS F07228
DEFINITION HSC1ZF101 normalized infant brain cDNA Homo sapiens cDNA clone
c-1zf10, mRNA sequence.
ACCESSION F07228
VERSION F07228.1 GI:672877
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 345)
AUTHORS Aufray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes
          ,M.D., Duprat,S., Houligatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F.,
          Mitchell,H., Mariage-Samson,R., Pletu,G., Poullet,Y.,
          Sebastiani-Kabakchis,C. and Tessier,A.
          IMAGE: molecular integration of the analysis of the human genome
          and its expression
          C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
          95277534
          Contact: Genethon
          Genexpress-Genethon
          Genethon Centre de recherche sur le Genome Humain
          1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
          Tel: 33169472800
          Fax: 33160778698
          Email: genexpress@genethon.fr
          Single read.
          Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-1zf10
          Seq primer: (-21)M13 universal.

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            /tissue_type="total brain"
            /dev_stage="3 months old"
            /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
            Site_2: NotI; sex=Female; dev_stage=3 months old;
            isolate=muscular atrophy patient; tissue_type=total brain
            ; total mRNA was oligo-(dT) primed and directionally
            cloned 5' -> 3' into the HindIII -> NotI sites of the
            lafmid BA vector. Clone library from B.Souares, Psychiatry
            Dept. Columbia University, USA. Normalization_method:
            Bento Soares, P.N.A.5 in press"

BASE COUNT 67 a 118 c 79 g 80 t 1 others

Query Match 27.1%; Score 344; DB 14; Length 345;
Best Local Similarity 99.7%; Pred. No. 3.9e-67;
Matches 344; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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BE647763
LOCUS BE647763
DEFINITION UI-M-BH1-ant-c-04-0-UI.r1 NIH_BMAP_M_S2 Mus musculus cDNA clone
UI-M-BH1-ant-c-04-0-UI 5', mRNA sequence.
ACCESSION BE647763 GI:9973583
VERSION BE647763
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 387)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: MEST@mail.nih.gov
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements
Seq primer: M13 Reverse.
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/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: PT7T3D-Pac (Pharmacia) with a modified
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NIH_BMAP_M_S2 library is a subtracted library derived from
NIH_BMAP_M_S1, which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hippocampus). The driver
used for subtraction consisted of a pool of 5,000 clones
from the NIH_BMAP_M_S1 library and a pool of 2,000 clones

BASE COUNT 84 a 121 c 102 g 80 t
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Best Local Similarity 92.9%; Pred.No.8.4e-55;
Matches 303; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
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Db 181 TCAATCCCTTTGTGTACATGACTCTGTGAGACCTTTCGAAACGCTTGTGTCTGTGG 240
QY 1184 TGAAGCCTGCAGCCCGAGGGGAGCCTTCGGCGTGTACGCAACGCTCAGACGCGCTGACGAGG 1243
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Db 241 TGAAGCCCGCGCGCCAGGGGAGCCTTCGCACGCTGACCAATGCTCAGACAGCTGACGAGG 300
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LOCUS BF313837
DEFINITION 601902234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4134848 5',
mRNA sequence.
ACCESSION BF313837 GI:11261906
VERSION BF313837
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1086)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: AFCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LICM1038 row: c column: 09
High quality sequence stop: 603.
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/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 12:07:02 ; Search time 56 Seconds
(without alignments)
2311.028 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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3	2212	100.0	1269	4	US-09-478-602-1 Sequence 1, Appli
4	2164	97.8	1385	3	US-08-984-288-1 Sequence 1, Appli
5	2000	90.4	3488	4	US-09-218-467B-1 Sequence 1, Appli
6	1783	80.6	1214	4	US-09-224-426-3 Sequence 3, Appli
7	1783	80.6	1214	4	US-09-478-601-3 Sequence 3, Appli
8	1783	80.6	1214	4	US-09-478-602-3 Sequence 3, Appli
9	1692	76.5	1316	3	US-08-602-809-1 Sequence 1, Appli
10	1692	76.5	1316	5	PCT-US95-16472-1 Sequence 1, Appli
11	1680	75.9	980	4	US-09-218-467B-6 Sequence 6, Appli
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17	522	23.6	1634	1	US-07-816-283-1	Sequence 1, Appli
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24	476	21.5	1796	1	US-07-816-283-11	Sequence 11, Appli
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ALIGNMENTS

RESULT 1

US-09-224-426-1

; Sequence 1, Application US/09224426

; Patent No. 6221613

; GENERAL INFORMATION:

; APPLICANT: Salon, John A

; APPLICANT: Laz, Thomas M

; APPLICANT: Nagorny, Raisa

; APPLICANT: Wilson, Amy E

; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone

; FILE REFERENCE: 57453/JPW/JHB

; CURRENT APPLICATION NUMBER: US/09/224,426

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patent Ver. 2.0 - beta

; SEQ ID NO 1

; LENGTH: 1269

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-224-426-1

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-885-478-2 (1-422) x US-09-224-426-1 (1-1269)

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QY	21	GLYC	SGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln	40
Db	61	GGCTG	CCAGGCTACGGAGGAAGACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGGACAA	120
QY	41	GlyGly	ArgArgTrpArgLeuProGlnProAlaTrpValGlyGlySerSerAlaArgLeu	60
Db	121	GGTGG	CAGGCGCTGAGAGCTGCCGACGCTGCGTGCGGTGGAGGGAGAGCTCAGCTCGGTTG	180
QY	61	TrpGlu	GlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly	80
Db	181	TGGGAG	CAGGCGGACCGGCACTGGCTGGATGGACTGGAAAGCCTCGTGTGCCCACTGGT	240
QY	81	ProAsn	AlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro	100
Db	241	CCCAAT	GCCAGCAACACACTCTGATGGCCCCGATTAACCTCACTTCAGCAGAGATCAACTCT	300
QY	101	ArgThr	GlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys	120
Db	301	CGCAG	GGGGAGCATCTCTCATCAATCATCATGCTTCGGTGTTCGGCACCATCTGC	360
QY	121	LeuLeu	GlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeu	140
Db	361	CTCTG	TGGCATCATCGGAACTCCACGGTCACTCTTCGGGTGTGAAGAAGTCCAAAGCTG	420
QY	141	HisTrp	CysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu	160
Db	421	CACGTG	GCAACAACGTCGCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTC	480
QY	161	PheLeu	LeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe	180
Db	481	TTTTCT	CTCTGGGCATGCCCTTCATGATCCACAGCTCATGGGCAATGGGCTGTGGCACTTT	540
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QY	241	PheIle	SerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla	260
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Db	781	GTGGG	CTGGGCAATGAGCCTGCCCCAACCCAGACACTGACCTTACTGTTCAACCCCTGAC	840
QY	281	GlnPhe	pheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle	300
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QY	301	LeuGln	ArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr	320
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QY	321	LysArg	ValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro	340
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QY	341	TyrTyr	ValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr	360
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QY	381	IleVal	LeuCysGlnThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln	400

Db	1141	ATCGTCTCTGTGAGACGTTCCGCCAACAGCTTGGTCTCTGCGGTGAAGCCTGCAGCCAC	1200
QY	401	GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluArgThrGluSerLys	420
Db	1201	GGGCGAGCTTCGGCGTGTACAGCAACGCTCAGACGGGCTGACGAGGAGAGACAGAAACGAAA	1260
QY	421	GlyThr	422
Db	1261	GGCACC	1266

RESULT 2

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US-09-478-601-1
; Sequence 1, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453z\JPW
; CURRENT APPLICATION NUMBER: US/09/478, 601
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224, 426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-478-601-1

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Alignment Scores:

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US-09-885-478-2 (1-422) x US-09-478-601-1 (1-1269)

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Db	1	ATGTCAGTGGAGACCATGAAGAAGGAGCTGGGAGGGGCACTGGGCTTGGAGCGCGCAGC	60
QY	21	GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln	40
Db	61	GGCTGCCAGGCTACGGAGGAAGAACCCCTTCCCGACTGCGGGGCTTCCGCTCCGGGACAA	120
QY	41	GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGlyGlySerSerAlaArgLeu	60
Db	121	GGTGGCAGGCGCTGGAGGCTGCCGAGCCTGCTGGGTGGAGGGGAGCTCAGCTCGGTTG	180
QY	61	TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly	80
Db	181	TGGGAGCAGGCGCAGCCGGCACCTGGCTGGATGGACCTGGAGACCTCGCTGCTGCCACCTGGT	240
QY	81	ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro	100
Db	241	CCCAATGCCAGCAACACACTCTGATGGCCCCGATAAACCCTCACTTCAGCAGGATCACCCTCT	300
QY	101	ArgThrGlySerIleSerTyrlleAsnIleIleMetProSerValPheGlyThrIleCys	120
Db	301	CGCAGCGGGAGCATCTCTCAACATCAACATCATCATGCTTCGGGTTCGGCACCATCTGC	360
QY	121	LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeu	140
Db	361	CTCCTGGGCATCATGGGAGACTCCACGGTCACTTCGGGGTCTGTGAGAGAGATCCCAAGCTG	420

QY	141	HISTPcYsAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu	160
Db	421	CACTGGTGCACAACAGTCCCGACATCTTCATCATCAACCTCTCGTAGTAGATCTCTC	480
QY	161	PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe	180
Db	481	TTTTCTCCGGGCATGCCCTTCATGATCCACCAAGCTCATGGGCAATGGGGTGTGGCACTTT	540
QY	181	GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr	200
Db	541	GGGAGAACCATGTGCACCCCTCATCATCCAGCCATGGATGGCAATAGTCAGTTCCACGACACC	600
QY	201	TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer	220
Db	601	TACATCCTGACCGCCCATGGCCATGACCCGCTACCTGGCCACTGTCCACCCCATCTCTTCC	660
QY	221	ThrIysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer	240
Db	661	ACGAAGTTCGGGAAGCCCTCTGTGGCCACCCGTGTGATCTGCCCTCTCGGGCCCTTCC	720
QY	241	PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla	260
Db	721	TTCATTCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGTGCA	780
QY	261	ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr	280
Db	781	GTGGGCTGCGGCATACGCTTGCCCAACCCAGACACTGACCTTACTGGTTCACCCCTGTAC	840
QY	281	GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle	300
Db	841	CAGTTTTCCTGGCCTTGCCCTTTTGTGTGTCATCACAGCCGCATACGTAGAGATC	900
QY	301	LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr	320
Db	901	CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTCCAGCGCAGCATCCGGCTGGCGACA	960
QY	321	LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro	340
Db	961	AAGAGGGTGACCCGCACAGCCATCGCCATCTGTCTGTCTTGTGTGCTGGGCACCC	1020
QY	341	TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr	360
Db	1021	TACTATGTGCTACAGCTGACCCAGTGTTCATCAGCCGCCGACCCCTACCTTTGTCTAC	1080
QY	361	LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr	380
Db	1081	TTATACAATGCGGCATCAGCTTGGGCTATGCCACAACAGCTGCCCTCAACCCCTTGTGTAC	1140
QY	381	IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln	400
Db	1141	ATCGTGCTCTGTGAGACGTTCCGCCAACAGCCTTGGTCTGTCTGGAAGCCTGCAGCCACG	1200
QY	401	GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGluSerLys	420
Db	1201	GGGCAGCTTCGGCGTGTCAACAACGCTCAGACGGCTGACGAGAGAGACAGAAACAAA	1260
QY	421	GlyThr 422	
Db	1261	GGCACC 1266	
RESULT 3			
US-09-478-602-1			
; Sequence 1, Application US/09478602			
; Patent No. 6291195			
; GENERAL INFORMATION:			
; APPLICANT: Salon, John A.			
; APPLICANT: Iaz, Thomas M.			
; APPLICANT: Nagorny, Raisa			
; APPLICANT: Wilson, Amy E.			
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone			
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof			
; FILE REFERENCE: 57453Y\JPW			
; CURRENT APPLICATION NUMBER: US/09/478,602			

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; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-478-602-1

Alignment Scores:
Pred. No.:      1,1e-206      length:      1269
Score:          2212.00      Matches:      422
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:    100.00%      Indels:      0
DB:             4             Gaps:        0

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US-09-885-478-2 (1-422) x US-09-478-602-1 (1-1269)

QY	1	MeterValGlyAlaMetLysGlyValGlyArgAlaValGlyLeuGlyGlySer	20
Db	1	ATGTCAGTGGAGCCATGAAGAAGGAGTGGGAGGGGACATTGGAGCGGCACG	60
QY	21	GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln	40
Db	61	GGCTGCCAGGCTACGGAGAGACCCCCCTTCCGCACTGGGGGGCTTGCGCTCCGGACAA	120
QY	41	GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGlyLysSerAlaArgLeu	60
Db	121	GGTGGCAGGCGCTGGAGGCTGCCGAGCCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTTG	180
QY	61	TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGlnAlaSerLeuLeuProThrGly	80
Db	181	TGGGAGCAGGCGACCGGCACTGGCTGGATGGACCTGGAGCCTCGCTGCCCCACTGGT	240
QY	81	ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerPro	100
Db	241	CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACTTCACCTTCAGCAGATCACCTCT	300
QY	101	ArgThrGlySerLysSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys	120
Db	301	CGCAGGGGAGCATCTCCTACATCAACATCATCATGCCCTTCGGTGTTCGCACCACTGCG	360
QY	121	LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeu	140
Db	361	CTCCTGGGCATCATCGGGAACCTCCACGGTCATCTTCGGGTGCTGAAGAAGTCCACGCTG	420
QY	141	HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu	160
Db	421	CACCTGGTGCACAACACGTCGCCGACATCTTCATCATCAACCTCTCGTAGTAGATCTCCTC	480
QY	161	PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe	180
Db	481	TTTCTCCTGGGCATGCCCTTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTT	540
QY	181	GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr	200
Db	541	GGGAGACCATGTGCACCCCTCATCAACGGCCATGGATGCCAATAGTCAGTTCCACCACAC	600
QY	201	TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer	220
Db	601	TACATCCTGACCGCCATGGCCATTGACCGGCTACCTGCGCCACTGTCCACCCCATCTCTCC	660
QY	221	ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer	240
Db	661	ACGAAGTCCGGAAGCCCTCTGTGGCCACCCCTGTGATCTGCCCTCTGTGGGCCCTCTCC	720
QY	241	PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla	260
Db	721	TTCATCAGCATCACCCCTGTGTGGCTGTATGCGACAGACTCATCCCTTCCACGAGAGGTGCA	780

QY 261 ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr 280
Db 781 GTGGGCTGGGCAATACGCTGCCCCAACCCAGACACTGACCTTACTGTGTACCCCTGTAC 840
QY 281 GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle 300
Db 841 CAGTTTTCCTGGCCTTTGCCCTTGTGTGTATCACAGCCCGCAATACGTGAGATC 900
QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
Db 901 CTGCAGCGCATGACGTCTCTCAGTGGCCCCCGCCTCCAGCGCAGCATCCGGCTGCGGACA 960
QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro 340
Db 961 AAGAGGGTGACCCGACAGCCATCGCCATCTGTCTGTCTTGTGTGTGTGGGCACCC 1020
QY 341 TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
Db 1021 TACTATGTGTACAGCTGACCCAGTTGTTCATCAGCCGCGCCGACCTCACCCTTGTCTAC 1080
QY 361 LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnPropheValTyr 380
Db 1081 TTATACAATGGCGCCATCAGCTTGGGCTATGCCAACACCTGCCCTCAACCCCTTGTGTAC 1140
QY 381 IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln 400
Db 1141 ATCGTCTCTGTGAGACGTTCGCCAAACGCTTGTCTGTCTGTGAAGCCTTCAGCCAC 1200
QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGluSerLys 420
Db 1201 GGGCAGCTTCGCGCTGTGACGACGCTCAGACGCGCTGACGAGAGAGACAGAAAGCAAA 1260
QY 421 GlyThr 422
Db 1261 GGCACC 1266

RESULT 4
US-08-984-288-1
; Sequence 1, Application US/08984288
; Patent No. 6033872
; GENERAL INFORMATION:
; APPLICANT: BERGMA, DEBK
; APPLICANT: ELLIS, CATHERINE
; TITLE OF INVENTION: NOVEL HUMAN 11CB SPLICE V
; TITLE OF INVENTION: ARIANT
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,288
; FILING DATE: 03-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,763
; FILING DATE: 11-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: P50599
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-984-288-1

Alignment Scores:
Pred. No.: 6.16e-202 Length: 1385
Score: 2164.00 Matches: 412
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.83% Indels: 0
Gaps: 0
DB: 3

US-09-885-478-2 (1-422) x US-08-984-288-1 (1-1385)
QY 11 GlyArgAlaValGlyLeuGlyGlyGlySerGlyCysGlnAlaThrGlnGluAspProLeu 30
Db 66 GGGAGGGCAGTTGGGCTTGGAGCGCGCAGCGGCTGCCAGGCTACGAGAGAACCCCTT 125
QY 31 ProAspCysGlyAlaCysAlaProGlyGlnGlyGlyArgArgTrpArgLeuProGlnPro 50
Db 126 CCCGACTGCGGGGCTTGGCTTCGGGACCAAGGTGGCAGCGCGCTGAGGCTGCCGACCT 185
QY 51 AlaTrpValGlnGlySerSerAlaArgLeuTrpGlnAlaThrGlyThrGlyTrpMet 70
Db 186 GCGTGGTGAGGGGAGCTCAGCTCGGTTGTGGAGACAGCGGACCGGACCTGGCTGATG 245
QY 71 AspLeuGluAlaSerLeuLeuProThrGlyProAsnAlaSerAsnThrSerAspGlyPro 90
Db 246 GACCTGAGACCTCGCTGTGCTGCCACTGTCCCAATGCCAGCAACCTCTGATGAGCC 305
QY 91 AspAsnLeuThrSerAlaGlySerProProArgThrGlySerIleSerTyrIleAsnIle 110
Db 306 GATAACCTCAGCTTGGGACAGATCACCTCTCGCACGGGAGCATCTCTACATCAACATC 365
QY 111 IleMetProSerValPheGlyThrIleCysLeuLeuGlyIleIleGlyAsnSerThrVal 130
Db 366 ATCATGCTTCGGGTGTTCGGCACCATCTGCTCTCTGGGCATCATCGGAACTCCACGG 425
QY 131 IlePheAlaValAlaLysLysSerLysLeuHisTrpCysAsnAsnValProAspIlePhe 150
Db 426 ATCTTCGCGGTGTGAAGAAGTCCAACTGCACTGGTGCACAACGTCCTCCGACATCTTC 485
QY 151 IleIleAsnLeuSerValValAspLeuLeuPheLeuLeuGlyMetProPheMetIleHis 170
Db 486 ATCATCAACCTCTCGGTAGTAGATCTCTCTTCTCTCGGCATGCCCTTCATGATCCAC 545
QY 171 GlnLeuMetGlyAsnGlyValTrpHisPheGlyGluThrMetCysThrLeuIleThrAla 190
Db 546 CAGCTCATGGGCAATGGGGTGTGGCACTTGGGGAGAGACCATGTGCACCTCATCACGCC 605
QY 191 MetAspAlaAsnSerGlnPheThrSerThrTyrIleLeuThrAlaMetAlaIleAspArg 210
Db 606 ATGATGCCAATAGTACGTTCACACGACCACTACATCTGACCGCATGGCCATTGACCGC 665
QY 211 TyrLeuAlaThrValHisProIleSerSerThrLysPheArgLysProSerValAlaThr 230
Db 666 TACCTGGCCACTGTCCACCCCATCTTCCACGAAAGTTCGGAAAGCCCTCTGTGGCCACC 725
QY 231 LeuValIleCysLeuLeuTrpAlaLeuSerPheIleSerIleThrProValTrpLeuTyr 250
Db 726 CTGGTGAATGCTCTCTGTGGCCCTTCTTCATCAGCATCACCCCTGTGTGCTGTAT 785
QY 251 AlaArgLeuIleProPheProGlyGlyAlaValGlyCysGlyIleArgLeuProAsnPro 270
Db 786 GCCAGACTCATCCCTTCCAGAGAGGTGAGTGGGCTGCGGCATACGCTGCCAACCCCA 845
QY 271 AspThrAspLeuTyrTrpPheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuProPhe 290

Db 846 GACACTGACCTCTACTGGTTCACCCCTGACAGTTTTCCTGGCCTTTGCCCTGCTTTT 905
QY 291 ValValIleThraIaIaTyrValArgIleuGlnArgMetThrSerSerValAlaPro 310
Db 906 GTGTCATCACAGCCGATACGTAGAGATCTTCAGCGCATGACGTCTCAGTGGCCCC 965
QY 311 AlasergIlnArgserIleArgLeuArgThrLysArgValThrArgThraIaIleAlaIle 330
Db 966 GCCTCCAGCGCAGCATCCGCTGCGGACAAGAAGGTGACCCGCACAGCCATCGCCATC 1025
QY 331 CysLeuValPhePheValCysTrpAlaProTyrTyrValIleuGlnLeuThrGlnLeuSer 350
Db 1026 TGTCTGTCTTCTTGTGTGCTGGGCACCTACTATGTGCTACAGCTGACCCAGTTGTCC 1085
QY 351 IleSerArgProThrLeuThrPheValTyrLeuTyrAsnAlaAlaIleSerLeuGlyTyr 370
Db 1086 ATCAGCCGCGCCGACCTTCACCTTGTCTACTTATACATGCGGCCATCAGCTTGGGCTAT 1145
QY 371 AlaAsnSerCysLeuAsnProPheValTyrIleValLeuCysGlnThrPheArgLysArg 390
Db 1146 GCCAACAGCTGCCCTCAACCCCTTGTGTACATCGTCTGTGAGACGTTCCGCAACGC 1205
QY 391 LeuValLeuSerValLysProAlaAlaGlnGlnLeuArgAlaValSerAsnAlaGln 410
Db 1206 TTGTCCTGTGCGGTGAGACCTTCAGACCCAGGGGACAGCTTCGCGCTGTACGAACGCTCAG 1265
QY 411 ThrAlaAspGluArgThrGluSerLysGlyThr 422
Db 1266 ACGGCTGACGAGAGAGACAGAAAGCAAGGCACC 1301

RESULT 5

US-09-218-467B-1
; Sequence 1, Application US/09218467B
; Patent No. 6362326
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: ELIS, CATHERINE
; APPLICANT: HALSEY, WENDY
; APPLICANT: BERGSMÄ DERK
; TITLE OF INVENTION: 11cby Genomic Sequence
; FILE REFERENCE: GP-50010
; CURRENT APPLICATION NUMBER: US/09/218,467B
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3488
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-218-467B-1

Alignment Scores:
Pred. No.: 2,77e-185 Length: 3488
Score: 2000.00 Matches: 422
Percent Similarity: 51.09% Conservative: 0
Best Local Similarity: 51.09% Mismatches: 0
Query Match: 90.42% Indels: 404
DB: 4 Gaps: 1

US-09-885-478-2 (1-422) x US-09-218-467B-1 (1-3488)

QY 1 MetSerValGlyAlaMetLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
Db 569 ATGTCAATGGAGCCATGAAGAAGGAGTGGAGGGGACAGTTGGGCTTGGAGGGCGGACG 628
QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
Db 629 GGCTGCCAGGCTACGAGGAGAAGACCCCTTCCGACTGCGGGGCTTGCCTCGGGACAA 688
QY 41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGlyLysSerSerAlaArgLeu 60
Db 689 GGTCGACGGCGCTGAGGCTGCAGCTGTGGGTGGAGGGGAGCTCAGCTCGGTTG 748

QY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGlnAlaSerLeuLeuProThrGly 80
Db 749 TGGAGACAGCGCAGCCGACCTGCTGATGACCTGGAAGCCTCGCTGCTGCCACTGCT 808
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAla----- 96
Db 809 CCCAATGCCAGCAACACCTCTGTATGGCCCCGATTAACCTCACTTCGCAGAGTGAAGTTGACT 868
QY 96 ----- 96
Db 869 GGGAGCCCTCCCTCCTCTGGGCTGTGGTGAAGAAATGGCAAGCTTTCACCCCTGAGCCAA 928
QY 96 ----- 96
Db 929 ACTGCTGGGAACCTTATACAGATTCTTGGGACAAATCTGTGTCTGTCTGTCTG 988
QY 96 ----- 96
Db 989 AGGGCAGAGAAAGGGGCAATGCTCCGACGGGACAGCGGCGACAGACAGAGGGAAGG 1048
QY 96 ----- 96
Db 1049 GGCGAAGCATATTCAGATGGCAAGGAAGGGGGCCAGCCGTGAGACAGAGGGGAAGG 1108
QY 96 ----- 96
Db 1109 CTCGCTGTGGGTTCCAAGATGCTTGGCAGAAAAAATTCAGGCTGGAAGCAAGCGA 1168
QY 96 ----- 96
Db 1169 GAGAACTGAGAGGTGGTATGTGGAGACAGCTGGGGGCTCACTCCTGCACTGTATAGCCT 1228
QY 96 ----- 96
Db 1229 CAGCTTTTACTCCCACTTGGATGATGAGGCTTGAGACATCTTACTGCCACTGGGAGA 1288
QY 96 ----- 96
Db 1289 GGCCCTGGGAAGGAAGACTTCACAGAGCCATGAGGGGATTAATTCTTGTGTAATTAA 1348
QY 96 ----- 96
Db 1349 GCTTCCTGACATTTCCAGAGCTGGGCTGCCCTGGATTCAGCTTGAAGGAGAAAGGAA 1408
QY 96 ----- 96
Db 1409 GGAAGGAAAAAGGAAAGGCTTATGTAGATAATTTTCCAGGCTGTGAGCTCCAAACAGA 1468
QY 96 ----- 96
Db 1469 CAGTTTCTGTCTGTCTTCACTCAAGAAAGCCAGGCTCAGAAAGATACCAATCAAGGAAT 1528
QY 96 ----- 96
Db 1529 CCCCCTAGGAAGCCTGGGGTAGGAGAGCTGTGGCTTGACCAAGGACAGCGGCCAATA 1588
QY 96 ----- 96
Db 1589 AGCCTCTACAAGACAGTCACCCACAGATATGCCCAAGAAATCAGTACACAGTTTCCAACCA 1648
QY 96 ----- 96
Db 1649 GAGATCTCCAAATGAACACTCAGGGCTACACATAGGAAAGACACACACACACACAC 1708
QY 96 ----- 96
Db 1709 ACACACACACAGCACTTACTTTTGTGTCTTCTTGCTATGCTGACGAGTTTCTCTGTG 1768
QY 96 ----- 96
Db 1769 AAGCCCGGGGCTCACAGAGTAATCTCTGACAGACAACCTGTGTCTTGCCTGTGGTGCCTG 1828
QY 96 ----- 96

Db 1829 CAGAGCGACGATGTGTCTCTCCAGACAGATGGCTCAGGGCACTGTGTAGATT 1888
QY 96 ----- 96
Db 1889 CACCAGAACTCATGAGAGGAAAGGACAAGATTAGCAACAGTGAAGGAGGAG 1948
QY 96 ----- 96
Db 1949 AATGTTGGAGAGATTCCAGATGAACGGTGGCTGAGGGTGAGCATGCCAGCAG 2008
QY 96 ----- 96
Db 2009 ATGTCAGTTCTCAGAGCAAAAGCCCATGTCAAAACAGCCACGCTTGCTCTCTGTCCCA 2068
QY 97 GlySerProProArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPhe 116
Db 2069 GGATCACCCTCTCGCAGGGGAGCATCTCTACATCAACATCATCATGCGTTCGGTGTTC 2128
QY 117 GlyThrIleCysLeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLys 136
Db 2129 GGCACCATCTGCTCTCGGGCATCATCGGGAACTCCACGGTCATCTTGGCGGTGTAAG 2188
QY 137 LysSerLysLeuHisTrpCysAsnValProAspIlePheIleIleAsnLeuSerVal 156
Db 2189 AAGTCCAAGCTGCACCTGTCACAACAACGTCGCCGACATCTTCATCATCAACCTCTCGGTA 2248
QY 157 ValAspLeuLeuPheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGly 176
Db 2249 GTAGATCTCTCTTCTCTGGGCATGCCCCCTTCATGATCCACAGCTCATGGCAATGGG 2308
QY 177 ValTrpHisPheGlyGlyThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGln 196
Db 2309 GTGTGGCAGCTTTGGGGAGACCATGTGCACCCCTCATCACGGCCATGGATGCCAATAGTCAG 2368
QY 197 PheThrSerThrTyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHis 216
Db 2369 TTCACCAAGCACCTACATCTCTGACCCGCCCATGGCCATGACCGCTACCTGGCCACTGTCAC 2428
QY 217 ProIleSerSerThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeu 236
Db 2429 CCCATCTCTTCCACGAAGTCCGGGAAGCCCTCTGTGGCCACCCCTGGTATCTGCCTCTG 2488
QY 237 TrpAlaLeuSerPheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPhe 256
Db 2489 TGGCCCTCTCTCATCAGCATTCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTC 2548
QY 257 ProGlyGlyAlaValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrp 276
Db 2549 CCAGAGGTGCAGTGGGCTGGGCATACGCCCTGCCCAACCCAGACACTGACCTTACTGG 2608
QY 277 PheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAla 296
Db 2609 TTCACCTGTACCAAGTTTTCCTGCGCTTGGCCCTGTGCTTGTGTCATCACAGCGCA 2668
QY 297 TyrValArgIleLeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIle 316
Db 2669 TACGTGAGGATCTCGACGCGCATGAGTCCCTCAGTGGCCCCCGCTCCAGCGCAGCATC 2728
QY 317 ArgLeuArgThrLysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheVal 336
Db 2729 CGGCTGCGGACAAGAAGGTTGACCCGACAGCCATCGCCATCTGTGTCCTTGTG 2788
QY 337 CysTrpAlaProTyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeu 356
Db 2789 TGCTGGGACCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCGCCAGCCCTC 2848
QY 357 ThrPheValTyrLeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsn 376
Db 2849 ACCTTTGTCTACTATATACATGCGGCATCAGCTTGGGCTATGCCAACAAGCTGCCTAAC 2908
QY 377 ProPheValTyrIleValLeuCysGlnThrPheArgLysArgLeuValLeuSerValLys 396

Db 2909 CCCTTTGTGTACATCGTGTCTGTGAGACGTTCCGCAACGCTTGGTCTGTGCGTGAAG 2968
QY 397 ProAlaAlaGlnGlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluArg 416
Db 2969 CCTGCAGCCCGAGGGGAGCTTCGCGCTGTCAACAACGCTCAGACGGCTGACGAGAGAGG 3028
QY 417 ThrGluSerLysGlyThr 422
Db 3029 ACAGAAAGCAAAAGGCACC 3046
RESULT 6
US-09-224-426-3
; Sequence 3, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salon, John A
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453/JPW/JHB
; CURRENT APPLICATION NUMBER: US/09/224,426
; CURRENT FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 3
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: rat
US-09-224-426-3
Alignment Scores:
Pred. No.: 8.22e-165 Length: 1214
Score: 1783.00 Matches: 344
Percent Similarity: 97.22% Conservative: 6
Best Local Similarity: 95.56% Mismatches: 10
Query Match: 80.61% Indels: 0
Gaps: 0
US-09-885-478-2 (1-422) x US-09-224-426-3 (1-1214)
QY 63 GlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGlyProAsn 82
Db 2 CAGGCGACCTGCACCGGCTGCATGATGATCTGCAAAACCTCGTGTGCTGCCACTGGCCCCAAT 61
QY 83 AlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProProArgThr 102
Db 62 GCCAGCAACATCTCCGATGGCCAGGATTAATCTCACATTTGCCGGGGTCACTCCTCGCACA 121
QY 103 GlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCysLeuLeu 122
Db 122 GGGAGTGTCTCATCATCAACATCATTAATGCTTCCGTGTTGGTACCATCTGTCTCTG 181
QY 123 GlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeuHisTrp 142
Db 182 GGCATGTTGGGAAACTCCACGGTCACTTGTGTTGGTGAAGAACTCCAAGCTTACACTGG 241
QY 143 CysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeuPheLeu 162
Db 242 TGCAGCAACGTCGCCGACATCTTCATCATCAACCTCTGTGTGGATCTGTCTTCTG 301
QY 163 LeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPheGlyGlu 182
Db 302 CTGGGCATGCTTTCATGATCCACCAAGCTCATGGGGAACGGGCTGACACTTTGGGGA 361
QY 183 ThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThrTyrIle 202
Db 362 ACCATGTGCACCTCATCAACAGCATGGAGGCCAACAAGTCAGTTCACTAGCACCTACATC 421
QY 203 LeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSerThrLys 222
Db 422 CTGACTGCCATGACCATTTGACCGCTACTTGGCCACCGTCCACCCCACTCTCTCCACCAAG 481

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1316 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-602-809-1

Alignment Scores:
Pred. No.: 7.23e-156 Length: 1316
Score: 1692.00 Matches: 340
Percent Similarity: 86.82% Conservative: 9
Best Local Similarity: 84.58% Mismatches: 22
Query Match: 76.49% Indels: 31
DB: 3 Gaps: 3

US-09-885-478-2 (1-422) x US-08-602-809-1 (1-1316)

QY 37 AlaProGlyGlnGlyArgArg-----44
Db 74 TCACCAGAACTCATGAGAGGAGGAAAAGGACACAGATTAGCAACAGTGAAGGGAGGGA 133
QY 45 -----Trp--ArgLeuProGlnProAlaTrpValGlnGlySerSerAlaArgLeuTrp 61
Db 134 GAATGGTGGAGAGATTCCAGATGAACGGGTGGCTGCTGGAGGCTGAGCATGCCAGCAG 193
QY 62 GlnGlnAlaThrGlyThrGlyTrpMetAspLeuGlnAlaSerLeuLeuProThr-GlyPr 81
Db 194 GATGTCA GTTCTCAGAGCAAAAGCCCATGTCAAAACAGCCAAAGCTTGCTCTCTGTCGCC 253
QY 81 cAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProProAr 101
Db 254 A-----GGATCACCTCTCG 268
QY 101 gThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCysLe 121
Db 269 CACGGGAGCATCTCCATCATCAACATCATGCGCTTCGGTTCGGCACCATCTGCCCT 328
QY 121 uLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValIleLysSerLysLeuHi 141
Db 329 CCTGGGCATCATCGGAACTCCACGGTCACTTCGCGGTGTAAGAAGTCCAAAGCTGCA 388
QY 141 sTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeuPh 161
Db 389 CTGGTGCACACACGTCGCCGACATCTTCATCAACCTCTCGGTAGTAGATCTCTCTT 448
QY 161 eleuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPheG1 181
Db 449 TCTCCTGGGCATGCCCTTCATGATCCACCACTCATGGGCAATGGGGTGTGGACATTGG 508
QY 181 yGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThTy 201
Db 509 GGAGACCATGTGCACCTCATCACGGGCCATGGATGCCAATAGTCAAGTTCACCAAGCACCTA 568
QY 201 rIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSerTh 221
Db 569 CATCCTGACCGCCATGGCCATTGACCGCTAAGTGGCCACTGTCCACCCCATCTCTTCCAC 628
QY 221 rLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSerPh 241
Db 629 GAAGTTCGGGAAGCCCTCTGTGGCCACCTGGGTGATCTGCTCTGTGGGCCCTCTCTT 688
QY 241 eIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAlaVa 261
Db 689 CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGCAGT 748
QY 261 lGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyrG1 281
Db 749 GGGCTGCGGCATACGCTGCGCCAAACCCAGACACTGACCTTACTGCTTACCCCTGTACA 808
QY 281 nPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIleLe 301

Db 809 GTTTTTCCTGGCCTTTCGCCCTTGCCCTTTTGTGTCATCACAGCCGCATACGTGAGATCCT 868
QY 301 uGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThrly 321
Db 869 GCAGCGCATGACGTCTCAGTGGCCCCCGCCCTCCAGCGCAGCATCCGGCTGCGGACAAA 928
QY 321 sArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaProTy 341
Db 929 GAGGTGACCCCGCACAGCCATCCCATCTGTCTGTCTTCTTGTGTGCTGGGCACCCCTA 988
QY 341 rTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyrLe 361
Db 989 CTATGTGTACAGCTGACCCAGTTGTCCATCAGCCGCCCGACCCCTCACCCTTGTCTACTT 1048
QY 361 uTyrAsnAlaAlaIleSerIleuGlyTyrAlaAsnSerCysLeuAsnProPheValTyrIl 381
Db 1049 ATACAATGGGGCCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTGTGTACAT 1108
QY 381 eValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGlnGl 401
Db 1109 CGTGCTGTGAGAGCGTTCGGAACAGCTTGCTGCTGTGCTGTAAGCCTGACGCCACGGG 1168
QY 401 yGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGlnSerLysGl 421
Db 1169 GCAGCTTCGCGCTGTACAGCAACGCTCAGACGGCTGACGAGAGAGACAGACAGAAAGG 1228
QY 421 yThr 422
Db 1229 CACC 1232

RESULT 10
PCr-US95-16472-1
; Sequence 1, Application PC/TUS9516472
; GENERAL INFORMATION:

; APPLICANT: Bergsma, Derk J
; APPLICANT: Ellis, Catherine E
; TITLE OF INVENTION: Human Somatostatin Receptor
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation/Corporate
; ADDRESSEE: Intellectual Proper
; STREET: P. O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCr/TUS95/16472
; FILING DATE:

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5024
; TELEFAX: 610 270 5090

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1316 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 27..1232
; OTHER INFORMATION: /note= "The coding sequence is from

Db 243 TGGCACTTTGGGAGACCATGTGCACCTTCATCAGCGCCATGATGCCAATAGTCAGTTTC 302
QY 198 ThrSerThrTyrIleuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisPro 217
Db 303 ACCAGCACCTACATCTGACCGCCATGGCCATGACCGCTACTGGCCACTGTCCACCCC 362
QY 218 IleSerSerThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrp 237
Db 363 ATCTCTTCACGAGAGTTCGGGAAGCCCTGTGGCCACCCCTGGTATCTGCCTCCTGTGG 422
QY 238 AlaLeuSerPheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPhePro 257
Db 423 GCCCTCTCCTTCATCAGCATCACCCCTGTGGCTGTATGCACAGACTCATCCCTCCCA 482
QY 258 GlyGlyAlaValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPhe 277
Db 483 GGAGGTGCAGTGGGCTGGGGCATACGCCCTGCCCAACCCAGACACTGACCTTACTGGTTC 542
QY 278 ThrLeuTyrGlnPhePheLeuAlaPheAlaLeuProPheValIleThrAlaAlaTyr 297
Db 543 ACCCTGTACCAGATTTCCTTGCGCTTGCCCTTGCCCTTTGTGTGTCATCAGACCGCATAC 602
QY 298 ValArgIleLeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArg 317
Db 603 GTGAGGATCCTGCAGCGCATGACGTCTCCTCAGTGGCCCCCGCCTCCAGCGCATCCGG 662
QY 318 LeuArgThrLysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCys 337
Db 663 CTGGCGACAAGAGGGGTGACCCGACAGCCCATCGCTGTCTTGTGTGTGC 722
QY 338 TrpAlaProTyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThr 357
Db 723 TGGGCACCCCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCGCCCGCCCTCACC 782
QY 358 PheValTyrLeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnPro 377
Db 783 TTTGTCTACTATACAAATGCGGCCATCAGCTTGGGCTATGCCAAGCTGCTCAACCCC 842
QY 378 PheValTyrIleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysPro 397
Db 843 TTTGTGTACATCGTCTCTGTGAGACGTTCGCAACGCTTGTGTCTGTGGTGAAGCCT 902
QY 398 AlaAlaGlnGlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluArgThr 417
Db 903 GCAGCCCGAGGGGAGCTTCGCGCTGTCAACAACGCTCAGACGGCTGACGAGAGAGAGACA 962
QY 418 GluSerLysGlyThr 422
Db 963 GAAAGCAAAAGGCACC 977

RESULT 12
US-07-816-283-7
; Sequence 7, Application US/07816283
; Patent No. 5436155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/816,283
; FILING DATE: 19911231
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1244 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-07-816-283-7

Alignment Scores:
Pred. No.: 6.11e-43 Length: 1244
Score: 535.50 Matches: 117
Percent Similarity: 52.57% Conservative: 77
Best Local Similarity: 31.71% Mismatches: 133
Query Match: 24.21% Indels: 42
DB: 1 Gaps: 8

US-09-885-478-2 (1-422) x US-07-816-283-7 (1-1244)

QY 61 TrpGluGlnAlaThrGly-ThrGlyTyrPheMetAspLeuGlnAlaSerLeuLeuProThrG1 80
Db 50 TGGAGGCCAAGTGTGGGTGTCTTCATTTGACCTCAACGGCTCAGTGGGGCCAAGC-- 107
QY 80 yProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPr 100
Db 108 ---AATGGCTTCCAACACGAGCCGAGCCATCTACGACATGACAAGC----- 149
QY 100 oArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCy 120
Db 150 -----AACGCCGTCTCAGCTTCATCTACTTCGTGTGTG 184
QY 120 sLeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValAlaLysSerLysLe 140
Db 185 TGTGTGGGGCTGTGCGGCAACACGCTGGTCATTATGTGATCTCCGCTATGCCAAGAT 244
QY 140 uHisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValAlaSpLeuLe 160
Db 245 G-----AAGACCATCACCAACATCTACATCCTTAACCTGGCCATTGCAGATGAAC 295
QY 160 uPheLeuLeuGlyMetProPhe-----MetIleHisGlnLeuMetG1 174
Db 296 CTTCATGTAGGGCTTCCCTTCTTGGCCATGCAGGTGGCGCTAGTCAC----- 344
QY 174 yAsnGlyValTrpHisPheGlyGluThrMetCysThrLeuLeuThrAlaMetAspAlaAs 194
Db 345 -----TGGCCCTTTTGGCAAGGCCATCTGCCGGGTGGTGCATGACTGTAGATGGCAT 394
QY 194 nSerGlnPheThrSerThrTyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaTh 214
Db 395 CAATCAGTTCAACAGATATCTTCTGCTGACGCGTCAATGACATGACACCGTACCTGGCCGT 454
QY 214 rValHisProIleSerSerThrLysPheArgLysProSerValAlaThrLeuValIleCy 234
Db 455 GCTGCACCCCATTAAGTACAGCAAAATGAGGCGACCCCGGACAGCCAAAGATGATCAATGT 514
QY 234 sLeuLeuTrpAlaLeuSerPheIleSerIleThrProValTrpLeuTyrAlaArgLeuI1 254
Db 515 AGCTGTGTGTGTGTCTCTGCTGCTCATTTTGGCCATCATGATATACGCGGCTCCG 574
QY 254 eProPheProGlyGlyAlaValGlyCysGlyIleArgLeuProAsnProAspThrAspLe 274
Db 575 GAGCAACACAGTGGGCGAGAGCAGAGCTGACCATCAACTGCGCAGGCAATCCGGGCGTGT 634
QY 274 uTyr---TrpPheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuProPheValI11 293

Db 635 GTACACAGGTTTCATTATCTACGCCCTTCATCTCGGGTTCCTGGTACCCCTTACCATCAT 694
QY 293 eThrAlaAlaTyrValArgIleLeuGlnArgMetThrSerSerValAlaProAlaSerGI 313
Db 695 TTGTCTCTGTACCTGTTTCATCATCATCAAGGTGAAGTCTCTGGAAATCCGAGTGGGATC 754
QY 313 nArgSerIleArgLeuArgThrLysArgValThrArgThrAlaIleAlaIleCysLeuVa 333
Db 755 ATCCAAGAGGAAAGTCAGAGAAAAAGGTGACCCGCGCATGTGTCCATCGTAGTGGCTGT 814
QY 333 lPhePheValCysTrpAlaProTyrTyrValLeuGlnLeuThrGlnLeuSerIleSer-- 352
Db 815 CTTCATCTCTGTGCTGGCTCCCTCTTCATCTTCAACGCTCTTCCGCTGTCTGTGGCCAT 874
QY 353 -ArgProThrIleuThrPheValTyrLeuTyrAsnAlaAlaIleSerIleuGlyTyrAlaAs 372
Db 875 CAGTCCCAACCCAGCCCTGAAGGATGTGTGACTTTGTGTGTGATGCTCACCCTATGCCAA 934
QY 372 nSerCysLeuAsnPropheValTyrIleValLeuCysGluThrPheArgLysArgLeuVa 392
Db 935 CAGCTGCGCAACCCCATCTCTGTACGCCCTTCTTGTCTGACAACTTCAAGAAG----- 986
QY 392 lLeuSerValLysProAlaAlaGlnGlyGlnLeuArgAlaValSerAsnAlaGlnThrAl 412
Db 987 -----AGCTTCCAGAAATGTTCTTGTGTGTGTCAGAGTGAGTGGTACGGA 1030
QY 412 aAspGluGluArgThrGluSerLys 420
Db 1031 GGATGGGAGAGAGAGACGACAGTAAG 1055
RESULT 13
US-08-417-103-7
; Sequence 7, Application US/08417103
; Patent No. 5723299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Saino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,103
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/816,283
; FILING DATE: 01-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1244 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; FEATURE: CDS
; NAME/KEY: LOCATION: 24..1130
; US-08-417-103-7
Alignment Scores:
Pred. No.: 6.11e-43 Length: 1244
Score: 535.50 Matches: 117
Percent Similarity: 52.57% Conservative: 77
Best Local Similarity: 31.71% Mismatches: 133
Query Match: 24.21% Indels: 42
DB: 1 Gaps: 8
US-09-885-478-2 (1-422) x US-08-417-103-7 (1-1244)
QY 61 TRPGlGlnAlaThrGly-ThrGlyTrpMetAspLeuGluAlaSerIleuLeuProThrGI 80
Db 50 TGGGAGCCCAAGTGTGGGTGCTCTCTCCATTGTGACCTCAACGGCTCAGTGGGCCAAGC-- 107
QY 80 yProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPr 100
Db 108 ----AATGGCTCCAACCAAGACGAGCCATACTACTGACATGACAAGC----- 149
QY 100 cArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCy 120
Db 150 -----AACGCCGTCTCAACGTTTCATCTACTTCGTGTGTG 184
QY 120 sLeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValAllyLysSerLysLe 140
Db 185 TGTGTGTGGGCTGTGGCGCAACAGCTGTGCATTTATGTATCTCCGCTATGCCAAGAT 244
QY 140 uHisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeu 160
Db 245 G-----AAGACCATCACCAACATCTACATCTTAACCTGGCCATTGCGATGAAGT 295
QY 160 uPheLeuLeuGlyMetProphe-----MetIleHisGlnLeuMetGI 174
Db 296 CTTCATGTAGGGCTTCCCTTGTGGCCATGCAGGTGGCGCTAGTCCAC----- 344
QY 174 yAsnGlyValTrpHisPheGlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAs 194
Db 345 -----TGCCCTTTTGGCAAGCCATCTGCCGGGTGTCATGACTGTAGATGCCAT 394
QY 194 nSerGlnPheThrSerThrTyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaTh 214
Db 395 CAATCAGTTCACCAAGTATCTTCCCTTGACGCGTCATGAGCATGACCGCTACCTGGCGGT 454
QY 214 rValHisProIleSerSerThrLysPheArgLysProSerValAlaThrLeuValIleCy 234
Db 455 GGTGACACCCATTAAAGTCAGCCAAATGAGAGCGACCCCGAGACCAAGATGATCAATGT 514
QY 234 sLeuLeuTrpAlaLeuSerPheIleSerIleThrProValTrpLeuTyrAlaArgLeuI 254
Db 515 AGCTGTGTGTGTGTCTCTGCTCGTCATTTTGGCCATCATGATATACGGCGGCTCCG 574
QY 254 ePropheProGlyGlyAlaValGlyCysGlyIleArgLeuProAsnProAspThrAspLe 274
Db 575 GAGCAACCAAGTGGGCGAGAGCAGCTGTACCATCAACTGGCCAGCGGAATCCGGGCGGTG 634
QY 274 uTyr--TrpPheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuPropheValValI 293
Db 635 GTACACAGGTTTCATTATCTACGCCCTTCATCTCGGGTTCCTGGTACCCCTTACCATCAT 694
QY 293 eThrAlaAlaTyrValArgIleLeuGlnArgMetThrSerSerValAlaProAlaSerGI 313
Db 695 TTGTCTCTGTACCTGTTTCATCATCATCAAGGTGAAGTCTCTGGAAATCCGAGTGGGATC 754
QY 313 nArgSerIleArgLeuArgThrLysArgValThrArgThrAlaIleAlaIleCysLeuVa 333
Db 755 ATCCAAGAGGAAAGTCAGAGAAAAAGGTGACCCGCGCATGTGTCCATCGTAGTGGCTGT 814
QY 333 lPhePheValCysTrpAlaProTyrTyrValLeuGlnLeuThrGlnLeuSerIleSer-- 352

Db 815 CTTCATCTTCTGCTGGCTCCCTTCTACATCTTCAACGTCTCTTCCGTGTCTGTGGCCAT 874
QY 353 -ArgProThrLeuThrPheValTyrLeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAs 372
Db 875 CAGTCCCAACCCACGCCCTGAAGGCATGTGTGACTTTGTGTGATCCTCACTATGCCAA 934
QY 372 nSerCysLeuAsnProPheValTyrIleValLeuCysGluThrPheArgLysArgLeuVa 392
Db 935 CAGTGGCCCAACCCCATCTCTGTACGCCCTTCTGTCTGACAACTTCAAGAAG----- 986
QY 392 lLeuSerValLysProAlaAlaGlnGlyGlnLeuArgAlaValSerAsnAlaGlnThrAl 412
Db 987 -----AGCTTCCAGAATGTCTTGTGCTGTCAGGTGAGTGTGACGGA 1030
QY 412 aAspGluGluArgThrGluSerLys 420
Db 1031 GGATGGGAGAGAGAGCCAGACTAAG 1055

RESULT 14
US-07-816-283-5
: Sequence 5, Application US/07816283
: Patent No. 5436155
: GENERAL INFORMATION:
: APPLICANT: Bell, Graeme I.
: APPLICANT: Yamada, Yuichiro
: APPLICANT: Saino, Susumu
: TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: PO Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/816,283
: FILING DATE: 19911231
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: McDaniel, C. Steven
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 713-787-1400
: TELEFAX: 713-789-2679
: TELEX: 79-0924
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1351 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-07-816-283-5

Alignment Scores:
Pred. No.: 1.53e-42 Length: 1351
Score: 532.00 Matches: 124
Percent Similarity: 49.76% Conservative: 81
Best Local Similarity: 30.10% Mismatches: 147
Query Match: 24.05% Indels: 60
DB: 1 Gaps: 12

US-09-885-478-2 (1-422) x US-07-816-283-5 (1-1351)

QY 28 AspProLeuProAspCysGlyAlaCysAlaProGlyGlnGlyLysArgArgTrpArgLeu 47
Db 2 GATCCTTGGCCT-----CCAGGGTCCATTAAAGGTGAGAATA 37

QY 48 ProGlnProAlaIrrpValGlu-----GlySerSerAlaArgLeuTrp 61
Db 38 AGATCTCTGGGCTGGCTGGAACTAGCCTAAGACTGAAGAACGCCATGGACATGGCGGAT 97
QY 62 GluGlnAlaThrGlyThr---GlyTyrMet-----AspLeuGluAlaSerLeu 76
Db 98 GAGCCACTCAATGGAAGCCACACATAGGCTATCCATTCCATTGACCTCAATGGCTCTGTG 157
QY 77 LeuProThrGlyProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAla 96
Db 158 GTGTCAACC-----AACACCTCAAACACAGACAGAGCCGTAATATGACCTGACAAGC--- 208
QY 97 GlySerProProArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPhe 116
Db 209 -----AATGCACTCCTCACATTCATCTAT 232
QY 117 GlyThrIleCysLeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValLys 136
Db 233 TTTGTGCTGCATCATTTGGTTGTGTGGCAACACACTTGCATTTATGTCACTCTCCGC 292
QY 137 LysSerLysLeuHisTyrCysAsnAsnValProAspIlePheIleAsnLeuSerVal 156
Db 293 TATGCCAAGATG-----AAGACATCACCAACACATTATCATCTCAACCTGGCCATC 343
QY 157 ValAspLeuLeuPheLeuLeuGlyMetProPhe-----MetIleHis 170
Db 344 GCAGATGAGCTTTCATGCTGGGTCTGCTTCTTGGCTATGCAGGTGGCTGTGGTCCAC 403
QY 171 GlnLeuMetGlyAsnGlyValTyrPheIleGlyGluThrMetCysThrLeuIleThrAla 190
Db 404 -----TGGCCCTTTGGCAAGGCCATTGTGCCGGGTGCTAGACT 442
QY 191 MetAspAlaAsnSerGlnPheThrSerThrTyrIleLeuThrAlaMetAlaIleAspArg 210
Db 443 GTGGATGGCARGATCAAGTTCACACAGATCTTCTGCTGCAGATCATGAGCATGACCGA 502
QY 211 TyrLeuAlaThrValHisProIleSerSerThrLysPheArgLysProSerValAlaThr 230
Db 503 TACCTGGCTGTGGTCCACCCCATCAAGTCGGCCAAAGTGAGAGAACCCGAGCGCCAAG 562
QY 231 LeuValIleCysLeuLeuTrpAlaLeuSerPheIleSerIleThrProValTyrLeuTyr 250
Db 563 ATGATCACCATGCGCTGTGTGGGAGTCTCTGCTGTCATCTTGCCCATCATGATATAT 622
QY 251 AlaArgLeuIleProPheProGlyGlyAlaValGlyCysGlyIleArgLeuProAsnPro 270
Db 623 GCTGGGCTCCGAGCAACACAGTGGGGAGAAAGCAGCTGCACATCAACTGGCCAGTGAA 682
QY 271 AspThrAspLeuTyr---TrpPheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuPro 289
Db 683 TCTGGGCTTGTATACACAGGTTTCATCTTACACTTTCATCTGGGTTCTCGTGAACC 742
QY 290 PheValValIleThrAlaAlaTyrValArgIleLeuGlnArgMetThrSerSerValAla 309
Db 743 CTCACCATCATCTGTCTTGTCTACCTGTTCATTATCATCAAGGTGAAGTCTCTGAATC 802
QY 310 ProAlaSerGlnArgSerIleArgLeuArgThrLysArgValThrArgThrAlaIleAla 329
Db 803 CGAGTGGGCTCCTCTAAGAGAAGACTGTGAGAAGAAGGTCAACCCGAATGTTCCATC 862
QY 330 IleCysLeuValPhePheValCysTrpAlaProTyrTyrValLeuGlnLeuThrGlnLeu 349
Db 863 GTGGTGGCTGTCTCATCTTCTGTGCTGCCCTTCTACATATTCAACGTTTCTCCGTC 922
QY 350 SerIleSer---ArgProThrLeuThrPheValTyrLeuTyrAsnAlaAlaIleSerLeu 368
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QY 389 LysArgLeuValLeuSerValLysProAlaAlaGlnGlyGlnLeuArgAlaValSerAsn 408

Db 1043 AAG-----AGCTTCAGATGTCCTCTGCTTGGTCAAGGTG 1078
QY 409 AlaglnThrAlaAspGluGluArgThrGluSerLys 420
Db 1079 AGCGGCACAGATGATGGGAGCGGAGTGAAGTAAG 1114

RESULT 15

US-08-417-103-5
; Sequence 5, Application US/08417103
; Patent No. 5723299

GENERAL INFORMATION:

APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 83..1189
US-08-417-103-5

Alignment Scores:

Pred. No.: 1.53e-42 Length: 1351
Score: 532.00 Matches: 124
Percent Similarity: 49.76% Conservative: 81
Best Local Similarity: 30.10% Mismatches: 147
Query Match: 24.05% Indels: 60
DB: 1 Gaps: 12

US-09-885-478-2 (1-422) x US-08-417-103-5 (1-1351)

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Db 2 GATCCTGGCCT-----CCAGGGTCCATTAGGTGAGATA 37
QY 48 ProGlnProAlaTrpValGlu-----GlySerSerAlaArgLeuTrp 61
Db 38 AGATCTCTGGGCTGGCTGGAAGCTAAGACTGAAGACGACCATGACATGCGGAT 97
QY 62 GluGlnAlaThrGlyThr--GlyTrpMet-----AspLeuGluAlaSerLeu 76

Db 98 GAGCCACTCAATGGAGGCCACACATGGCTATTCATTCCATTGTCACCTCAATGGCTCTGTG 157
QY 77 LeuProThrGlyProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAla 96
Db 158 GTGTCAACC-----AACACCTCAACACGACAGAGCCGTACTATGACCTGACAAGC--- 208
QY 97 GlySerProProArgThrGlySerIleSerThrIleAsnIleIleMetProSerValPhe 116
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Thu Feb 20 11:14:37 2003

us-09-885-478-2.rni

Page 15

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Search completed: February 19, 2003, 13:50:21
Job time : 69 secs

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4

5
6

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 13:15:13 ; Search time 78 Seconds
(without alignments)
2755.572 Million cell updates/sec

Title: US-09-885-478-2

Perfect score: 2212
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 424239 segs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2212	100.0	1269	10	US-09-885-478-1 Sequence 1, Appli
2	2164	97.8	1385	10	US-09-925-776-1 Sequence 1, Appli
3	2085	94.3	2138	10	US-09-895-686-8 Sequence 8, Appli
4	1783	80.6	1214	10	US-09-885-478-3 Sequence 3, Appli

5	1708	77.2	1478	10	US-09-864-761-9721	Sequence 9721, Ap
6	1224	55.3	720	10	US-09-864-761-21946	Sequence 21946, A
7	886	40.1	519	10	US-09-895-686-25	Sequence 25, Appl
8	777	35.1	459	10	US-09-864-761-10236	Sequence 10236, A
9	565.5	25.6	1023	9	US-09-990-940-1	Sequence 1, Appli
10	565.5	25.6	1965	9	US-09-791-932-57	Sequence 57, Appl
11	552.5	25.0	336	10	US-09-895-686-22	Sequence 22, Appl
12	539	24.4	575	10	US-09-864-761-9017	Sequence 9017, Ap
13	521	23.6	304	10	US-09-895-686-57	Sequence 57, Appl
14	519	23.5	1427	10	US-09-967-768A-296	Sequence 296, App
15	498	22.5	274	10	US-09-864-761-26601	Sequence 26601, A
16	475	21.5	279	10	US-09-895-686-24	Sequence 24, Appl
17	475	21.5	1773	9	US-10-112-599A-3	Sequence 3, Appli
18	472	21.3	271	10	US-09-895-686-56	Sequence 56, Appl
19	462	20.9	1610	10	US-09-761-962-16	Sequence 16, Appl
20	462	20.9	2229	10	US-09-214-904-1	Sequence 1, Appli
21	456.5	20.6	1981	10	US-09-823-114-15	Sequence 15, Appl
22	455	20.6	1149	10	US-09-993-844-10	Sequence 10, Appl
23	453.5	20.5	1334	10	US-09-761-962-3	Sequence 3, Appli
24	453.5	20.5	1365	10	US-09-761-962-11	Sequence 11, Appl
25	453.5	20.5	1423	10	US-09-761-962-1	Sequence 1, Appli
26	453.5	20.5	1542	10	US-09-761-962-4	Sequence 4, Appli
27	453.5	20.5	1729	10	US-09-761-962-9	Sequence 9, Appli
28	453.5	20.5	2045	10	US-09-761-962-10	Sequence 10, Appl
29	453	20.5	2218	10	US-09-214-904-3	Sequence 3, Appli
30	453	20.5	2219	9	US-10-112-599A-1	Sequence 1, Appli
31	444.5	20.1	1829	9	US-09-823-114-7	Sequence 7, Appli
32	423	19.1	2602	9	US-09-905-186A-1	Sequence 1, Appli
33	421.5	19.1	1408	10	US-09-214-904-5	Sequence 5, Appli
34	418.5	18.9	1346	10	US-09-761-962-12	Sequence 12, Appl
35	414	18.7	1829	9	US-09-905-186A-7	Sequence 7, Appli
36	414	18.7	1829	9	US-09-905-186A-8	Sequence 8, Appli
37	414	18.7	1829	9	US-09-905-186A-9	Sequence 9, Appli
38	414	18.7	1829	9	US-09-905-186A-10	Sequence 10, Appl
39	414	18.7	1829	9	US-09-905-186A-11	Sequence 11, Appl
40	413.5	18.7	1602	10	US-09-804-551B-27	Sequence 27, Appl
41	413	18.7	1805	10	US-09-823-114-18	Sequence 18, Appl
42	412.5	18.6	1452	10	US-09-170-919-3	Sequence 3, Appli
43	412	18.6	1404	10	US-09-804-551B-9	Sequence 9, Appli
44	377	17.0	223	10	US-09-895-686-20	Sequence 20, Appl
45	372	16.8	1238	10	US-09-761-962-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-885-478-1
; Sequence 1, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-885-478-1

Alignment Scores: 6.13e-199 Length: 1269
Pred. No.: 2212.00 Matches: 422
Score: 100.00% Conservative: 0
Percent Similarity:

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-885-478-2 (1-422) x US-09-885-478-1 (1-1269)

QY 1 MetSerValGlyAlaMetLysGlyValGlyArgAlaValGlyLeuGlyGlyGlySer 20
DB 1 ATGTCAGTGGAGGCCATGAGAAGGAGTGGGGAGGGCAGTTGGCTTGAGGGCGGACG 60
QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
DB 61 GGCTGCCAGGCTACGGAGGAGAACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGGACAA 120
QY 41 GlyGlyArgArgTTrpArgLeuProGlnProAlaTTrpValGlyGlySerSerAlaArgLeu 60
DB 121 GGTGGCAGGCGCTGAGAGGCTGCCGACCTGCGGTGGGTGGAAGGGAGAGCTCAGCTCGGTTG 180
QY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly 80
DB 181 TGGAGACGCGGACCGGACCGGACCTGGATGAGACCTGGAACTCGCTGCTGCCACCTGGT 240
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
DB 241 CCCAATGCCAGACACACCTGATGGCCCCGATAACCTCACTTCAGCAGATCACTCCT 300
QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
DB 301 CGCAGGGGAGCATCTCCTACATCAACATCATCATGCTTCGGGTGTCGGCACCATCTGC 360
QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeu 140
DB 361 CTCTGGGCATCATCGGGAAGCTCCACGGTCATCTTCGGCGTCGTGAAGAAGTCCAAGCTG 420
QY 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160
DB 421 CACTGGTGCAACAACAGCTCCCGACATCTTCATCATCAACTCTCGGTAGTAGTCTCCTC 480
QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180
DB 481 TTTCCTCTGGGCATGCCCTTCATGATCCACAGCTCATGGGCAATGGGGTGTGCCACTTT 540
QY 181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
DB 541 GGGAGACCATGTGCACCCCTCATCGGCCATGGATGCCAATAGTCAGTTCCACGACACC 600
QY 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220
DB 601 TACATCCTGACCGGCATGGCCATTGACCGCTACCTGGCCACTGTCACCCCATCTCTCC 660
QY 221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer 240
DB 661 ACGAAGTTCCGGAAGCCCTCTGTGGCCACCCCTGGTGAATCTGCTCTCTGCGCCCTCTCC 720
QY 241 PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla 260
DB 721 TTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCACAGAGGTGCA 780
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DB 781 GTGGCTGCGGCATACGCGCTGCCCAACCCAGACACTGACTCTACTGTTACACCTGTAC 840
QY 281 GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle 300
DB 841 CAGTTTTCCTGGCCTTTGCCCTTGTGTGTCATCACAGCCGATACGTAGAGATC 900
QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
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DB 961 AAGAGGTGACCCGACAGCCATCGCATCTGTGTCTCTTTGTGTGTGGGACACC 1020

QY 341 TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
DB 1021 TACTATGTGCTACAGCTGACCCAGTTGTTCATCAGCCGCCGACCTCACCCTTGTGTAC 1080
QY 361 LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr 380
DB 1081 TTATACAATGGCGGCATCAGCTTGGGCTATGCCAACAGAGCTCTCAACCCCTTGTGTAC 1140
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QY 401 GlyGlnLeuArgAlaValaSerAsnAlaGlnThrAlaAspGluGluArgThrGlySerLys 420
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QY 421 GlyThr 422
DB 1261 GGCACC 1266

RESULT 2

US-09-925-776-1
; Sequence 1, Application US/09925776
; Patent No. US20020038007A1
; GENERAL INFORMATION:
; APPLICANT: AMES, ROBERT S., JR.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: FOLEY, JAMES J.
; APPLICANT: BERGSMAN, DEK J.
; APPLICANT: ELLIS, CATHERINE E.
; APPLICANT: CHAMBERS, JON K.
; TITLE OF INVENTION: A METHOD OF FINDING AGONIST AND
; TITLE OF INVENTION: ANTAGONIST TO HUMAN 11CB SPLICE VARIANT
; FILE REFERENCE: GP-50003-D2
; CURRENT APPLICATION NUMBER: US/09/925,776
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/032,763
; PRIOR FILING DATE: 1996-12-11
; PRIOR APPLICATION NUMBER: 08/984,288
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: 60/073,747
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 09/060,504
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1385
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-925-776-1

Alignment Scores:

Pred. No.: 2,27e-194 Length: 1385
Score: 2164.00 Matches: 412
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.83% Indels: 0
DB: 10 Gaps: 0

US-09-885-478-2 (1-422) x US-09-925-776-1 (1-1385)

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QY 31 ProAspCysGlyAlaCysAlaProGlyGlnGlyArgArgTTrpArgLeuProGlnPro 50
DB 126 CCCGACTGCGGGCTTGGCTCCGGGACAAAGGTGGCAGCGCTGAGGCTGCCGCAAGCT 185
QY 51 AlaTrpValGluGlySerSerAlaArgLeuTrpGluGlnAlaThrGlyThrGlyTrpMet 70

Db 186 GCGTGGGTGAGGGAGAGCTCAGCTCGGTGTGTGGAGACAGCGCAGCCGGCACTGGCTGATG 245

QY 71 ASPLEUGLUALaserLeuLeuProThrglyProAsnAlaSerAsnThrSerAspGlyPro 90

Db 246 GACCTGGAAGCCTCGCTGCTGCCACTGTGTCCTCCAATGCCAACAACACCTCTGATGGCCCC 305

QY 91 AspasnLeuThrSerAlaGlySerProProArgThrGlySerIleSerTyrIleAsnIle 110

Db 306 GATAACCTCAGTTCGGCAGATCACCTCTCGCACGGGAGCATCTCCTACATCAACATC 365

QY 111 IleMetProSerValPheGlyThrIleCysLeuLeuGlyIleIleGlyAsnSerThrVal 130

Db 366 ATCATGCCCTTCGGTGTTCGGCACCATCTGCCTCCTGGGCATCATCGGAACCTCCAGCGTC 425

QY 131 IlePheAlaValValLysSerLysLeuHisTrpCysAsnAsnValProAspIlePhe 150

Db 426 ATCTTCGGCGTCTGGAAGAGTCCAAGCTGCACCTGGTGCACAACGTCCTCCGACATCTTC 485

QY 151 IleIleAsnLeuSerValValAspLeuLeuPheLeuLeuGlyMetProPheMetIleHis 170

Db 486 ATCATCAACCTCTCGGTAGATCTCCTCTTCTCTCGGCATGCCCCCTCATGATCAGCAC 545

QY 171 GlnLeuMetGlyAsnGlyValTrpHisPheGlyGlyIleThrMetCysThrLeuIleThrAla 190

Db 546 CAGCTCATGGCAATGGGTGTGGCACTTTGGGGAGACCATGTGCACCCCTCATCAGCGCC 605

QY 191 MetAspAlaAsnSerGlnPheThrSerThrTyrIleLeuThrAlaMetAlaIleAspArg 210

Db 606 ATGATGCCAATAGTACAGTTCACACAGACACCTACATCCTGACCGGCATGGCCATGACCGC 665

QY 211 TyrLeuAlaThrValHisProIleSerSerThrLysPheArgLysProSerValAlaThr 230

Db 666 TACCTGGCCACTGTCCACCCCATCTCTCCACGAAGTCCGGAAGCCCTCTGTGGCCACC 725

QY 231 LeuValIleCysLeuLeuTrpAlaLeuSerPheIleSerIleThrProValTrpLeuTyr 250

Db 726 CTGGTGAATCTGCCTCGTGTGGCCCTCTCCTCATCAGCATCACCCCTGTGTGGCTGAT 785

QY 251 AlaArgLeuIleProPheProGlyGlyAlaValAlaGlyCysGlyIleArgLeuProAsnPro 270

Db 786 GCCAGACTCATCCCTTCCAGAGAGGTGCAGTGGGCTGGGCATACGCCCTGCCAACCCA 845

QY 271 AspThrAspLeuTyrTrpPheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuProPhe 290

Db 846 GACACTGACCTTACTGTTCAACCTGTACACAGTTTTCCTGGCCCTTGGCCCTGCTTTT 905

QY 291 ValValIleThrAlaAlaThrValArgIleLeuGlnArgMetThrSerSerValAlaPro 310

Db 906 GTGGTCATCACAGCCGATACGTGAGGATCCTCGACGGCATGACGTCCTCAGTGGCCCC 965

QY 311 AlaSerGlnArgSerIleArgLeuArgThrLysArgValThrArgThrAlaIleAlaIle 330

Db 966 GCCTCCAGCGCAGCATCCGGCTGCGGACAAGAAGGGGTGACCCGACAGCCATCGCCATC 1025

QY 331 CysLeuValPhePheValCysTrpAlaProTyrTyrValleuGlnLeuThrGlnLeuSer 350

Db 1026 TGTCTGGTCTTCTTGTGTGTGGCACCCCTACTATGTGTACAGCTGACCCAGTGTGCC 1085

QY 351 IleSerArgProThrLeuThrPheValTyrLeuTyrAsnAlaAlaIleSerLeuGlyTyr 370

Db 1086 ATCAGCCGCGCCGACCTTGTCTACTTATACAAATCGGGCCATCAGCTTGGGCTAT 1145

QY 371 AlaAsnSerCysLeuAsnPropheValTyrIleValleuGlyGluThrPheArgLysArg 390

Db 1146 GCCAACAGCTGCCTCAACCCCTTGTGTACATCGTCTGTGAGACGTTCGCAACGCG 1205

QY 391 LeuValleuSerValLysProAlaAlaGlnGlyGlnLeuArgAlaValSerAsnAlaGln 410

Db 1206 TTGTCCTCTCGTGTGAAGCCTGCAGCCAGCGGCGAGCTTCGCGCTGTACAGCAACGCTCAG 1265

QY 411 ThrAlaAspGluGluArgThrGluSerLysGlyThr 422

Db 1266 ACGGCTGACGAGAGAGAGAGCAAAAGCAAAAGGCACC 1301

RESULT 3

US-09-895-686-8

; Sequence 8, Application US/09895686

; Patent No., US20020106655A1

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Lal, Preeti

; APPLICANT: Tang, Y. Tom

; APPLICANT: Baughn, Mariah R.

; TITLE OF INVENTION: HUMAN GPCR PROTEINS

; FILE REFERENCE: PC-0044 CIP

; CURRENT APPLICATION NUMBER: US/09/895,686

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PERL Program

; SEQ ID NO 8

; LENGTH: 2138

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc-feature

; OTHER INFORMATION: Incyte ID No. US20020106655A1 1459432CB1

US-09-895-686-8

Alignment Scores:

Pred. No.:	1,15e-186	length:	2138
Score:	2085.00	Matches:	400
Percent Similarity:	98.53%	Conservative:	3
Best Local Similarity:	97.80%	Mismatches:	6
Query Match:	94.26%	Indels:	1
DB:	10	Gaps:	0

US-09-885-478-2 (1-422) x US-09-895-686-8 (1-2138)

QY 14 ValGlyLeuGlyGlyGlySerGlyCysGlnAlaThrGluGluAspProLeuProAspCys 33

Db 21 ATTGGGCTTGAGAGCGCGCAC-GGCTGCCAGGCTACGAGAGGTAGACCCCTTCCCAACTGC 79

QY 34 GlyAlaCysAlaProGlyGlnGlyIlyArgArgTrpArgLeuProGlnProAlaTrpVal 53

Db 80 GGGGCTTGGCTCCGGGACAAGGTGGCAGGCGCTGGAGGCTGCCGACAGCCCTGCGTGGGTG 139

QY 54 GluGlySerSerAlaArgLeuTrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGlu 73

Db 140 GAGGGAGCTCAGCTCGGTGTGGCAGCATGCGACCGGACCTGCTGATGGACCTGGAA 199

QY 74 AlaSerLeuLeuProThrGlyProAsnAlaSerAsnThrSerAspGlyProAspAsnLeu 93

Db 200 GCCTCGCTGCTGCCCACTGTGCCAATGCAACAACACCTCTGATGGCCCCGATAACTTC 259

QY 94 ThrSerAlaGlySerProProArgThrGlySerIleSerTyrIleAsnIleIleMetPro 113

Db 260 ACTTGGCAGGATCACCTCTCGCAGCGGGAGCATCTCCTACATCAACATCATGCGCT 319

QY 114 SerValPheGlyThrIleCysLeuLeuGlyIleIleGlyAsnSerThrValIlePheAla 133

Db 320 TCGGTGTTCGGCACCATCTGCTCTGCGGCATCATCGGGAACCTCCAGGTCATCTTCGGC 379

QY 134 ValValLysLysSerLysLeuHisTrpCysAsnAsnValProAspIlePheIleAsn 153

Db 380 GTCGTGAAGAAGTCCAAGCTGCACCTGGTGCAACAACGTCCTCCGACATCTTCATCATCAAC 439

QY 154 LeuSerValValAspLeuLeuPheLeuLeuGlyMetProPheMetIleHisGlnLeuMet 173

Db 440 CTCGTGAGTAGATCTCCTCTTCTCTGCGGCATGCCCCCTGATGATCCACAGCTCATG 499

QY 174 GlyAsnGlyValTrpHisPheGlyGluThrMetCysThrLeuLeuThrAlaMetAspAla 193

Db 500 GGCATGGGGGTGGCACCTTGGGAGAGACCATGTGCACCCCTCATCACGGCCATGATGCC 559

QY 194 AsnSerGlnPheThrSerThrTyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAla 213

Db 560 AATAGTCAGTTCAACCAGCACCTACATCTGACCGCCATGGCCATTGACCGGTACTGCGCC 619

QY 214 ThrValHisProIleSerSerThrLysPheArgLysProSerValAlaThrLeuValIle 233

Db 620 ACTGTCCACCCCATCTCTTCCACGAAGTTCCGGAAGCCCTGTGTGGCCACCCCTGGTGAATC 679

QY 234 CysLeuLeuTrpAlaLeuSerPheIleSerIleThrProValTrpLeuTyrAlaArgLeu 253

Db 680 TGCCCTCTGTGGGCCCTCTCTCTTCATCAGCATCACCCCTGTGTGGCTGTATGCGAGACTC 739

QY 254 IleProPheProGlyGlyAlaValGlyCysGlyIleArgLeuProAsnProAspThrAsp 273

Db 740 ATCCCTTCCCAAGGAGGTGACAGTGGGCTGGCGCATACGCTGCCCAACCCAGACACTGAC 799

QY 274 LeuTyrTrpPheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuPropheValIle 293

Db 800 CTCTACTGTGTCAACCTGTACCAAGTTTTCCTGGCCTTGGCCCTTGTGTGGTCAATC 859

QY 294 ThrAlaAlaTyrValArgIleLeuGlnArgMetThrSerSerValAlaProAlaSerGln 313

Db 860 ACAGCCGCATACGTGAGGATCCTGCAGCGCATGACGTCTCAGTGGCCCCCACCCTCCAG 919

QY 314 ArgSerIleArgLeuArgThrLysArgValThrArgThrAlaIleAlaIleCysLeuVal 333

Db 920 CGCAGCATCCGGCTGCGGACAAAGAGGGTGACCCGCGACAGCCATCGCATGTGTGTC 979

QY 334 PhePheValCysTrpAlaProTyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArg 353

Db 980 TTCTTTGTGTGTGGGACCCCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGC 1039

QY 354 ProThrLeuThrPheValTyrLeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSer 373

Db 1040 CCGACCCCACTTTGTCTACTTATACATGCGGCATCAGCTTGGGCTATGCCAACAGC 1099

QY 374 CysLeuAsnPropheValTyrIleValLeuCysGluThrPheArgLysArgLeuValLeu 393

Db 1100 TGCCCTCAACCCGTTGTGTACATCGTCTCTGTGAGACGTTCCGCAACGCTTGGTCTG 1159

QY 394 SerValLysProAlaAlaGlnGlyInLeuArgAlaValSerAsnAlaGlnThrAlaAsp 413

Db 1160 TCGGTGAAGCTGCAGCCCGAGGGGAGCTTCGCGCTGTACGCAACGCTCAGGGCGGTGAC 1219

QY 414 GluGluArgThrGluSerLysGlyThr 422

Db 1220 GAGGAGAGACAGAAAGCAAGGCAC 1246

RESULT 4

US-09-885-478-3

: Sequence 3, Application US/09885478

: Patent No. US20020111306A1

: GENERAL INFORMATION:

: APPLICANT: SALON, JOHN A

: APPLICANT: LAZ, THOMAS M

: APPLICANT: NAGORNY, RAISA

: APPLICANT: WILSON, AMY E

: TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH1

: TITLE OF INVENTION: USES THEREOF

: FILE REFERENCE: 1795/57453-A-PCF-US

: CURRENT APPLICATION NUMBER: US/09/885,478

: CURRENT FILING DATE: 2001-09-24

: PRIOR APPLICATION NUMBER: PCT/US99/31169

: PRIOR FILING DATE: 1999-12-30

: NUMBER OF SEQ ID NOS: 28

: SOFTWARE: PatentIn version 3.1

: SEQ ID NO 3

: LENGTH: 1214

: TYPE: DNA

: ORGANISM: RATTUS NORVEGICUS

US-09-885-478-3

Alignment Scores: 1.25e-158 Length: 1214

Pred. No.: 1783.00 Matches: 344

Percent Similarity: 97.22% Conservative: 6

Best Local Similarity: 95.56% Mismatches: 10

Query Match: 80.61% Indels: 0

DB: 10 Gaps: 0

US-09-885-478-2 (1-422) x US-09-885-478-3 (1-1214)

QY 63 GlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGlyProAsn 82

Db 2 CAGCGACCTGCACCGGCTGCATGATATGCAAACTCGTGTGCTGTCCACTGGCCCCAAT 61

QY 83 AlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProArgThr 102

Db 62 GCCAGCAACATCTCCGATGGCCAGGATATATCTCACATTTGCCGGGGTCACCTCCTGCACA 121

QY 103 GlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCysLeuLeu 122

Db 122 GGGAGTGTCTCTACATCAACATCATATAGCCTTCCGTGTGTGTACCATCTGTCTCTG 181

QY 123 GlyIleIleGlyAsnSerThrValIlePheAlaValAlaLysLysSerLysLeuHistrp 142

Db 182 GGCATCGTGGAACTCCACGGTCAATCTTGTGTGTGTAAGAGATCCAAAGCTACACTGG 241

QY 143 CysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuPheLeu 162

Db 242 TGCAGCAACGTCCTCCGACATCTTCATCATCAACCTCTCTGTGTGATCTGCTTCTCTG 301

QY 163 LeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPheGlyGlu 182

Db 302 CTGGGCATGCTTTTCATGATCCACAGCTCATGGGGAACGGCGTCTGGCACTTTGGGGAA 361

QY 183 ThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThrTyrIle 202

Db 362 ACCATGTGACACCTTCATCACAGCCATGAGCAAGCCAAACAGTCACTGATCAACACTACATC 421

QY 203 LeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSerThrLys 222

Db 422 CTGACTGCCATGACCATTTGACCGCTACTTGGCCACCGTCCACCCCATCTCCTCACCAAG 481

QY 223 PheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSerPheIle 242

Db 482 TTCGGAAGCCCTTCATGCGCACCCGTGTGATCTGCCTCTGTGGCGCTCTCCTTCATC 541

QY 243 SerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAlaValGly 262

Db 542 AGTATCACCCCTGTGTGTGCTCTACGCCAGGCTCATTTCCCTTCCAGGGGGTGTGTGGGC 601

QY 263 CysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyrGlnPhe 282

Db 602 TGTGGCATCCGCTGCCAAACCCGAGACTGACCTTACTGTGTCACTGTGTACCAAGTTT 661

QY 283 PheLeuAlaPheAlaLeuProPheValIleThrAlaAlaTyrValArgIleLeuGln 302

Db 662 TTCCTGGCTTTGCCCTTCCGTTGTGTGATTTACCGCGGCATACGTGAATAATACATACAG 721

QY 303 ArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThrLysArg 322

Db 722 CGCATGACGTTCTGGTGGCCCAAGCTTCCCAACGACGATCCGCTTGGACAAAGAGG 781

QY 323 ValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaProTyrTyr 342

Db 782 GTGACCCGCGAGGCCATTGCCATCTGTGTGCTTCTTGTGTGTGTGGCGACCCCTACTAT 841

QY 343 ValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyrLeuTyr 362

Db 842 GTGTGACAGTGAACCAAGCTGTCCATCAGCGCCGACCCCTCAGCTTGTCTACTTGTAC 901

QY 363 AsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnPropheValTyrIleVal 382

Db 902 AACGGCGGCATCAGCTTGGGCTATGCTAACAGCTGCCTGAACCCCTTGTGTACATATG 961

QY 383 LeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGlnGlyGln 402

Db 962 CTCTGTGAGACCTTTGCAAAACGCTTGTGTTCACGTGAGACCTGCAGCCAGGGGCGAC 1021

QY 403 LeuArgAlaValSerAsnAlaGlnThrAlaAspGluArgThrGluSerLysGlyThr 422

Db 1022 CTCGGCAGCGGTACAGCAGCGCTCAGACAGCTGATGAGAGAGAGACAGAAAGCAGCAC 1081

RESULT 5

US-09-864-761-9721

; Sequence 9721, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aecmlca-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; PRIOR APPLICATION NUMBER: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 9721

; LENGTH: 1478

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO 286090.10

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.1

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7

; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3

US-09-864-761-9721

Alignment Scores:

Pred. No.: 1.87e-151 Length: 1478

Score: 1708.00 Matches: 346

Percent Similarity: 82.22% Conservative: 10

Best Local Similarity: 79.91% Mismatches: 17

Query Match: 77.22% Indels: 60

DB: 10 Gaps: 6

US-09-885-478-2 (1-422) x US-09-864-761-9721 (1-1478)

QY 32 AspCysGlyAlaCysAlaProGlyGlnGlyArgArgTrpArgLeuProGln----- 49

Db 152 AACGTGTGCTCTTGCCCTC-----TGGTGCTGCAGAGGCGAGGC 190

QY 50 -----ProAlaTrpValGlnGlySer-----SerAlaArgLeuTrpGlnAla 64

Db 191 ATGTTGTGTCCTTCCAAAGACAGATGCTCAGGGCAGCTGTGTAGATTCCACGAAACT 250

QY 65 ThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGlyProAsnAlaSer 84

Db 251 CATGGAGAGGGAAGGAGC-----AAGATTAGC 280

QY 85 AsnThrSerAspGlyProAspAsn----- 92

Db 281 AAC--AGTGAAGGAGGAGAGATGTTGGAGAGATTCAGATGAACGGTGGTCGCTG 337

QY 92 ----- 92

Db 338 GAGGCTGACATGCCAGCAGATGTCACTTCTCAGACCAAGCCCATGTCAACAGCCAA 397

QY 93 -----LeuThrSerAlaGlySerProProArgThrGlySerIleSerTyrIleAsn 109

Db 398 CGCTTGCTTCCTTGTGCCAGAGATCACCTCTCGCAGGGGAGCATCTCTACATCAAC 457

QY 110 IleIleMetProSerValPheGlyThrIleCysLeuLeuGlyIleIleGlyAsnSerThr 129

Db 458 ATCATCATGCGCTTCGGTGTTCGGCACCATCTGCCCTGGGCATCATCGGAACCTCACAG 517

QY 130 ValIlePheAlaValValLysIleSerLysLeuHisTrpCysAsnAsnValProAspIle 149

Db 518 GTCATCTTCGCGGTCGTGAAGAATCCAAAGCTGCACGTGTGCAACAACGTCGCCGACATC 577

QY 150 PheIleIleAsnLeuSerValValAspLeuLeuPheLeuLeuGlyMetProPheMetIle 169

Db 578 TTCATCATCAACCTCTCGGTAGATATCTCTCTTCTCTGGGCATGCCCTTCATGATC 637

QY 170 HisGlnLeuMetGlyAsnGlyValTrpHisPheGlyGluThrMetCysThrLeuIleThr 189

Db 638 CACCAGCTCATGGGCAATGGGGTGTGGCACTTTGGGGAGACCATGTGCACCCCTCATCAGC 697

QY 190 AlaMetAspAlaAsnSerGlnPheThrSerThrTyrIleLeuThrAlaMetAlaIleAsp 209

Db 698 GCCATGGATGCCAATAGTCAGTTCACCAAGCACCTACATCTTGACCGCCATGGCCATTGAC 757

QY 210 ArgTyrLeuAlaThrValHisProIleSerSerThrLysPheArgLysProSerValAla 229

Db 758 CGCTACCTGGCCACTGTCCACCCCATCTCTTCACGAGAAGTCCGGAAGCCCTCTGTGGCC 817

QY 230 ThrLeuValIleCysLeuLeuTrpAlaLeuSerPheIleSerIleThrProValTrpLeu 249

Db 818 ACCCTGGTGTCTGCTCTCTGTGGGCCCTCTCTTCATCAGCATCACCCCTGTGTGGCTG 877

QY 250 TyrAlaArgLeuIleProPheProGlyGlyAlaValGlyCysGlyIleArgLeuProAsn 269

Db 878 TATGCCAGACTCATCCCTTCCCAAGAGGTGCAAGTGGGCTGCGGCATACGCCCAAC 937

QY 270 ProAspThrAspLeuTyrTrpPheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuPro 289

Db 938 CCAGACACTGACCTTACTGTGTTACCCCTGACCAAGTTTTCCTGCGCTTTGCCCTGCTG 997

QY 290 PheValValIleThrAlaAlaTyrValArgIleLeuGlnArgMetThrSerSerValAla 309

Db	998	TTTGTGTCATCACAGCCGCATACGTGAGGATCCTGCAGCGCATGACGCTCTCAGTGGCC	1057
QY	310	ProAlaSerGlnArgSerIleArgLeuArgThrIysArgValThrArgThrAlaIleAla	329
Db	1058	CCCCGCTCCCAAGCGCAGCATCCGGCTCGCGACAAGAAGGTGACCCCGCACAGCCATCGCC	1117
QY	330	IleCysLeuValPhePheValCysTrpAlaProIleTyrValLeuGlnLeuThrGlnLeu	349
Db	1118	ATCTGTCTGTCTTCTTTGTGTGCTGGGCACCCCTACTATGTGTCTACAGCTGACCCAGTTG	1177
QY	350	SerIleSerArgProThrLeuThrPheValTyrIleuTyrAsnAlaAlaIleSerLeuGly	369
Db	1178	TCCATCAGCCGCCCGACCCCTCACCTTTGTCTACTTATACAAATGCGGCCATCAGCTTGGGC	1237
QY	370	TyrAlaAsnSerCysLeuAsnProPheValTyrIleValLeuCysGlnThrPheArgLys	389
Db	1238	TATGCCACACAGCTGCCTCAACCCCTTTGTGTACATCTGCTCTGTGAGCAGTTCCGCAAA	1297
QY	390	ArgLeuValLeuSerValLysProAlaAlaGlnGlnLeuArgAlaValSerAsnAla	409
Db	1298	CGCTTGCTCTGTGCGTGAAAGCCTGCAGCCACAGGGGACGCTTGCGCGCTGTGCAGCAACGCT	1357
QY	410	GlnThrAlaAspGlnGlnArgThrGlnSerLysGlyThr	422
Db	1358	CAGACGGCTGACGAGGAGAGAGACAGAAAGCAAGGCAACC	1396

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RESULT 6
US-09-864-761-21946
; Sequence 21946, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408

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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21946
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO 286090.10
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
; OTHER INFORMATION: SMTSSPROT HIT: Q99705, EVALU0 0.00e+00
; OTHER INFORMATION: NT HIT: g11418166, EVALU0 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: BE701073.1, EVALU0 0.00e+00
US-09-864--761-21946

```

Alignment Scores:	
Pred. No.:	2.1e-106
Score:	1224.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	55.33%
DB:	10
Length:	720
Matches:	239
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-885-478-2 (1-422) x US-09-864-761-21946 (1-720)

QY	184	Me	Cys	Thr	Ile	Leu	Ile	Thr	Ala	Met	Asp	Ala	Asn	Ser	Gln	Phe	Thr	Ser	Thr	Tyr	Ile	Leu	203		
Db	1	AT	GTG	CAC	CCCT	CA	TAC	GGG	CCAT	GGC	ATG	CA	TGCA	TGCA	TAG	TCA	GTTC	ACC	CAG	CA	CC	TAC	ATC	CTG	60
QY	204	Thr	Ala	Met	Ala	Ile	Asp	Arg	Tyr	Leu	Ala	Thr	Val	His	Pro	Ile	Ser	Ser	Thr	Leu	Phe			223	
Db	61	ACC	GCC	ATG	GGC	CA	TGAC	CGG	CTAC	CTGG	CA	CTG	TCAC	CTG	TCAC	CCCA	CTC	TTCC	AC	GGA	AG	TTTC		120	
QY	224	Arg	Lys	Pro	Ser	Val	Ala	Thr	Leu	Val	Ile	Cys	Leu	Leu	Thr	Pal	Ala	Leu	Ser	Phe	Ile	Ser		243	
Db	121	CGG	AAG	CCCT	CTG	TGG	CCAC	ACC	CTG	TGAT	CTG	CCCT	CTG	TGG	CCCT	CTC	CTT	CA	TAC	A	G	C		180	
QY	244	Ile	Thr	Pro	Val	Thr	Leu	Tyr	Ala	Arg	Leu	Ile	Pro	Phe	Pro	Gly	Gly	Ala	Val	Gly	Cys			263	
Db	181	ATC	ACCC	CTG	TGG	CTGT	ATG	CCAG	ACAT	CA	TCC	CCCT	TCC	CAG	AGG	TG	CAG	TGG	GG	CTGC			240		
QY	264	Gly	Ile	Arg	Leu	Pro	Asn	Pro	Asp	Thr	Asp	Leu	Tyr	Trp	Phe	Thr	Leu	Tyr	Gln	Phe			283		
Db	241	GGC	ATAC	GCCT	GTG	CCCA	ACC	CAG	ACAC	TA	CACT	CACT	CTG	TTC	AC	CCCT	GTAC	CCAG	TTT	TC			300		
QY	284	Leu	Ala	Phe	Ala	Leu	Pro	Phe	Val	Ile	Thr	Ala	Ala	Tyr	Val	Arg	Ile	Leu	Gln	Arg			303		
Db	301	CTG	GCT	TG	CCCT	GTG	CCCT	TTT	GTG	TCA	TAC	ACAG	CCG	CA	TAC	GTG	AGG	ATC	CTG	CAG	GC		360		
QY	304	Met	Thr	Ser	Ser	Val	Ala	Pro	Ala	Ser	Gln	Arg	Ser	Ile	Arg	Leu	Arg	Thr	Lys	Arg	Val			323	
Db	361	ATG	ACG	TCT	CA	TG	GGC	CCCG	CCCT	CCCA	CGC	AGC	AGC	ATC	CGG	CTG	CGG	ACAA	AGG	GGT	G		420		
QY	324	Thr	Arg	Thr	Ala	Ile	Ala	Ile	Cys	Leu	Val	Phe	Phe	Val	Cys	Trp	Pal	Pro	Tyr	Tyr	Val			343	
Db	421	ACC	CGC	AC	AGC	CA	TG	CCAT	CTG	TCT	GTG	CTT	CTT	TGT	GTG	CGG	CA	CCCT	AC	CA	TAT	CTG		480	
QY	344	Leu	Gln	Leu	Thr	Gln	Leu	Ser	Ile	Ser	Arg	Pro	Thr	Leu	Thr	Phe	Val	Tyr	Leu	Tyr	Asn			363	
Db	481	CTA	CAG	CTG	AC	CCCA	GTG	TG	CCAT	CA	AGC	CGC	CGA	CCCT	CA	CCCT	TTG	CTA	CTA	TACA	CA	T		540	
QY	364	Ala	Ala	Ile	Ser	Leu	Gly	Tyr	Ala	Asn	Ser	Cys	Leu	Asn	Pro	Phe	Val	Tyr	Ile	Val	Leu			383	

Db 541 GCGGCCATCAGCTTGGCTATGCCAACAGCTGCTCAACCCCTTTGTGTACATCGTGCTC 600
QY 384 CysgluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGlnGlyGlnLeu 403
Db 601 TGTGAGACGTTCCGCAACGCTTGGTCTGCTGGTGAAGCCTGCAGCCCGAGGGCAGCTT 660
QY 404 ArgAlaValSerAsnAlaGlnThrAlaAspGluArgThrGluSerLysGlyThr 422
Db 661 CGCGCTGTACAGCAACGCTCAGACGGCTGACGAGAGAGACAGAGAAGCAAGCAGCACC 717

RESULT 7

US-09-895-686-25
; Sequence 25, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 25
; LENGTH: 519
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020106655A1 SAAB00250R1
US-09-895-686-25

Alignment Scores:
Pred. No.: 7.84e-75 Length: 519
Score: 886.00 Matches: 171
Percent Similarity: 99.42% Conservative: 0
Best Local Similarity: 99.42% Mismatches: 1
Query Match: 40.05% Indels: 0
DB: 10 Gaps: 0

US-09-885-478-2 (1-422) x US-09-895-686-25 (1-519)

QY 179 HispHeGlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThr 198
Db 3 CACTTGGGGAGACCATGTGCACCCCTCATCAGGGCCATGGATGCCAATAGTCAGTTCCACC 62
QY 199 SerThrTyrlleLeuThrAlaMetAlaIleAspArgTyrlleuAlaThrValHisProIle 218
Db 63 AGCACCTACATCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGCCACCCCATC 122
QY 219 SerSerThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAla 238
Db 123 TCTTCCAGGAAGTCCGGAAAGCCCTGTGTGGCCACCTGTGATCTGCTCTGTGGGCC 182
QY 239 LeuSerPheIleSerIleThrProValTrpLeuTyrlaArgLeuIleProPheProGly 258
Db 183 CTCTCTTCATCAGCATCACCCCTGTGTGGTGTATGCCAGACTCATCCTCCCTCCAGGA 242
QY 259 GlyAlaValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrlTrpPheThr 278
Db 243 GGTGACATGGGCTGCGGCATACGCCCTGCCCAACCCAGACACTGACCTTACCTGTTCCACC 302
QY 279 LeuTyrlGlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrlVal 298
Db 303 CTGTACCAAGTTTCTTCCCTGGCTTGGCCCTGCTTGTAGTGTGCATCACAGCCGATACGTG 362
QY 299 ArgIleLeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeu 318
Db 363 AGGATCCTGCAGCGCATGACGTCCTCAGTGGCCCGCCCTCCAGCGCAGCATCCGGCTG 422
QY 319 ArgThrLysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrp 338

Db 423 CGACAAAGAGGGTGACCCGACAGCCATCGCCATCTGTCTGTCTTGTGTGCTGG 482
QY 339 AlaProTyrlValLeuGlnLeuThrGlnLeuSer 350
Db 483 GCACCTACTATGTGCTACAGCTGACCCAGTTGTCC 518

RESULT 8

US-09-864-761-10236
; Sequence 10236, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10236
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO Z86090.10
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
US-09-864-761-10236

Alignment Scores: 1.16e-64 Length: 459
Pred. No.: 777.00 Matches: 152
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 35.13% Indels: 0
Query Match: 10 Gaps: 0
DB:

US-09-885-478-2 (1-422) x US-09-864-761-10236 (1-459)

QY 183 ThrMetCysThrIleuIleThrAlaMetAspAlaAsnSergInPheThrSerThrTyrIle 202
Db 3 ACCATGTGCACCTCATCATCAGCGCCATGGATGCCAATAGTCAGTTCCACCAGACCTACATC 62
QY 203 LeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSerThrLys 222
Db 63 CTGACCGCCATGGCCATGTGACCGGCTACCTGGCCACCTGTCACCCCATCTCTCCACGGAAG 122
QY 223 PheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSerPheIle 242
Db 123 TTCGGGAAGCCCTCTGTGGCCACCCCTGGTATCTGCCCTCTGTGGCCCTCTTCATC 182
QY 243 SerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyAlaValGly 262
Db 183 AGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCACGAGAGTGCGGC 242
QY 263 CysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyrGlnPhe 282
Db 243 TGCGGCATACGCTGCCCAACCCAGACACTGACCTCTACTGTGTACCCCTGTACAGTTT 302
QY 283 PheLeuAlaPheAlaLeuProPheValIleThrAlaAlaTyrValArgIleLeuGln 302
Db 303 TTCCTGGCTTTGGCCCTGCTTTGTGTGTCATCACAGCCGATACGTGAGATCCTGCAG 362
QY 303 ArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThrLysArg 322
Db 363 CGCATGACGTCTCTCAGTGGCCCCCGCTCCAGCGCATCCGGCTCGGACAAAGAGG 422
QY 323 ValThrArgThrAlaIleAlaIleCysLeuValPhe 334
Db 423 GTGACCCGACACGATCGCCATCTGTGTCTTC 458

RESULT 9

US-09-990-940-1
; Sequence 1, Application US/09990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiayang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupte, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030027252A1el Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1023)
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR342,
; OTHER INFORMATION: melanin-concentrating hormone receptor 2 (MCHR2)
US-09-990-940-1

Alignment Scores: 2.89e-44 Length: 1023
Pred. No.: 565.50 Matches: 113
Score: 55.95% Conservative: 61
Percent Similarity: 36.33% Mismatches: 114
Best Local Similarity: 25.57% Indels: 23
Query Match: 9 Gaps: 4
DB:

US-09-885-478-2 (1-422) x US-09-990-940-1 (1-1023)

QY 110 IleIleMetProSerValPheGlyThrIleCysLeuLeuGlyIleIleGlyAsnSerThr 129
Db 103 GTCATCCCTCCCTTCCATGATGGGATTAATCTGTTCACACAGGGCTGTGGCAACATCCTC 162
QY 130 ValIlePheAlaValValLysLysSerLysLeuHisTrpCysAsnValProAspIle 149
Db 163 ATGTATTCACATATAATAGATCCAGAAA-----AAACAGTCCCTGCATC 210
QY 150 PheIleIleAsnLeuSerValValAspLeuPheLeuLeuGlyMetProPheMetIle 169
Db 211 TATATCTGCACACCTGGCTGTGGCTGATTGTGTCACATAGTGGCATGCCCTTTCTTATT 270
QY 170 HisGlnLeuMetGlyAsnGlyValTrpHisPheGlyGluThrMetCysThrLeuIleThr 189
Db 271 CACCAATGGGCCCGAGGGGGAGAGTGGGTGTGGGGGCTCTCTGCACCATCATACA 330
QY 190 AlaMetAspAlaAsnSergInPheThrSerThrTyrIleLeuThrAlaMetAlaIleAsp 209
Db 331 TCCCTGGATCTTGTAAACCAATTGGCCTGTAGTGCATCATGACTGTAATGAGTGTGAC 390
QY 210 ArgTyrLeuAlaThrValHisProIleSerSerThrLysPheArgLysProSerValAla 229
Db 391 AGGTACTTTGCCCTCGTCCACCAATTTCGACTGCACAGCTTGAGAGACAAGTACAAGACC 450
QY 230 ThrLeuValIleCysLeuLeuTrpAlaLeuSerPheIleSerIleThrProValTrpLeu 249
Db 451 ATCCGGATCAATTGGGGCTTTGGGACAGCTTCTTATCTGCGCATTCCTGTGGGTC 510
QY 250 TyrAlaArgLeuIleProPheProGlyAlaValAlaGlyCysGlyIleArgLeuProAsn 269
Db 511 TACTCGAAGTTCATCAAAATTAAAGACGGGTGTGAGAGTGTGCTTTTGATTTGACATCC 570
QY 270 ProAspThrAspLeuTyrTrpPheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuPro 289
Db 571 CCTGAC---GATGTACTCTGTGTATACACTTATTTGACGATAACAACCTTTTTCCT 627
QY 290 PheValValIleThrAlaAlaTyrValArgIleLeu----- 301
Db 628 CTACCCCTGATTTTGGTGTGCTATATTTTAATTTTATGCTATCTTGGAGATGATCA 687
QY 302 -----GlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArg 317
Db 688 CAGAATAGAGATGCCAGATGCTCAATCCACAGTGTACCA-----AAA 729
QY 318 LeuArgThrLysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCys 337
Db 730 CAGAGAGTGAATGAAGTTGACAAAGATGGTGTGCTGTGCTGTGTGTAAGTCTTATCC 789
QY 338 TrpAlaProTyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThr 357
Db 790 GCTGCCCTTATCATGTGATCAACTGTGTAACCTTACAGATGGAACGCCACACACTGGCC 849
QY 358 PheValTyrLeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSergCysLeuAsnPro 377

Db 850 TTCTATGTGGGTTATTAACCTCTCCATCTGTCTCAGCTATGCGACAGCAGCATTAACCT 909
QY 378 pheValTyrIleValIleuCysGluThrPheArgLysArgLeuValIleuSerValLysPro 397
Db 910 TTTCCTACATCCCTGCTGAGTGGAATTTCCAGAAACGCTGCTCAATCCAAGAGA 969
QY 398 AlaAlaGlnGlyGlnLeuArgAlaValSerAsn 408
Db 970 GCGACTGAGAAGAAATCAACATATGGGAAC 1002
RESULT 10
US-09-791-932-57
; Sequence 57, Application US/09791932
; Publication No. US20030003451A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030003451A1e1 G Protein-Coupled Receptors Cross-Referen
; FILE REFERENCE: 00325 US1
; CURRENT APPLICATION NUMBER: US/09/791,932
; PRIOR APPLICATION NUMBER: 2001-02-23
; PRIOR FILING DATE: 60/184,305
; PRIOR APPLICATION NUMBER: 2000-02-23
; PRIOR FILING DATE: 60/184,304
; PRIOR APPLICATION NUMBER: 2000-02-23
; PRIOR FILING DATE: 60/184,303
; PRIOR APPLICATION NUMBER: 2000-02-23
; PRIOR FILING DATE: 60/184,397
; PRIOR APPLICATION NUMBER: 2000-02-23
; PRIOR FILING DATE: 60/184,247
; PRIOR APPLICATION NUMBER: 2000-02-23
; PRIOR FILING DATE: 60/188,880
; PRIOR APPLICATION NUMBER: 2000-03-13
; PRIOR FILING DATE: 60/217,369
; PRIOR APPLICATION NUMBER: 2000-07-11
; PRIOR FILING DATE: 60/217,370
; PRIOR APPLICATION NUMBER: 2000-07-11
; PRIOR FILING DATE: 60/218,492
; PRIOR APPLICATION NUMBER: 2000-07-20
; PRIOR FILING DATE: 60/186,810
; PRIOR APPLICATION NUMBER: 2000-03-03
; PRIOR FILING DATE: 60/188,064
; PRIOR APPLICATION NUMBER: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/194,344
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/218,337
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 57
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-791-932-57
Alignment Scores:
Pred. No.: 7.51e-44 Length: 1965
Score: 565.50 Matches: 113
Percent Similarity: 55.95% Conservative: 61
Best Local Similarity: 36.33% Mismatches: 114
Query Match: 25.57% Indels: 23
DB: 9 Gaps: 4

US-09-885-478-2 (1-422) x US-09-791-932-57 (1-1965)
QY 110 IleIleMetProSerValPheGlyThrIleCysLeuLeuGlyIleIleGlyAsnSerThr 129
Db 160 GTCAATCCCTCCCTTCATGATGGGATTTATCTGTCAACAGGCGCTGGTGGCAACATCCGC 219
QY 130 ValIlePheAlaValValLysSerLysLeuHisTrpCysAsnAsnValProAspIle 149
Db 220 ATTGATTCACATTAATAAGATCCAGAAA-----AAACAGTCCCTGCATC 267
QY 150 PheIleIleAsnLeuSerValValAspLeuPheLeuLeuGlyMetProPheMetIle 169
Db 268 TATATCTGCAACCTGGCTGGCTGATTTGGTCCACATAGTTGGAATGCCCTTTCTTAT 327
QY 170 HisGlnLeuMetGlyAsnGlyValTrpHisPheGlyGluThrMetCysThrLeuIleThr 189
Db 328 CACCAATGGGCGCCGAGGGGAGAGTGGGTGTTGGGGGCCCTCTGCACCATCATCACA 387
QY 190 AlaMetAspAlaAsnSerGlnPheThrSerThrTyrIleLeuThrAlaMetAlaIleAsp 209
Db 388 TCCCTGATCTACTGTGTAACCAATTTGCCCTGAGTGCATCATGACTGTATGAGTGTGAC 447
QY 210 ArgTyrIleuAlaThrValHisProIleSerSerThrLysPheArgLysProSerValAla 229
Db 448 AGGTACTTGGCCCTCGTCCACCACTTTCGACTGCACAGCTGGAGAACAGGTACAAGACC 507
QY 230 ThrLeuValIleCysLeuLeuTrpAlaLeuSerPheIleSerIleThrProValTrpLeu 249
Db 508 ATCCGATTCATTTGGGCCCTTGGGCGACCTTCCTTATCCTGGCATTCGCTGTGGGTC 567
QY 250 TyrAlaArgLeuIleProPheProGlyGlyAlaValGlyCysGlyIleArgLeuProAsn 269
Db 568 TACTCGAAGCTCATCAATTTAAAGACGGGTGTGAGAGTGTGCTTTGATTTGACATCC 627
QY 270 ProAspThrAspLeuTyrTrpPheThrLeuTyrGlnDhePheLeuAlaPheAlaLeuPro 289
Db 628 CCTGAC--GATGACTCTGTGTATACACTTTATTTGACGATAACAACTTTTTCCT 684
QY 290 pheValValIleThrAlaAlaTyrValArgIleLeu----- 301
Db 685 CTACCCCTGATTTTGGTGTGCTATATTTTAACTTAACTTACTTGGAGATGTATCAA 744
QY 302 -----GlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArg 317
Db 745 CAGAATAAGGATGCCAGATGCTCAATCCAGTGTACCA-----AAA 786
QY 318 LeuArgThrLysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCys 337
Db 787 CAGAGAGTGATGAAGTTGACAAAGATGGTGTGCTGCTGGTGTAGTCTTATTCCTGAGT 846
QY 338 TrpAlaProTyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThr 357
Db 847 GCTGCCCTTATCATGTGATACACTGGTGAACCTTACGATGGAACGCCACACTGGCC 906
QY 358 pheValTyrLeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnPro 377
Db 907 TTCTATGTGGGTTATTAACCTCTCCATCTGTCTCAGCTATGCGACAGCAGCATTAACCT 966
QY 378 pheValTyrIleValIleuCysGluThrPheArgLysArgLeuValIleuSerValLysPro 397
Db 967 TTTCCTACATCCCTGCTGAGTGAATTTCCAGAAACGCTCTGCCCTCAATCCAAGAGA 1026
QY 398 AlaAlaGlnGlyGlnLeuArgAlaValSerAsn 408
Db 1027 GCGACTGAGAAGAAATCAACATATGGGAAC 1059
RESULT 11
US-09-895-686-22
; Sequence 22, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga

```

; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020106655A1 1459432X12
US-09-895-686-22

Alignment Scores:
Pred. No.:          9.43e-44          Length:          336
Score:             552.50             Matches:         106
Percent Similarity: 94.83%             Conservative:    4
Best Local Similarity: 91.38%           Mismatches:     1
Query Match:       24.98%             Indels:         5
DB:                10                 Gaps:          1

US-09-885-478-2 (1-422) x US-09-895-686-22 (1-336).
QY      65 ThrGlyThrGlyTrpMetAspLeuGlAlaSerLeuLeuProThrGlyProAsnAlaSer 84
      Db      2 TCCGGGACTGGA-----ACCTCGCTGCTGCCACACTGGTCCCAACGCCAGC 46

QY      85 AsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProProArgThrGlySer 104
      Db      47 AACACCTCTGATGGCCCCGATACCTCACTTCGGCAGGATCACCTCTCGCACGGGAGC 106

QY      105 IleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCysLeuLeuGlyIle 124
      Db      107 ATCTCCTACATCGACATCATCATGCTTCGGTGTTCGGCACCATCTGCTCTCGGCATC 166

QY      125 IleGlyAsnSerThrValIlePheAlaValIleValysSerIleuHisTrpCysAsn 144
      Db      167 ATCGGGAAGTCCACGGTCACTTCGGCGTGTGAAGAAGTCCAAAGCTGCACATGTGTGCAAC 226

QY      145 AsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeuPheLeuLeuGly 164
      Db      227 AAGTCCCGGACATCTTCATCATCAACCTCTCGGTAGATGATCTCTCTCTCTCGGGC 286

QY      165 MetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180
      Db      287 ATGCCCTTCGTGATCCACAAAGCTCATGGCAATGGGGTGTGTGCACATT 334

RESULT 12
US-09-864-761-9017
; Sequence 9017, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9017
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO Z86090.10
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
US-09-864-761-9017

Alignment Scores:
Pred. No.:          3.85e-42          Length:          575
Score:             539.00             Matches:         100
Percent Similarity: 95.33%             Conservative:    2
Best Local Similarity: 93.46%           Mismatches:     1
Query Match:       24.37%             Indels:         4
DB:                10                 Gaps:          1

US-09-885-478-2 (1-422) x US-09-864-761-9017 (1-575)
QY      1 MetSerValGlyAlaMetIleLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
      Db      156 ATGTCAGTGGAGCCATGAAGAAGAGGAGTGGGAGGCGAGTTGGGCTTGAGGCGCAGC 215

QY      21 GlyCysGlnAlaThrGlnGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
      Db      216 GCGAGCCAGGCTACGAGGAAGAAGCCCTCCCAACTGCGGGCTTGCGCTCCGGACAA 275

QY      41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGlnGlySerSerAlaArgLeu 60
      Db      276 GGTGGCAGGCGCTGAGGCTGCCGACGCTGGCTGGAGGGGAGCTCAGCTCGGTTG 335

QY      61 TrpGlnGlnAlaThrGlyThrGlyTrpMetAspLeuGlAlaSerLeuLeuProThrGly 80
      Db      336 TGGGAGCAGGCGACCGCACTGGCTGATGGACCTGGAAGCCCTCGCTGCCCACTGTG 395
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Thu Feb 20 11:14:39 2003

us-09-885-478-2.rnpb

Page 11

QY	81	ProAsnAlaSer	asnThrSer	aspGlyPro	aspAsnLeu	thrSer	Ala-----	96
Db	396	CCCAACGCCAG	CAACACCTCT	GTATGGCCCG	ATACCTACTT	CGGCAGGTG	AGTTGACT	455
QY	97	GlySerPro	ProArgThr	Gly				103
Db	456	GGGAGCCCTC	CTCCTCTGGG					476

RESULT 13
US-09-895-686-57

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; Sequence 57, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 57
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO. US20020106655A1 701899983H1
US-09-895-686-57

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Alignment Scores:	
Pred. No.:	7.46e-41
Score:	521.00
Percent Similarity:	100.00%
Best Local Similarity:	98.02%
Query Match:	23.55%
DB:	10
Length:	304
Matches:	99
Conservative:	2
Mismatches:	0
Indels:	0
Gaps:	0

US-09-885-478-2 (1-422) x US-09-895-686-57 (1-304)

QY	216	HisProIleSerSerThrLysPheArgLysProSerValAlaThrLeuValIleCysLeu	235
Db	2	CACCCCACTCTCTCCACCAAGTCCGGAAGCCCTCCATGGCCACCCCTGGTGA	61
QY	236	LeuTrpAlaLeuSerPheIleSerIleThrProValTrpLeuTyraAlaArgLeuIlePro	255
Db	62	CTGTGGGGCGCTCTCTTCATCATCAGTATCACCCCTGTGTGGCTCTACGCCAGGCTCAT	121
QY	256	PheProGlyGlyAlaValAlaGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTy	275
Db	122	TTCCCAAGGGGTGCTGTGGGCTGTGGCATCCGCCTGCCAACCCGGACACTGACCTTCAC	181
QY	276	TrpPheThrLeuTyrlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAla	295
Db	182	TGGTTCACCTCTGTACCAAGTTTTTCCTTGCCCTTTGCCCTTCGGTTCATTACCGCC	241
QY	296	AlaTyrlValArgIleLeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSer	315
Db	242	GCATACGCTGAATACTACTACAGCGCATGACGCTTCGGTGGCTCCAGCCTCCCAACGCAGC	301
QY	316	Ile 316	
Db	302	ATC 304	

RESULT 14
US-09-967-768A-296
; Sequence 296, Application US/09967768A

APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature

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; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 296
; LENGTH: 1427
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-967-768A-296

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Alignment Scores:	
Pred. No.:	1,11e-39
Score:	519.00
Percent Similarity:	50.40%
Best Local Similarity:	30.67%
Query Match:	23.46%
DB:	10
US-09-885-478-2 (1-422) x US-09-967-768A-296 (1-1427)	
	Length: 1427
	Matches: 115
	Conservative: 74
	Mismatches: 124
	Indels: 62
	Gaps: 11

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QY      48  ProGlnProAla-----TrpValGluGlySerSerAlaArgLeu----- 60
      |||  |||||  |||  |||||  |||
Db      21  CCTGGGCGCCCGCGCGCGCTCTTGCGGCAGCGCTAGCTCCGCGCGCTCAGCTGCCCT 80

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QY	61	-----TPrpGlUGlnAla	64
		:	
- Db	81	GGCCCGGACCCCTGTGCATGAGCGGCCCTTCAGCGCTGCCCCCCGGGGGGGAGAGAAGG	140
QY	65	ThrGlyThrGlyTrpMetaspLeuGIuaIaserleuPurThrGlyProAsnAlaser	84
Db	141	CTGGGACGGGCGCTGG-----CCCTCTGCAGCC	167

[illegible]

QY 145 AsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeuPheLeuLeuGly 164
||| |||:|||||:||||| ||| ||| |||:|||||
Db 345 AAC-----ATCTAAGCTGCTCAACCTGGCCGTAGCCGACGACACTCTTCATGCTGAGC 395

QY 165 MetProPhemeIle-----HisGlnLeuMetGlyAsnGlyValTrp 178
:::|||||::: ||| |||
Db 396 GTGCCCTTCGTGGCCTGCTGGCGGCCCTGGCCAC-----TGG 434

Qy 179 HispheglglutthrmctCysthrleuilethralametaspaalaasnserglInphethr 198
 ||||| ::||| ::::||| ::| |||||
 Db 435 CCCTTCGGCTCCGTCCTGTGCGCGCGGTGCTCAGCGTGCAGCGGCTCAACATGTTAC 499

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QY 199 SerThrTyrIleLeuThralaMetalaIleaspArgTyrLeualaThralHisProIle 218
    ||| ::| ||||| :::::|||||:::|||||:::
Db 495 AGCGTCTTCTGTCACCGTGCTCAGCGTGGACCGCTACGTCGGCCGTGGTGCACCCCTCTG 554
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QY 219 SerSerThrIysPheArgIysProSerValAlaThrLeuValIleCysLeuLeuTrpAla 238
::: :::::||||| 111::: ::::|
DB 555 CGCGCGGCAGTACCGCGGCCACGCTGCGCCAAAGCTCATCTACACCTGGCGGTGTGGCTG 614

QY 239 LeuSerPheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGly 258

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Db 615 GCATCCCTGTTGTACTCTCCCATCGCATCTTCGACAGACACAGACCGGCTCGCGGC 674
QY 259 G1Y---AlaValG1Ycysg1YleArgleuProAsnProAspThrAspleuYrTrp--- 276
Db 675 GGCCAGGCCGTGGCTGCAACCTGCAGTGGCCACACCCG-----GCCTGGTGG 722
QY 277 -----PheThrleuYrGlnPhePheleuAlaPheAlaPheProPheValIleThr 294
Db 723 GCAGTCTCGTGTCTACACTTTCCTGCTGGGCTTCCTGCTGCCCGTGTGGCATTGGC 782
QY 295 AlaAlaTyrValArgIleleuGlnArgMetThrSerSerValAlaProAlaSerGlnArg 314
Db 783 CTGTGCTACCTGCTCATGCTGGGCAAGATGGCGCGCTGGCCCTGGCGCTGGCGCAG 842
QY 315 SerIleArgLeuArgThrIysArgValThrArgThrAlaIleAlaIleCysleuValPhe 334
Db 843 CAGCGCAGGCGCTCGAGAGAAATACACAGGCTGTGTGATGTGTGTGTGTCTT 902
QY 335 PheValCysTrpAlaProTyrTyrValleuGlnleuThrGlnleuSerIleSerArgPro 354
Db 903 GTGCTCTGCTGATGCTTCTACGTGGTGCAGCTGCTGAACCTCGTGTGACCAAGCCTT 962
QY 355 ThrIleuThrPheValTyrleuTyrAsnAlaAlaIleSerleuGlyTyrAlaAsnSerCys 374
Db 963 GATGCCACC-----GTCAACACAGCGTCCCTTATCTCAGCTATGCCAACAAGCTGC 1013
QY 375 LeuAsnProPheValTyrIleValleuGlyGluThrPheArgLys 389
Db 1014 GCCAACCTATTTCTCTATGGCTTCCCTCCGACAACTTCGCCGA 1058

RESULT 15
US-09-864-761-26601
; Sequence 26601, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 26601
; LENGTH: 274
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO Z86090.10
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
; OTHER INFORMATION: EST_HUMAN HIT: BE312542.1, EVALU0 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P97639, EVALU0 1.00e-04
; OTHER INFORMATION: NT HIT: AE004060.1, EVALU0 1.10e-02
US-09-864-761-26601

Alignment Scores:
Pred. No.: 9.32e-39 Length: 274
Score: 498.00 Matches: 90
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.90% Mismatches: 0
Query Match: 22.51% Indels: 0
DB: 10 Gaps: 0

US-09-885-478-2 (1-422) x US-09-864-761-26601 (1-274)
QY 6 MetIysIysGlyValGlyArgAlaValGlyLeuGlyGlySerGlyCysGlnAlaThr 25
Db 1 ATGAAGAAGGAGTGGGGAGGGCAGTTGGGCTTGAGAGCGGCAAGGCTGCCAGGCTACG 60
QY 26 GluGlnAspProLeuProAspCysGlyAlaCysAlaProGlyGlnGlyGlyArgArgTrp 45
Db 61 GAGGAGAGACCCCTTCCCAACTGCGGGGCTTGCCTCCGGGACAAGTGGCAGCGCTGG 120
QY 46 ArgLeuProGlnProAlaTrpValGluGlySerSerAlaArgLeuTrpGluGlnAlaThr 65
Db 121 AGGCTGCCGACGCTGCTGGGTGGAGGGGAGCTCAGCTCGGTTGTGGAGGAGCGGACC 180
QY 66 GlyThrGlyTrpMetAspLeuGlnAlaSerLeuLeuProThrGlyProAsnAlaSerAsn 85
Db 181 GGCACGTGGCTGGATGGACCTGGAAGCCTCGCTGCCCCACTGTGCCAACCGCAGCAAC 240
QY 86 ThrSerAspGlyProAspAsnLeuThrSerAla 96
Db 241 ACCTCTGATGGCCCGATTAACCTCACTTCGCA 273
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Search completed: February 19, 2003, 14:50:23
Job time : 85 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 12:02:37 ; Search time 2053 Seconds
(without alignments)
3329.028 Million cell updates/sec

Title: US-09-885-478-2
Perfect score: 2212
Sequence: 1 MSVGAMKKGVGRAVGLGGGS.....LRAVSNQOTADEERTESKGT 422

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: em_esthum:*
3: em_estinu:*
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5: em_estov:*
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23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB ID	Description
		Match	Length	DB		
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2	1578.5	71.4	958	13	BI754621	BI754621 603025173
3	1395	63.1	872	13	BI757659	BI757659 603027991
4	1369	61.9	797	13	BI818742	BI818742 603037572
5	1368.5	61.9	921	13	BG913631	BG913631 602811509
6	1097.5	49.6	834	12	BF342364	BF342364 602013155
7	1086	49.1	845	12	BF966511	BF966511 602286863
8	1057	47.8	869	12	BG519797	BG519797 602578956
9	1014	45.8	685	13	BI818110	BI818110 603032324
10	880.5	39.8	859	10	BE312747	BE312747 601150756
11	691	31.2	600	10	BE312542	BE312542 601150023
12	591	26.7	345	14	F07228	F07228 HSC1ZF101 n
13	539	24.4	387	10	BE647763	BE647763 UI-M-BH1 -
14	491.5	22.2	1086	12	BF313837	BF313837 601902234
15	484	21.9	497	12	BF600078	BF600078 264555 MA
16	449	20.3	313	12	BE701073	BE701073 CMO-NN013
17	402	18.2	440	12	BF600064	BF600064 264640 MA
18	400	18.1	264	10	BB586291	BB586291 BB586291
19	391.5	17.7	794	17	CNS01WC1	AL1170218 Tetraodon
20	370	16.7	642	10	BE252309	BE252309 601114162
21	362.5	16.4	937	17	CNS03GSG	AL243385 Tetraodon
22	357.5	16.2	720	13	BI753905	BI753905 603022907
23	355	16.0	904	12	BG329444	BG329444 602429002
24	349	15.8	901	17	CNS01SK5	AL165326 Tetraodon
25	347	15.7	1029	17	CNS03SOZ	AL258812 Tetraodon
26	330	14.9	960	13	BI914562	BI914562 603179505
27	327	14.8	1141	17	CNS04CF7	AL284380 Tetraodon
28	325.5	14.7	2702	11	AK004730	AK004730 Mus muscu
29	320.5	14.5	995	17	CNS04RQE	AL304223 Tetraodon
30	316	14.3	1053	17	CNS04C2T	AL283934 Tetraodon
31	311.5	14.1	1377	11	AK010895	AK010895 Mus muscu
32	304.5	13.8	916	17	CNS02EZx	AL194406 Tetraodon
33	300	13.6	1026	17	CNS04NIQ	AL298151 Tetraodon
34	297	13.4	2402	11	AK018203	AK018203 Mus muscu
35	295	13.3	755	13	BI772443	BI772443 603058608
36	295	13.3	1051	13	BM545259	BM545259 AGENCOURT
37	294	13.3	2020	11	BC013202	BC013202 Homo sapi
38	292	13.2	741	13	BI224313	BI224313 602940621
39	291	13.2	656	9	AL119185	AL119185 DKFZp761N
40	291	13.2	3336	11	AK018543	AK018543 Mus muscu
41	290.5	13.1	848	13	BI908815	BI908815 603066279
42	289.5	13.1	3005	11	AK019478	AK019478 Mus muscu
43	287.5	13.0	1082	14	BM922776	BM922776 AGENCOURT
44	287	13.0	980	13	BM543468	BM543468 AGENCOURT
45	286.5	13.0	971	9	AU091121	AU091121 AU091121

ALIGNMENTS

RESULT 1
BM805549
LOCUS BM805549 1114 bp mRNA linear EST 05-MAR-2002
DEFINITION AGENCOURT_6498483 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5729087
5', mRNA sequence.
ACCESSION BM805549
VERSION BM805549.1 GI:19122372
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1114)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: L1AM12725 row: m column: 24
High quality sequence start: 52
High quality sequence stop: 684.

FEATURES
source

Location/Qualifiers
1. 1114
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5729087"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."

BASE COUNT 198 a 375 c 299 g 241 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 9.68e-161 Length: 1114
Score: 1662.50 Matches: 332
Percent Similarity: 92.62% Conservative: 7
Best Local Similarity: 90.71% Mismatches: 25
Query Match: 75.16% Indels: 4
DB: 14 Gaps: 0

US-09-885-478-2 (1-422) x BM805549 (1-1114)

QY 10 ValGlyArgAlaValGlyLeuGlyGlySerGlyCysGlnAlaThrGlnGluAspPro 29
Db 22 ATGGGAGAGGCGAGTTGGGCTTGTACGCGGCTTCGCTGCGACGCTACGAGGAAGACCCC 81
QY 30 LeuProAspCysGlyAlaCysAlaProGlyGlnGlyArgArgTrrArgLeuProGln 49
Db 82 CTTCGCCGACTGCGGGGCTTGGCTCCGGGACAGAGTGGCAGCGCTGAGGCTGCCGACG 141
QY 50 ProAlaTrpValGluGlySerSerAlaArgLeuTrpGluGlnAlaThrGlyThrGlyTrp 69
Db 142 CCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTGTGGGAGACAGCGACCGGCACTGGCTGG 201
QY 70 MetAspLeuGluAlaSerLeuLeuProThrGlyProAsnAlaSerAsnThrSerAspGly 89
Db 202 ATGGACCTGGAAAGCCTCGCTGCTGCCCACTGTGCCAATGCCAGCAACACCTCTGATGGC 261
QY 90 ProAspAsnLeuThrSerAlaGlySerProProArgThrGlySerIleSerTyrIleAsn 109
Db 262 CCCGATAACCTCACCTCGGCGAGGATCACCTCCGCGACGCGGAGCATCTCTACATCAAC 321
QY 110 IleIleMetProSerValPheGlyThrIleCysLeuLeuGlyIleIleGlyAsnSerThr 129
Db 322 ATCATCATGCGCTTCGTTGCGGACCATCTGCTCTGGGCATCATCGGGAACCTCCACG 381
QY 130 ValIlePheAlaValAllylsSerIleuHisTrpCysAsnAsnValProAspIle 149
Db 382 GTCATCTTCGGCGTGTGAGAAGATCCAAAGCTGCACACTGGTGCAACAACAGTCCCCGACATC 441
QY 150 PheIleIleAsnLeuSerValValAspLeuLeuPheLeuLeuGlyMetProPheMetIle 169
Db 442 TTCATCATCAACCTCTCGGTAGATCTCTTCTCTCTGCGGACATGCCCTTCATGATC 501

QY 170 HisGlnLeuMetGlyAsnGlyValTrpHisPheGlyGluThrMetCysTrhrLeuIleThr 189
Db 502 CACGAGCTCATGGGCAATGGGGTGTGGCAGCTTTGGGAGACCATGTGCACCCCTCATCAGC 561
QY 190 AlaMetAspAlaAsnSerGlnPheThrSerThrTyrIleLeuThrAlaMetAlaIleAsp 209
Db 562 GCCATGGATGCCAATAGTCAGTTACACGACGACCTACATCTTGACCGCCATGGCATTTGAC 621
QY 210 ArgTyrLeuAlaThrValHisProIleSerSerThrIlySpheArgLysProSerValAla 229
Db 622 CGCTAGCTGGCCACTGTCCACCCCATCTCTTCCACGAAAGTTCGGAAAGCCCTCTGTGGCC 681
QY 230 ThrLeuValIleCysLeuLeuTrpAlaLeuSerPheIleSerIleThrProValTrpLeu 249
Db 682 ACCCTGGTATCTGCCTCTGTGGGCCCTCTCTTCATCAGCATCACCCCTGTGTGGCTG 741
QY 250 TyrAlaArgLeuIleProPheProGlyGlyAlaValGlyCysGlyIleArgLeuProAsn 269
Db 742 TATGCCAGACTCATCCCTCCCTCCAGAGAGTGCAGATGAGGCTGCGGATACGCTGCCAAC 800
QY 270 ProAspThrAspLeuTyrTrpPheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuPro 289
Db 801 CCAGACACTGACCTCTACTGTGTCACCCGTACACAGNTTTCCTGGCCTTGGCCTGCCCT 860
QY 290 PheValValIleThrAlaAlaTyrValArgIleLeuGlnArgMetThrSerSerValAla 309
Db 861 TTGTGTGTCATCACAGCCCGCATACGTGAGGATCTCTGCAACGCAATGACGTCTTCTAGTGGGC 920
QY 310 ProAlaSerGlnArgSerIleArgLeuArgTrrLysArgValThrArgThrAlaIleAla 329
Db 921 CCCGGCTTCCAGGA-AGCATCCGGCTGCGGACCAAGAGGGGTGACCCGACAGCATCCGCC 979
QY 330 IleCysLeuValPhe-PheValCysTrpAlaProTyrTyrValLeuGlnLeuThrGlnLe 349
Db 980 ATCTGTCTGGGCTTCTTGGGGGCTGGGACACCTTACTATGTGCTACAGCTGACCCAGTT 1039
QY 349 uSerIleSerArgPro-ThrLeuThrPheValTyrIleuTyrAsnAlaIleSerLeuG 369
Db 1040 GTCCATTAAACCGCGGACCTCACCCCTTGCCAACTAAACCAAGCGGCGCATCACCTTGG 1099

QY 369 lYTyraAlaAsnSer 373
Db 1100 GCTATTCCACGCT 1113

RESULT 2
LOCUS B1754621 958 bp mRNA linear EST 25-SEP-2001
DEFINITION 603025173F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5195443 5',
mRNA sequence.

ACCESSION B1754621
VERSION B1754621.1 GI:15746199
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 958)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

CONTACT: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: L1AM11489 row: b column: 20
High quality sequence stop: 862.
Location/Qualifiers

source	1. .958	
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	/clone="IMAGE:5195443"	
	/lab_host="NIH_MGC_114"	
	/lab_host="DH10B"	
	/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."	
BASE COUNT	168 a 329 c 256 g 205 t	
ORIGIN		
Alignment Scores:		
Pred. No.:	3.62e-152	Length: 958
Score:	1578.50	Matches: 309
Percent Similarity:	96.88%	Conservative: 1
Best Local Similarity:	96.56%	Mismatches: 9
Query Match:	71.36%	Indels: 4
DB:	13	Gaps: 0
US-09-885-478-2 (1-422) x B1754621 (1-958)		
QY	20	SerGlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGly 39
Db	1	AGCGGCTGCCAGGCTACGAGAGAGACCCCTTCCGACTGCGGGGCTTGCGCTCCGGGA 60
QY	40	GlnGlyArgArgTrpArgLeuProGlnProAlaTrpValGluGlySerSerAlaArg 59
Db	61	CAAGGTGGCAGGCGCTGAGAGCTGCCGACGCTCGGTGGAGGGGAGGCTCAGCTCGG 120
QY	60	LeuTrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThr 79
Db	121	TTGTGGGAGCAGGCGACCGGCACTGGCTGGATGGACTGGGAAGCCTCGCTGTCGCCACT 180
QY	80	GlyProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerPro 99
Db	181	GGTCCCAATGCCAGCAACACCTCTGATGGCCCGATTAACCTCACTTCGGCAGATCACCT 240
QY	100	ProArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIle 119
Db	241	CCTCGCACGGGGAGCATCTCTACATCAACATCATGCTTCGCTGTCGCAACCATC 300
QY	120	CysLeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysSerLys 139
Db	301	TGCCTCTGGGCATCATCGGGAACCTCCACGGTCACTTCGCGGTCTGAAGAAGTCCAAG 360
QY	140	LeuHisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeu 159
Db	361	CTGCACCTGGTGCAACAAGTCCCGACATCTTCATCAATCAACCTCTCGGTAGATCTTC 420
QY	160	LeuPheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHis 179
Db	421	CTCTTCTCTCTGGGCATGCCCTTCATGATCCACCACTCATGGGCAATGGGGTGTGGCAC 480
QY	180	PheGlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSer 199
Db	481	TTTGGGAGAGACCATGTGCACCCCTCATCAGCGGCATGGATGCCAATAGTCAGTTCCACGAC 540
QY	200	ThrTyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSer 219
Db	541	ACCTACATCTGTGACCGCATGGCCATGTACCTGACCTGGCCACTGTCCACCCCATCTCT 600
QY	220	SerThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeu 239
Db	601	TCCACGAAGTCCGGAAGCCCTCTGTGGCCACCTGTGATCTGCTCTGTGGGCCCTC 660
QY	240	SerPheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGly 259

Db	661	TCCTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCCAGAGGT 720
QY	260	AlaValGlyCysGlyIleArgLeu-ProAsnProAspThrAspLeuTyrTrpPheThrIle 279
Db	721	GCAGTGGGCTGGCGGATACGCCTTGCCCAACCCAGACACTGACCTCTACTGTTACCCCT 780
QY	279	uTyrGlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValAr 299
Db	781	GTACCAAGTTTTCCTGGCCTTTGCCCTGCCCTTTTGTGTCATCACAGC-GCATACGTAG 839
QY	299	gIleLeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuAr 319
Db	840	GATCCTGCAGCGCATGACGTCTCTCAAGTGGCCCGGCTCCAAAGCGCAGCATCCGGCTGC 899
QY	319	gThrLysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrp 338
Db	900	GACAACAAGGGTGACCCGGCA-GGCATCGCCATCTGTGTC--TTCTTTGTGTGCTGG 954
RESULT	3	872 bp mRNA linear EST 25-SEP-2001
BI757659		
LOCUS	603027991F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5198231 5',	
DEFINITION	mRNA sequence.	
ACCESSION	BI757659	
VERSION	BI757659.1 GI:15749237	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	1 (bases 1 to 872)	
TITLE	NIH-MGC http://mgc.nci.nih.gov/.	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://Image.llnl.gov Plate: L1AM11496 row: f column: 24 High quality sequence stop: 829.	
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	/lab_host="DH10B"	
	/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."	
BASE COUNT	156 a 306 c 208 g 202 t	
ORIGIN		
Alignment Scores:		
Pred. No.:	2.72e-133	Length: 872
Score:	1395.00	Matches: 283
Percent Similarity:	97.93%	Conservative: 1
Best Local Similarity:	97.59%	Mismatches: 5
Query Match:	63.07%	Indels: 4
DB:	13	Gaps: 0

US-09-885-478-2 (1-422) x B1757659 (1-872)

QY	65	ThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGlyProAsnAlaSer	84
Db	3	ACCGGCACTGGCTGATGGAACCTGGAGAGCCCTGCTGCCACATGGTCCCAATGCCAGC	62
QY	85	AsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProProArgThrGlySer	104
Db	63	AACACCTCTGATGGCCCCGATAACCTCACTTCGGCAGGATCACCTCTCCGACAGGGAGC	122
QY	105	IleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCysLeuLeuGlyIle	124
Db	123	ATCTCTACATCAACATCATCATGCTTCGGTTCGGCACCATCTGCCCTCTGGGCATC	182
QY	125	IleGly-AsnSerThrValIlePheAlaValIleLysLysSerLysLeuHisTrpCysAs	144
Db	183	ATCGCGGAACCTCCACGGTCACTCTTCGGGGTCTGGAAGAAGTCCAAAGCTGCACCTGGTCAA	242
QY	144	nasnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeuPheLeuLeuG	164
Db	243	CAACGTCGCCGACATCTTCATCATCAACCTTCGCTAGTAGATCTCTTTTCTCTCTGGG	302
QY	164	YmetProPheMetIleHisClnLeuMetGlyAsnGlyValTrpHisPheGlyGluThrMe	184
Db	303	CATGCCCTTCATGATCCACACGCTCATGGGCAATGGGGTGTGGCACTTGGGGAGACCAT	362
QY	184	tCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThrTyrIleLeuTh	204
Db	363	GTGCACCCCTCATCACGGCCATGGATGCCATAGTCAGTTCACACGACCATCATCTGAC	422
QY	204	rAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSerThrLysPheAr	224
Db	423	CGCCATGGCCATTGACCCGCTACCTGGCCACTGTCCACCCCATCTCTTCCACGAAGTCCG	482
QY	224	glysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSerPheIleSerIl	244
Db	483	GAAGCCCTCTGTGGCCACCTGGTGTATCTGCTCTGTGGGCCCTCTCTTCATCATGACAT	542
QY	244	eThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAlaValGlyCysGl	264
Db	543	CACCCCTGTGTGGCTGTATGCAGACTCATCCCTTCCAGAGGTGCAGTGGCTGGCG	602
QY	264	YIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyrGlnPhePheLe	284
Db	603	CATACGCTGCCCCAACCCAGACACTGACCTCTACTGTGTACACCTGTACAGTTTTCCT	662
QY	284	uAlaPheAlaLeuProPheValIleThrAlaAlaTyrValArgIleLeuGlnArgMe	304
Db	663	GGCCTTGGCCCTGCTTTGTGTGCATCACAGCCGCAATGAGGATCCTGCAGCGCAT	722
QY	304	tThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThrLysArgValTh	324
Db	723	GACGTCTCAGTGGCCCCCGCTCCAGGCGCAGCATCCGGCTGCGGAC-AAAGAGGTGAC	781
QY	324	rArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaProTyrTyrValLe	344
Db	782	CCGTACAGC-ATCGCCATCTGTCTGTCTTCTTGTGTGTGGTGGCCACC-TACTATGTGCT	839
QY	344	uGlnLeuThrGlnLeuSerIleSerArg	353
Db	840	ACAGTTGACCCAGTTGTCCATCAGGCGC	867
RESULT 4			
B1818742			
LOCUS			
B1818742			
DEFINITION			
603037572F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178856 5',			
mRNA sequence.			
B1818742			
ACCESSION			
B1818742			
VERSION			
B1818742.1 GI:15930292			
KEYWORDS			
EST.			
SOURCE			
human.			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 797)			
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Incyte Genomics, Inc. clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11445 row: 0 column: 17 High quality sequence stop: 774. Location/Qualifiers			
FEATURES	1..797			
source	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5178856" /clone_1lb="NIH_MGC_115" /lab_host="DH10B" /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."			
BASE COUNT	144	a	262	c 228 g 163 t
ORIGIN				
Alignment Scores:				
Pred. No.:	1.15e-130	Length:	797	
Score:	1369.00	Matches:	262	
Percent Similarity:	98.87%	Conservative:	1	
Best Local Similarity:	98.50%	Mismatches:	2	
Query Match:	61.89%	Indels:	2	
DB:	13	Gaps:	0	
US-09-885-478-2 (1-422) x B1818742 (1-797)				
QY	7	LysLysGlyValGlyArgAlaValGlyLeuGlyGlySerGlyCysGlnAlaThrGlu	26	
Db	3	AAGAAGGAGTGGGAGGGCAGTTGGCTTGAGGGCGCAGCGGCTGCCAGGCTACGGAG	62	
QY	27	GluAspProLeuProAspCysGlyAlaCysAlaProGlyGlnGlyGlyArgArgTrpArg	46	
Db	63	GAAGACCCCTTCCGACTGCGGGGCTTGCGCTCCGGGACAAGGTGGCAGCGCTGAGG	122	
QY	47	LeuProGlnProAlaTrpValGluGlySerSerAlaArgLeuTrpGluGlnAlaThrGly	66	
Db	123	CTGCCGCAAGCTGCGTGGTGAGGAGGAGCTCAGCTCGTTGTGTGGAGACAGGCGAGCGG	182	
QY	67	ThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGlyProAsnAlaSerAsnThr	86	
Db	183	ACTGGCTGGATGACCTTGAAGCCTCGCTGCTGCCACTGTGCCAATGCCAGCAACACC	242	
QY	87	SerAspGlyProAspAsnLeuThrSerAlaGlySerProProArgThrGlySerIleSer	106	
Db	243	TCTGATGGCCCGGATAACCTCACTTCGGCAGGATCACCTCTCTGCCACGGGAGCATCTCC	302	
QY	107	TyrIleAsnIleIleMetProSerValPheGlyThrIleCysLeuLeuGlyIleIleGly	126	
Db	303	TACATCAACATCATATGCTTCGGTGTGGCACCACATCTGCTCTCTGGGCATCATCGGG	362	
QY	127	AsnSerThrValIlePheAlaValValLysLysSerLysLeuHisTrpCysAsnAsnVal	146	
Db	363	AACTCCACGGTCACTTCGCGGTGTGAAGAAGTCCAAAGCTGCACTGGTGCACAACAGTC	422	

Oy	147	Proaspilpheilleleashleuservalvalaspleuleupheleuglymetpro	166
Db	423	CCCCACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTTTCTCCCTGGGCATGCC	482
Oy	167	PhemetilehisglnleumetciyasnglyvaltrphispheligluThrmetystr	186
Db	483	TTCATGATCCACCAGCTCATGSCAATGGGGTGTGSCACTTTGGGGAGACCATGTGCACC	542
Oy	187	leuillethrAlametaspaiaasnserglinpherhserrthyrtyleuthrAlamet	206
Db	543	CTCATCACGGCCATGATGCCAATAAGTACAGTTCACACACCTACATCATGCCCATG	602
Oy	207	AlalieaspargyrrleualathrvalHisproileserserThrlysphearglyspr	226
Db	603	GCCATTCACCGCTACCTGGCCACTGTCCACCCCACATCTCTCCACGAAGTCCGGAAGCCC	662
Oy	227	ServalaIathrleuvalillecysleuleutrpalaleuserpheilleserillethrpro	246
Db	663	TCTGTGGCCACCCCTGTGATGTGCTCTGCTGTGGGCCCTCTCCATCATGATCAC - CCT	721
Oy	247	Valtrpleutryrralaaargleullepropheprogilylala-Valglycysglyllear	266
Db	722	GTGTGGCTGTATGCCAGACTCATCCCTTCCACAGAGGTGCATGTGGGCTGCGGCATACG	781
Oy	266	gleuproasnproasp 271	
Db	782	CCTGCCCAAGCCAGAG 797	
RESULT 5			
LOCUS	BG913631	921 bp mRNA linear EST 05-JUN-2001	
DEFINITION	602811509F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4943498		
ACCESSION	BG913631		
VERSION	BG913631.1 GI:14294107		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 921)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: David N. Louis, M.D. CDNA library Preparation: Life Technologies, Inc. CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10887 row: a column: 03 High quality sequence stop: 731. Location/Qualifiers 1..921 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4943498" /clone_1bp="NCI_CGAP_Brn67" /tissue_type="anaplastic oligodendroglioma with 1p/19q loss" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: brain; Vector: pCMV-SPOrt6; site_1: NotI; site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."		
BASE COUNT	174 a	309 c	247 g
ORIGIN			191 t

Pred. No. :	1,59e-130	Length:	921
Score:	1368.50	Matches:	273
Percent Similarity:	90.76%	Conservative:	2
Best Local Similarity:	90.10%	Mismatches:	26
Query Match:	61.87%	Indels:	4
DB:	13	Gaps:	1
US-09-885-478-2 (1-422) x BG913631 (1-921)			
QY 19	glyserglycsglnalathrgrlucgluaspProleuProaspcysglyAlacysAlapro		38
Db 1	GGCAGCGGCTGCCAGGCTACGGAGGAAGACCCCTTCCCGACTGGGGGCTTGGCGTCCG		60
QY 39	glylngllyglyargArgTrpargleuProglInProAlatrpaValgluglySerSerAla		58
Db 61	GGACAAGGTGGCAGGGCGCTGGAGGCTGCCGACGCTGCGTGGGTGGAGGGAGCTCAGCT		120
QY 59	ArgleuTrpGlucInAlaThrGlythrGlyTrpMetaspleuGluaIaSerleuLeupro		78
Db 121	CGGTGTGGAGCAGCGGACCGGCGACTGGCTGATGGACCTGGAACCTCGCTGTGCC		180
QY 79	ThrGlyProasnaIaSerasnThrSeraspGlyProaspaInleuthrSerAlaGlySer		98
Db 181	ACTGGTCCCAATGCCAGCAACACCCTGTATGGCCCCGATAACTTCACTTCGGCAGATCA		240
QY 99	ProProArgthrglySerIleSerTyrIleasnIleIleMetProSerValPheGlyThr		118
Db 241	CCTCCTCGCAGCGGAGCATCTCTCATATCAATCATATGCTTCGGTGTCCGCACC		300
QY 119	IleCysleuLeuGlyIleIleGlyasnSerThrValIlePheAlaValValLysLysSer		138
Db 301	ATCTGCCTCTCGGCAATCATCGGGAACCTCCACGGTCACTTTCGGCGTGTGAAGAAGTCC		360
QY 139	LysleuHistTrpCysasnValProaspIlePheIleIleasnLeuSerValValasp		158
Db 361	AAGCTGCACCTGGTGCAACAACGTCGCCGACATCTTCATCATCAACCTCTCGGTAGTAGAT		420
QY 159	LeuLeuPheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyasnGlyValTrp		178
Db 421	CTCCTCTTCTCTGGGCGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGG		480
QY 179	HisPheGlyGluThrMetCysThrIleuIleThrAlaMetaspaIaasnSerGlnPheThr		198
Db 481	CACPTTGGGAGACCATGTGCACCCCTCATACGTCATGATGAGCAATAGTCAGTTACAC		540
QY 199	SerThrTyrIleLeuThrAlaMetAlaIleasparGlyLeuAlatrValHisProIle		218
Db 541	AGCACCTACATCTTGACCGGCATGGCCATGTGACCGCTACCTGGCCACTGTCCACCCCATC		600
QY 219	SerSerThrLysPheArgLysProSerValAlatrLeuValIleCysleuLeuTrpAla		238
Db 601	TCTTCCACGAAGTTCGGGAAGCCCTGTGGGCCACCTG-GTGAATGTGCCTCTGTGGGC-		658
QY 239	LeuSerPheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGly		258
Db 659	CTCTCCTTCATCAGATCACCCCTGTGTGGCTGTATGCCAGACATCATCCCTTCCACAGA		718
QY 259	GlyAlaValGlyCysGlyIleArgLeuProasnProasPThrAspleuTyrTrpPheThr		278
Db 719	GGTGCAGTGGGCTGGGCATACGCGCTGACAACAACACACTGAAGCTCTACTGTTCACC		778
QY 279	-LeuTyrGlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrVa		298
Db 779	ACTGTACCAAGTATTCCTGGCCTTTGACCCGCTTTTGTGGCAATTACACGCGCAATCC		838
QY 298	1--ArgIleLeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleAr		317
Db 839	GTGAGGATCCCTGCAGCGCATGACGGTCCCCAAGTGGCCCCGGCTTCCAACGACGATCACG		898
QY 317	gLeuArg 319		
Db 899	CCGGAGA 905		

RESULT 6
BF342364
LOCUS
DEFINITION BF342364 834 bp mRNA linear EST 22-NOV-2000
602013155F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4148940
5', mRNA sequence.
ACCESSION BF342364
VERSION BF342364 GI:11289365
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 834)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9409 row: n column: 13
High quality sequence start: 20
High quality sequence stop: 730.
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1..834
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4148940"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: PCMV-SPORE6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP library."
BASE COUNT 142 a 271 c 232 g 188 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 1.27e-102 Length: 834
Score: 1097.50 Matches: 235
Percent Similarity: 88.24% Conservative: 5
Best Local Similarity: 86.40% Mismatches: 28
Query Match: 49.62% Indels: 10
DB: 12 Gaps: 2
US-09-885-478-2 (1-422) x BF342364 (1-834)
QY 20 SerGlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGly 39
||||| :|||
DB 21 AGCGGCTGCAG-GCTACGAGAGATGACCCCTTCCCACTGCGGGCTTGGCTCCGGGA 79
QY 40 GlnGlyArgArgTrpArgLeuProGlnProAlaTrpValGluGlySerSerAlaArg 59
||||| :|||
DB 80 CAAGGTGGCAGGCGCTGAGAGCTGCCGAGCCTGCGTGGGTGAGAGGAGCTCAGCTCGG 139
QY 60 LeuTrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThr 79
||||| :|||
DB 140 TTGTGGAGACAGCGGAC-GGCACTGGCTGATGAGACTGGAAGCCTCGCTGCCACT 198
QY 80 GlyProAsnAlaSer-AsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerPr 99
||||| :|||
DB 199 GGTCCCAAGCCACGACACCTCTGATGCGCCGCACTAACCCTCAGTCCGACGATCACC 258
QY 99 oProArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrI 119
||||| :|||
DB 259 TCCTCGCACGGGGAGCATCTCTACATCAACATCATCATGCGCTTCGGTTCGGCACCAT 318

QY 119 ecysLeuLeuGlyIleIlelegLyAsnSerThrValIlePheAlaValValIlySlySerly 139
||||| :|||
DB 319 CTGCCTCCTGGGCATCATCGGGAAGCTCAGCGGTCTCTCGGGTCTGGAAGAAGTCCAA 378
QY 139 sleuHisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLe 159
||||| :|||
DB 379 GCTGCACGTGTGCACACAGCTCCCGACATCTTCATCATCAACCTCTCGTAGATATCT 438
QY 159 uLeuPheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHi 179
||||| :|||
DB 439 CCTCTTCTCTCGGCATGCCCCCTTCATGATCCACAGCTCATGGGCAATGGGTTGGGA 498
QY 179 sPheGlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSe 199
||||| :|||
DB 499 CTTTGGGAGAGACCATGTGCACCCCTCATGCAGGGCCATGGATGCCAATAGTCAAGTCAACCAG 558
QY 199 rThrTrpIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSe 219
||||| :|||
DB 559 CACCTACATCCTGNACGC-ATGGCCATTGACCG-TACCTGGCCACTGTCCACCCCAATCTC 616
QY 219 rSerThrIlyspheArgIlyspSerSerValAlaThrLeuValIleCysLeuLeuTrpAlaLe 239
||||| :|||
DB 617 TTCCACGAAAGTTCCGGAAGCCCTCTGTGGC-ACCCTGGTGTCTTCTCCTGTGGGCCCT 675
QY 239 uSerPheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyG1 259
||||| :|||
DB 676 CTCCTTCATCAGCATCACCCCTGTGTGGT--GTTTGACAGACTCATCCCTTCCACAGAGG 733
QY 259 yAlaValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLe 279
||||| :|||
DB 734 TTGCAGTGGGGTGGG--CATACGCTTGGCAACAGAAATGACTCTACTTGGTTCCCTTG 790
QY 279 uTyrGlnPhePheLeuAlaPheAlaLeuProPhe 290
||||| :|||
DB 791 TCCAGTTTCTGTGGCTT-----TGCCCTGCCCTTGG 818
RESULT 7
BF966511
LOCUS
DEFINITION BF966511 845 bp mRNA linear EST 23-JAN-2001
602286863F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4375863 5',
mRNA sequence.
ACCESSION BF966511
VERSION BF966511 GI:12333726
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 845)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10041 row: m column: 16
High quality sequence stop: 661.
FEATURES
source
1..845
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4375863"
/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified

Db 455 CCCAATGCCAGACACACCTCTGATGGCCCCGATTAACCTTCACTTCGGCAGGATCACCTCCT 514

QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
|||||
Db 515 CGCACGGGGAGCATCTCTACATCAACATCATCATGCTTCGGTGTGGCACCACATCTGC 574

QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysSerLysLeu 140
|||||
Db 575 CTCCTGGGCATCATCGGAACCTCACCGGTCACTTCGGCGTCTGAAGAAGTCCAAAGCTG 634

QY 141 -HistPcCysAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLe 160
:::|||||
Db 635 CAACTGGTGCACAACAGCTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCT 694

QY 160 uPheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPh 180
|||||
Db 695 CTTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGCAATGGGGTGTGGCACTA 754

QY 180 eGlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerTh 200
:|||||
Db 755 TGGGAGACCAATGTGCACCCCTCATCACCGGCATGGATTGCCATAGTCAATTCCACGAGAC 814

QY 200 rTyrIleLeuThrAla 205
|||||
Db 815 CTACATCCTGACCGCA 830

RESULT 9
BI818110 685 bp mRNA linear EST 04-OCT-2001
LOCUS 60303232F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173852 5',
DEFINITION mRNA sequence.
ACCESSION BI818110
VERSION BI818110.1 GI:15928318
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 685)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM11432 row: 0 column: 05
High quality sequence stop: 679.
Location/Qualifiers
1. 685
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5173852"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

BASE COUNT 132 a 205 c 212 g 136 t
ORIGIN

Alignment Scores:
Pred. No.: 3.94e-94 Length: 685
Score: 1014.00 Matches: 188
Percent Similarity: 99.47% Conservative: 0
Best Local Similarity: 99.47% Mismatches: 1
Query Match: 45.84% Indels: 0
DB: 13 Gaps: 0
US-09-885-478-2 (1-422) x BI818110 (1-685)

QY 1 MetSerValGlyAlaMetLysLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
|||||
Db 115 ATGTCAGTGGAGGCCATGAAGAAGGAGTGGGAGGCGCAGTTGGCCTTGAGAGCGGCAGC 174

QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
|||||
Db 175 GGCTGCCAGGCTACCGGAGGAAGACCCTTCCCGACTGCGGGGCTTGGCGTCCGGGACAA 234

QY 41 GlyGlyArgArgTyrPargLeuProGlnProAlaTrpValGluGlySerSerAlaArgLeu 60
|||||
Db 235 GGTCGACAGCGCTGAGAGCTGCCGCAACCTGCGTGGGTGGAGGGAGAGCTACAGCTCGGTTG 294

QY 61 TyrGluGlnAlaThrGlyThrGlyTyrMetAspLeuGluAlaSerLeuLeuProThrGly 80
|||||
Db 295 TGGGAGCAGGCGCAGACCGGCACCTGGCTGATGACACTGGAAAGCTCGCTGCTGCCACTGGT 354

QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
|||||
Db 355 CCCAATGCCAGACACACCTCTGATGGCCCCGATTAACCTCACTTCGGCAGATCACTCCT 414

QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
|||||
Db 415 CGCACGGGGAGCATCTCTACATCAACATCATCATGCTTCGGTGTTCGGCACCACATCTGC 474

QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeu 140
|||||
Db 475 CTCCTGGGCATCATCGGAACCTCCACGGTTCATCTTCGGGTGCGTGAAGAAGTCCAAGCTG 534

QY 141 HistPcCysAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160
|||||
Db 535 CAACTGGTGCACAACAGCTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTC 594

QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180
|||||
Db 595 TTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTA 654

QY 181 GlyGluThrMetCysThrLeuIleThr 189
|||||
Db 655 GGGGAGACCATGTGCACCTCATCAGC 681

RESULT 10
BE312747 859 bp mRNA linear EST 26-OCT-2000
LOCUS 601150756F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503484 5',
DEFINITION mRNA sequence.
ACCESSION BE312747
VERSION BE312747.1 GI:9131846
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM176 row: p column: 13
High quality sequence start: 3
High quality sequence stop: 733.

FEATURES

source
1. 859
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3503484"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 151 a 267 c 254 g 186 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 3.24e-80 length: 859
Score: 880.50 Matches: 183
Percent Similarity: 91.58% Conservative: 2
Best Local Similarity: 90.59% Mismatches: 10
Query Match: 39.81% Indels: 7
DB: 10 Gaps: 1

US-09-885-478-2 (1-422) x BE312747 (1-859)

QY 1 MetSerValGlyAlaMetLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
DB 194 ATGTCAAGTGGAGCCATGAAGAAGGAGTGGGAGGCGAGTTGGCTTGGAGCGGCAGC 253
QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
DB 254 GGCTGCCAGGCTACGAGGAGAACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGACAA 313
QY 41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGluGlySerSerAlaArgLeu 60
DB 314 GGTGGCAGGCGCTGGAGGCTGCCGACCTGCTGGTGGAGGGAGCTCAAGCTCGTTG 373
QY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThr-G1 80
DB 374 TGGAGCAGGCGGAGCCTCTCTACATCAACATCATGCTTCGGTTCGGCACCATCT 433
QY 80 Y-ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProp 100
DB 434 TTCCCAATGCCAGCAACACCTCTGATGGCCCCGATTAACCTCACTTCGGCAGGATCACCTC 493
QY 100 roArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleC 120
DB 494 CTGCACGGGGAGCATCTCTACATCAACATCATGCTTCGGTTCGGCACCATCT 553
QY 120 yslLeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysSerLysL 140
DB 554 GCCTCCTGGGCATCATCGGAACTCCACGGTCACTTCGCGGTGCTGAAGAAGTCCAAAGC 613
QY 140 euHisTrpCysAsnAsnValProAspIle-PheIleIleAsnLeuSerVal-ValAspIle 159
DB 614 TGCACGTGGTGCACACAGTCCCGACATCTTTCATCATCAACCTCTCGGTAAGTAGATCT 673
QY 159 u---LeuPheLeuLeuGly-MetProPheMetIleHisGlnLeuMetGlyAsnGlyValT 178
DB 674 CCTTCTTTCTCTCTGGCATTTGCNCTTCATGATCCACCAAGCTCATGGGAGGGGTGT 733
QY 178 rPHis-PheGlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSer 195
DB 734 GGCACTTTTGGGAGACCTGTGTCCTCATCACGGCATGGGTTGCCCTGTGCG 787

RESULT 11
BE312542 600 bp mRNA linear EST 26-OCT-2000
LOCUS 601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5',
DEFINITION mRNA sequence.

ACCESSION BE312542
VERSION BE312542
KEYWORDS BE312542.1 GI:9131383
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 600)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM175 row: m column: 05
High quality sequence start: 7
High quality sequence stop: 574.

FEATURES

source
1. 600
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3503020"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 113 a 174 c 197 g 116 t
ORIGIN

Alignment Scores:

Pred. No.: 6.92e-61 length: 600
Score: 691.00 Matches: 132
Percent Similarity: 99.25% Conservative: 0
Best Local Similarity: 99.25% Mismatches: 1
Query Match: 31.24% Indels: 1
DB: 10 Gaps: 0

US-09-885-478-2 (1-422) x BE312542 (1-600)

QY 1 MetSerValGlyAlaMetLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
DB 195 ATGTCAAGTGGAGCCATGAAGAAGGAGTGGGAGGCGAGTTGGCTTGGAGCGGCAGC 254
QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
DB 255 GGCTGCCAGGCTACGAGGAGGAAGAACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGACAA 314
QY 41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGluGlySerSerAlaArgLeu 60
DB 315 GGTGGCAGGCGCTGGAGGCTGCCCGACCTCGCTGGTGGAGGGAGCTCAGCTCGTTG 374
QY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly 80
DB 375 TGGAGCAGGCGGAGCCTGCTGGATGGACCTGAAGCCTCGCTGCTGCCACATGCT 434
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100

|||||
Db 435 CCCATGCCAGCACACCTCTGATGGCCCCCGATTAACCTTCGCGCAGGATCACCTCCT 494
QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
Db 495 CGCAGCGGAGCATCTCCATCATCAACATCATCATGCCCTTCGGTGTTCGGACCATCTGC 554
QY 121 LeuLeuGlyIleIleIleGlyAsnSerThrValIlePheAla 133
Db 555 CTCCTGGGCATCATCGGAGACTCCCG-GTCATCTTCGCG 592
RESULT 12
F07228 345 bp mRNA linear EST 20-FEB-1995
LOCUS HSC12F101 normalized infant brain cDNA Homo sapiens cDNA clone
DEFINITION c-12f10, mRNA sequence.
ACCESSION F07228
VERSION F07228.1 GI:672877
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 345)
Aufray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes
,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F.,
Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabakchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
and its expression
TITLE and its expression
JOURNAL C. R. Acad. Sci. IIR, sci. Vie 318 (2), 263-272 (1995)
MEDLINE 95277534
COMMENT Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-12f10
Seq primer: (-21)M13_universal.
FEATURES
source
1..345
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-12f10"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain
; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soaes, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"

Alignment Scores:
Pred. No.: 6.51e-51 Length: 345
Score: 591.00 Matches: 114
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 1
Query Match: 26.72% Indels: 0
DB: 14 Gaps: 0

US-09-885-478-2 (1-422) x F07228 (1-345)

QY 122 LeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysSerLysLeuHis 141

|||||
Db 1 CTGGGCATCATCGGAGACTTCACGGTCACTCTTCGCGGTGTGAGAGAAGTCCAGCTGCAC 60
QY 142 TrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuPhe 161
Db 61 TGGTGACACAACGTCCTCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTTT 120
QY 162 LeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPheGly 181
Db 121 CTCCTGGGCATGCCCTTCATCATCCACACGCTCATGGCAATGGGCTGTGGACATTTGGG 180
QY 182 GluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThrTyr 201
Db 181 GAGACCATGTGCACCCCTCATCATCCACGCGCATGATGCCAATAGTCAGTTCACACGACCTTAC 240
QY 202 IleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSerThr 221
Db 241 ATCTGACCGCCATGGCCATTGACCGCTTACCTGGCCACTGTCCACCCCATCTNTTCCACG 300
QY 222 LysPheArgLysProSerValAlaThrLeuValIleCysLeuLeu 236
Db 301 AAGTTCGGAGAAGCCCTCTGTGGCCACCCCTGTGATCTGCCTCTG 345
RESULT 13
BE647763 387 bp mRNA linear EST 06-SEP-2000
LOCUS UI-M-BH1-ant-c-04-0-UI.r1 NIH_BMAP_M_S2 Mus musculus cDNA clone
DEFINITION UI-M-BH1-ant-c-04-0-UI 5', mRNA sequence.
ACCESSION BE647763
VERSION BE647763
KEYWORDS BE647763.1 GI:9973583
SOURCE EST.
ORGANISM house mouse.
Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 387)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: MEST@mail.nih.gov
cDNA library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements
Seq primer: M13 Reverse.
FEATURES
source
1..387
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH1-ant-c-04-0-UI"
/clone_lib="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S2 library is a subtracted library derived from
NIH_BMAP_M_S1, which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hippocampus). The driver
used for subtraction consisted of a pool of 5,000 clones

from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries."

BASE COUNT 84 a 121 c 102 g 80 t
ORIGIN

Alignment Scores:

Pred. No.: 1.78e-45 Length: 387
Score: 539.00 Matches: 106
Percent Similarity: 99.07% Conservative: 0
Best Local Similarity: 99.07% Mismatches: 1
Query Match: 24.37% Indels: 0
DB: 10 Gaps: 0

US-09-885-478-2 (1-422) x BE647763 (1-387)

QY 316 ILEArgLeuArgThrLysArgValThrArgThrAlaIleAlaIleCysLeuValPhephe 335
|||
Db 3 ATCCGGCTTCGGACAAAGAGGGGTGACCCGACACCATTCATCTCTGCTCTCTTT 62
QY 336 ValCysTrpAlaProTyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThr 355
|||
Db 63 GTGTGCTGGGGCCCTACTACTGCTGCTGCAGCTGACCCAGTTGTCCATCAGCCGCCGACC 122
QY 356 LeuThrPheValTyrLeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeu 375
|||
Db 123 CTCACATTCGTCTACCTGTACATATGCGGCTATCAAGCTTGGGCTATGCCAACAGCTGCCTC 182
QY 376 AsnProPheValTyrIleValLeuCysGluThrPheArgLysArgLeuValLeuSerVal 395
|||
Db 183 AATCCCTTTGTGTACATAGTACTCTGTGAGACCTTTCCAAACGCTTGGTGTGCTGCGGTG 242
QY 396 LysProAlaAlaGlnGlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGlu 415
|||
Db 243 AAGCCCGCGGCCAGGGGCGCTTCGCACGGTCCAGCAATGCTCAGACAGCTGACGAGAG 302
QY 416 ArgThrGluSerLysGlyThr 422
|||
Db 303 AGGACAGAAAGCAAGGCACC 323

RESULT 14
BF313837 1086 bp mRNA linear EST 21-NOV-2000
LOCUS 601902234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4134848 5',
DEFINITION mRNA sequence.

ACCESSION BF313837 GI:11261906
VERSION BF313837
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1086)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LICM1038 row: c column: 09
High quality sequence stop: 603.

FEATURES
source Location/Qualifiers
1..1086
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4134848"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"

/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; site_1: XhoI; site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 326 a 303 c 310 g 147 t
ORIGIN

Alignment Scores:

Pred. No.: 6.22e-40 Length: 1086
Score: 491.50 Matches: 121
Percent Similarity: 82.24% Conservative: 4
Best Local Similarity: 79.61% Mismatches: 20
Query Match: 22.22% Indels: 10
DB: 12 Gaps: 2

US-09-885-478-2 (1-422) x BF313837 (1-1086)

QY 1 MetSerValGlyAlaMetLysGly--ValGlyArgAlaValGlyLeuGlyGly 20
|||
Db 216 ATGTCAGTGGGAGCCCATGAAGACGGGAGCGTGGGAGGGCAGTTGGCTTGAGGGCGCA 275
QY 20 erGlyCysGlnAlaThrGlu-GluAsp-ProLeuProAspCysGlyAlaCysAlaProGl 39
|||
Db 276 GTGGCTGCCAGGCTACGAGCGGAAGACCCCTTACCCGACTGCGGGCTTGCGCTCCGGG 335
QY 39 yGlnGlyArgArgTrpArgLeuProGlnProAlaTrpVal--GluGlySerSerAl 58
|||
Db 336 ACAAGGTGGCAGGCGCGCTGGAGGCTGCCGAGCCCTGGGTGGCGACGGGAGAGCTCAGAC 395
QY 58 aArgLeuTrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGlnAlaSerLeuLeuPr 78
|||
Db 396 TCGGTGCTGGAGACGACGGCGACCGGCACTGGCTGATGAGCACTGGAAGCTCGCTGCC 455
QY 78 oThrGlyProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySe 98
|||
Db 456 ACATGGTCCCAATGCCAGCAA-ACCTCTGATGGCCGATAA--CTCACTTCGGCAGGATC 512
QY 98 rProProArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyTh 118
|||
Db 513 ACCTCCTCGCAGCGGGAGAGATCTCCTACATCAACATCATGCGCTTGGTGC CGGAC 572
QY 118 rIleCysLeuLeuGlyIleIleGlyAsnSerThrValIlePhe-AlaValValLysLys 138
|||
Db 573 ATC-TGGCTACTGGGCATCATCGGGAACCTCCAGGTCCATCTACAGCGGACGTAAGAAGT 631
QY 138 erLysLeu--HisTrpCysAsnAsn 145
|||
Db 632 CCATGCTCGAACATGATGCAACAC 657

RESULT 15
BF600078 497 bp mRNA linear EST 25-APR-2001
LOCUS 264555 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

DEFINITION BF600078
ACCESSION BF600078
VERSION BF600078.1 GI:11697183
KEYWORDS EST.
SOURCE cow.

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 497)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Perteaux,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keeler,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 11:05:52 ; Search time 283 Seconds
(without alignments)
3358.103 Million cell updates/sec

Title: US-09-885-478-2

Perfect score: 2212

Sequence: 1 MSVGAMKKGVGRAVLGGGS.....LRASNAQTADERTESKGT 422

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09885478/runat_13022003_105050_12757/app.query.fasta_1.583
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09885478_@CGN_1_1_187_@runat_13022003_105050_12757 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002: *
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2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT: *
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14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT: *
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17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT: *
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT: *
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20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT: *
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT: *
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT: *
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT: *
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	2212	100.0	1269	21	AAA63240	Human MCH1 recepto
2	2212	100.0	1269	24	ABK14548	Human cDNA encodin
3	2207	99.8	1269	22	AAD13654	Human melanin-conc
4	2207	99.8	1269	22	AAA91189	Human MCH-R3 codin
5	2207	99.8	1269	22	AAH47297	Human long form MC
6	2207	99.8	1275	21	AAA72918	Human SLC-1 cDNA s
7	2207	99.8	1275	22	AAF86229	Human melanin conc
8	2207	99.8	1275	22	AAF86975	Human SLC-1 coding
9	2207	99.8	1275	24	ABK10854	DNA encoding human
10	2207	99.8	1275	24	ABA92411	Human SLC-1 encod1
11	2207	99.8	1275	24	AAI69442	Human SLC-1 cDNA.
12	2207	99.8	1283	21	AAA72924	Human SLC-1 (L) CD
13	2207	99.8	1283	22	AAF86235	Human melanin conc
14	2207	99.8	1283	22	AAF86981	Human SLC-1 coding
15	2207	99.8	1283	24	ABA92417	Human SLC-1 (L) nu
16	2207	99.8	1283	24	AAI69448	Human SLC-1(L) CDN
17	2197	99.3	1269	22	AAH47302	Human long form/mo
18	2197	99.3	1254	22	AAH47311	Human long form/mo
19	2184	98.7	1254	22	AAD13653	Human melanin-conc
20	2184	98.7	1254	22	AAA91188	Human MCH-R2 codin
21	2164	97.8	1385	19	AAV28115	Human 11CB splice
22	2164	97.8	1385	20	AAK60230	Nucleotide sequenc
23	2164	97.8	1385	22	AAD09345	Human 11CBY cDNA.
24	2085	94.3	2152	21	AAZ90522	Human GPCR protein
25	2000	90.4	3488	21	AAA30875	Human 11cby gene.
26	1971	89.1	2483	22	AAA91191	Human MCH-R3 full
27	1968	89.0	2148	21	AAA53886	Murine 11cby recep
28	1880	85.0	2080	22	AAH47299	Mouse MCHIR cDNA.
29	1824	82.5	1062	22	AAD13652	Human melanin-conc
30	1824	82.5	1062	22	AAA91187	Human MCH-R1 codin
31	1824	82.5	1062	22	AAH47298	Human short form M
32	1824	82.5	1062	24	ABK10702	Human melanin-conc
33	1824	82.5	1074	21	AAA72923	Human SLC-1 (S) cd
34	1824	82.5	1074	22	AAF86234	Human melanin conc
35	1824	82.5	1074	22	AAF86980	Human SLC-1 coding
36	1824	82.5	1074	24	ABA92416	Human SLC-1 (S) nu
37	1824	82.5	1074	24	AAI69447	Human SLC-1(S) CDN
38	1824	82.5	2133	23	ABT98036	TSHR-Gs-alpha fusi
39	1819	82.2	1062	23	ABT97927	Non-endogenous hum
40	1818	82.2	1062	23	ABT97897	Non-endogenous hum
41	1818	82.2	1062	23	ABT97921	Non-endogenous hum
42	1817	82.1	1062	23	ABT97924	Non-endogenous hum
43	1814	82.0	1062	22	AAH47301	Human short form/m
44	1814	82.0	1062	23	ABT97909	Non-endogenous hum
45	1814	82.0	1062	23	ABT97915	Non-endogenous hum

ALIGNMENTS

RESULT 1
AAA63240
ID AAA63240 standard; DNA; 1269 BP.
XX
AC AAA63240;
XX
DT 17-NOV-2000 (first entry)
XX
DE Human MCH1 receptor coding sequence.
XX
KW Human; MCH1 receptor; melanin concentrating hormone; neuroregulator;
KW G-protein coupled; PEXU.HR-TL231; feeding; water balance;
KW energy metabolism; arousal; attention; memory; cognitive function;
KW psychiatric disorder; diabetes; cardiovascular; gastrointestinal;
KW hypertension; balance; diabetes; respiratory; asthma; reproductive function;
KW electrolyte balance; asthma; reproductive function;
KW immune; endocrine; musculoskeletal; Alzheimer's disease;
KW sensory modulation; transmission; motor coordination;

KW	Parkinson's disease; olfaction; urinary; depression; seizure; pain;
KW	schizophrenia; morphine tolerance; opiate addiction; migraine; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..1269
XX	/+tag= a
XX	/product= "Human MCH1 receptor"
PN	MO200039279-A2.
XX	
PD	06-JUL-2000.
XX	
PF	30-DEC-1999; 99WO-US31169.
XX	
PR	31-DEC-1998; 98US-0224426.
XX	
PA	(SYNA-) SYNAPTIC PHARM CORP.
XX	
PI	Salon JA, Laz TM, Nagorny R, Wilson AE;
XX	
DR	WPI: 2000-548644/50.
DR	P-PSDB; AAB13436.
XX	
PT	Novel nucleic acid encoding human melanin concentrating hormone
PT	receptor useful for treating cardiovascular disorders, hypertension and
PT	diabetes, whose mutant form is activated by melanin concentrating
PT	hormone -

Claim 26; Fig 1; 173pp; English.

Neuroregulators modulate communication in the nervous system. Melanin concentrating hormone 1 (MCH1) is one such neuroregulator. MCH may serve as an integrative neuropeptide, involved in stress response, feeding regulation and sexual activity. Also, MCH is thought to participate in water balance regulation, energy metabolism, general arousal/attention state, memory and cognitive functions and psychiatric disorders. The present sequence is the coding sequence of human MCH1 receptor. MCH1 receptor is a G-protein coupled receptor. The present sequence may be used in the therapy for a variety of disorders: steroid or pituitary hormone disorder, epinephrine release disorder, gastrointestinal disorder, cardiovascular disorder, electrolyte balance disorder, hypertension, diabetes, respiratory disorder, asthma, reproductive function disorder, immune disorder, endocrine disorder, musculoskeletal disorder, neuroendocrine disorder, cognitive disorder, memory disorder, e.g. Alzheimer's disease, sensory modulation and transmission disorder, motor coordination disorder, sensory integration disorder, dopaminergic function disorder e.g. Parkinson's disease, olfaction disorder, sympathetic innervation disorder, depression, stress, fluid-imbalance disorder, urinary disorder e.g. urinary incontinence, seizure, pain, psychotic behaviour e.g. schizophrenia, morphine tolerance, opiate addiction or migraine. The present sequence is also contained in plasmid pEXT-HR-TL231 (ATCC 203197).

Sequence 1269 BP; 234 A; 419 C; 347 G; 269 T; 0 other;

Alignment Scores:			
Pred. No.:	7.19e-185	Length:	1269
Score:	2212.00	Matches:	422
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-885-478-2 (1-422) x AAA63240 (1-1269)

QY 1 MetSerValGlyAlaMetLysLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
 |||||
 Db 1 ATGTCAAGTGGAGCATGACAGAAGGAGTGGGAGGCGCACTGGGCTTGAGAGCGGCAGC 60
 |||||
 QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyCln 400
 |||||

Db	61	GGCTGCCAGGCTACGGAGGAAGACCCCTTCCCGACTGCGGGGCTTGCCTCCGGGACAA	120
QY	41	GLYGLYArgArgTrpArgLeuProGlnProAlaTrpValGluGlySerSerAlaArgLeu	60
Db	121	GGTGGCAGGCGCTGGAGGCTGCGCAGCCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTTG	180
QY	61	TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly	80
Db	181	TGGGAGCAGGCGCACCAGCACTGGCTGGATGACCTGGAAGCCTCGCTGTCGCCACTGTT	240
QY	81	ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro	100
Db	241	CCCAATGCCAGCACACACTCTGATGGCCCCGATAACCTCATTACAGCAGGATCACCTCCT	300
QY	101	ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys	120
Db	301	CGCACGGGAGCATCTCTTACATCAACATCATCATGCTTCGGTGTTCGGCACCATCTGC	360
QY	121	LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeu	140
Db	361	CTCCTGGGCATCATCGGGAACCTCCACGGTCATCTTCGGGTCGTGAAGAGTCCAAGCTG	420
QY	141	HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu	160
Db	421	CACGTGGTGCACAACAACGTCGCCGACATCTTCATCATCAACCTCTCGGTAGATCTCCTC	480
QY	161	PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe	180
Db	481	TTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGGCACCTTT	540
QY	181	GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr	200
Db	541	GGGGAGACCATGTGACACCCCTCATCAAGGCCATGATGCCAATAGTCAGTTACACAGCACC	600
QY	201	TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer	220
Db	601	TTACATCTGACCGCCATGGCCATTGACCGCTACCTGGCCACCTGTCACCCCATCTCTTCC	660
QY	221	ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer	240
Db	661	ACGAGTTCCGGAAGCCCTGTGTGGCCACCCTGTGATCTGCCTCTGTGGGCCCTCTCC	720
QY	241	PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla	260
Db	721	TTTCATGACATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCACAGAGGTGCA	780
QY	261	ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr	280
Db	781	GTGGGCTCGGCATACGCGCTGCCCAACCCAGACACTGACTCTACTGTTCACCCCTGTAC	840
QY	281	GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle	300
Db	841	CAGTTTTCCTGGCCTTTGCCCTGCTTTTGTGTCAATCAGCCGATACGTGAGATC	900
QY	301	LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr	320
Db	901	CTGCAGCGCATGACGCTCTCAGTGGCCCCCGCCTCCACAGCGACATCCGGCTGGGACA	960
QY	321	LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro	340
Db	961	AAGAGGGTACCCGCACAGCCATCGCCATCTGTCTGTCTTCTTTGTGTGTGGGCAACC	1020
QY	341	TyrTrpValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr	360
Db	1021	TACTATGTGTACAGCTGACCCAGTTGTTCATCAGCCGCCCGCACCTCACCTTTGTCTAC	1080
QY	361	LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr	380
Db	1081	TTATACAATGGGGCCATCAGCTTGGGCTATGCCAACAGAGCTGCTCAACCCCTTGTGTAC	1140
QY	381	IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln	400
Db	1141	ATCGTGTCTGTGAGACAGTTCGCCGAACGCTTGTCTCTGTGTGTAAGCCTGCAGCCAG	1200

QY	401	GlycInLeuAArgAlaValSerAsnAlaGlnThrAlaSpGIuArgThrGluserylS	420
Db	1201	GGGCAGCTTCGCCGTGTACAGAACGCTCAGACGCGTGTACGAGAGAGAGACAGAACA	1260
QY	421	GlyThr	422
Db	1261	GGCACCC	1266
RESULT 2			
ID	ABK14548	standard; cDNA; 1269 BP.	
XX	AC	ABK14548;	
XX	DT	08-MAY-2002 (first entry)	
DE		Human cDNA encoding melanin concentrating hormone receptor, MCH1.	
KW		Human; ss; gene; melanin concentrating hormone receptor; MCH1;	
KW		steroid hormone disorder; pituitary hormone disorder;	
KW		epinephrine release disorder; gastrointestinal disorder;	
KW		cardiovascular disorder; hypertension; diabetes; respiratory disorder;	
KW		asthma; reproductive function disorder; immune disorder;	
KW		musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;	
KW		memory disorder; motor coordination disorder; obesity; eating disorder;	
KM		dopaminergic function disorder; pain; psychosis; opiate addiction;	
KW		affective disorder; migraine; transgenic.	
XX			
OS		Homo sapiens.	
FH			
XX			
FT	CDS	Location/Qualifiers	
FT		1..1269	
FT		/*tag= a	
FT		/product= "MCH1"	
PN		WO200202744-A2.	
XX			
PD		10-JAN-2002.	
XX			
Pf		05-JUL-2001; 2001WO-US21350.	
XX			
PR		05-JUL-2000; 2000US-0610635.	
PA		(SYNA-) SYNAPTIC PHARM CORP.	
PI		Salon JA, Laz TM, Nagorny R, Wilson AE;	
XX			
DR		WPI; 2002-164532/21.	
Dt		P-PsDB; AAU75853.	
PT		Purified human melanin concentrating hormone receptor protein and	
PT		polynucleotides for screening modulator useful for treating memory	
PT		disorder, sensory modulation and transmission disorder, motor	
PT		coordination disorder -	
XX			
PS		Claim 2; Fig 1; 524pp; English.	
XX			
CC		The invention relates to a purified human melanin concentrating hormone	
CC		(MCH1) receptor protein and its encoding nucleic acid (or mutant	
CC		activated by MCH or its analogue or homologue). Also included are	
CC		expression vectors, probes, transformed insect cells, antisense	
CC		oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting	
CC		the binding of the antibody to MCH1, a transgenic animal expressing the	
CC		protein, or a homologous knockout or antisense complementary to the MCH1	
CC		nucleic acid, ant/agonists of MCH1, and methods of isolating chemical	
CC		compounds which activate MCH1. The protein, nucleic acid, antibody,	
CC		ant/agonists and compound are useful for diagnosing and treating a	
CC		steroid or pituitary hormone disorder, an epinephrine release disorder, a	
CC		gastrointestinal disorder, cardiovascular disorder, electrolyte balance	
CC		disorder, hypertension, diabetes, respiratory disorder, asthma,	
CC		reproductive function disorder, immune disorder, endocrine disorder,	
CC		musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,	
CC			

```

CC memory disorder, sensory modulation and transmission disorder, motor
CC coordination disorder, sensory integration disorder, motor integration
CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder,
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC encodes human MCH1.
XX
SQ Sequence 1269 BP; 234 A; 419 C; 347 G; 269 T; 0 other;

Alignment Scores:
Pred. NO.: 7.19e-185 Length: 1269
Score: 2212.00 Matches: 422
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-885-478-2 (1-422) x ABK14548 (1-1269)

```

50	Sequence 1269 BP; 234 A; 419 C; 347 G; 269 T; 0 other;
Alignment Scores:	
Pred. No.:	7.19e-185
Score:	2212.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	24
US-09-885-478-2 (1-422) x ABK14548 (1-1269)	
	Length: 1269
	Matches: 422
	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0
QY	1 MetSerValGlYAlaMetLysLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
Db	1 ATGTCAGTGGAGACCATGAAGAAGGAGTGGGAGGGCAGTTGGGCTTGAGAGCGGCAGC 60
QY	21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
Db	61 GGCTGCCAGGCTACGAGGAGAACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGGACAA 120
QY	41 GlyGlyArgArgTrrPargLeuProGlnProAlaTrrPvalGlyGlySerSerAlaArgLeu 60
Db	121 GGTGGCAGGGCGCTGGAGGCTGCCGACGCTGCGTGGGAGGGGAGCTCAGCTCGGTTG 180
QY	61 TrpGluGlnAlaThrGlyThrGlyTrrMetAspLeuGluAlaSerLeuLeuProThrGly 80
Db	181 TGGAGCAGGCGGACCGGCACCTGGCTGGATGGACCTGGAAGCCTCGCTGCTGCCACTGCT 240
QY	81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
Db	241 CCCAATGCCAGCAACACCTTGATGGCCCCGATAACCTCAGCTTCAAGAGATCACCTCCT 300
QY	101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
Db	301 CGCAGCGGAGCATCTCCTACATCAACATCATCATGCCCTTCGGTTCGGCACCATCTGC 360
QY	121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValAllyLysSerLysLeu 140
Db	361 CTCCTGGGCATCATCGGGAAGCTCCAGGTCATCTTCGGGTCGTGAAGAAGTCCAAAGCTG 420
QY	141 HisTrrCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160
Db	421 CACTGGTGCACAACGTCGCCGACATCTTCATCATCAACCTTCGGGTAGATCATCTCTC 480
QY	161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrrPheIsphe 180
Db	481 TTTCTCCTGGGCATGCCCTTCATGATGCACACAGCTCATGGGCAATGGGGTGTGCACATT 540
QY	181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
Db	541 GGGAGACCATGTGCACCCCTCATGCAGGCCCATGGATGCCAATAGTCAGTTCACACGACCC 600
QY	201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220
Db	601 TACATCCTTAACCGCCATGGCCATTAACCGCTACCTGGCCACATGTCCACCCCATCTTCC 660
QY	221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrrPalaleuSer 240
Db	661 ACGAAGTTCGGAAGCCCTGTGTGCCAACCCCTGGTGATTCGCTCTGTGGGCCCTTCC 720
QY	241 PheIleSerIleThrProValTrrPleuTrrAlaArgLeuIleProPheProGlyGlyAla 260
Db	721 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCACGAGAGGTGCA 780

QY 261 ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr 280
|||||
Db 781 GTGGGCTGGCGCATACGCCCTGGCCCAACCCAGACACTGACCTCTACTGTGTCAACCTGTAC 840
QY 281 GlmphepheLeuAlaIleAlaLeuProPheValValIleThrAlaIleTyrValArgIle 300
|||||
Db 841 CAGTTTTCCTGGCCCTTTGCCCTTGCCCTTTGTGTATCATCACAGCCGCATACGTGAGGATC 900
QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
|||||
Db 901 CTGCAGCGCATGACGTCTCTCAGTGGCCCCCGCCCTCCAGCGCAGCATCCGGCTGGGACA 960
QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro 340
|||||
Db 961 AAGAGGGTGACCCGACAGCCATCGCCATCTGTCTGTCTTGTGTGTGGGACACC 1020
QY 341 TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
|||||
Db 1021 TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCGACCCCTCACCTTGTCTAC 1080
QY 361 LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr 380
|||||
Db 1081 TTATACATATGGCGCATACGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTGTGTAC 1140
QY 381 IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaIleGln 400
|||||
Db 1141 ATCGTGCTCTGTGAGACGCTCCGCCAAACGCTTGCTCTGTGGTGAAGCCTGCAGCCAG 1200
QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGlnSerLys 420
|||||
Db 1201 GGGCAGCTTCGGCGTGTACGACAACGCTCAGACGGCTGACGAGAGAGAGACAAAGCAAA 1260
QY 421 GlyThr 422
|||||
Db 1261 GGCACC 1266
RESULT 3
AAD13654
ID AAD13654 standard; cDNA; 1269 BP.
XX AC AAD13654;
XX DT 06-NOV-2001 (first entry)
XX DE Human melanin-concentrating hormone receptor variant #3 cDNA.
XX KW Human; melanin-concentrating hormone; MCH analogue; signal transduction;
KW appetite; therapy; anorexia; acquired immune deficiency syndrome; AIDS;
KW wasting; cachexia; frail elderly; weight maintenance; cancer; anorectic;
KW pain reduction; stress reduction; sexual dysfunction; variant; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FT Key Location/Qualifiers
FT CDS 1..1269
FT /*tag= a
FT /product= "Human MCH receptor protein variant #3"
XX PN WO200157070-A1.
XX PD 09-AUG-2001.
XX PF 01-FEB-2001; 2001WO-US03293.
XX PR 03-FEB-2000; 2000US-0179967.
XX PA (MERI) MERCK & CO INC.
XX PI Bednarek M;
XX DR WPI; 2001-483416/52.
DR P-PSDB; AAE07330.

XX
PT Novel peptide encoding a melanin-concentrating hormone analog useful
PT for increasing weight or appetite
XX
PS Disclosure; Page 33; 66pp; English.
XX
CC The present invention relates to truncated melanin-concentrating hormone
CC (MCH) analogues active at the MCH receptor. The truncated MCH analogues
CC are optionally modified peptide derivatives of mammalian MCH. The MCH
CC analogues can bind to the MCH receptor and bring about signal
CC transduction. The MCH agonists can be used to facilitate a weight gain,
CC maintenance of weight and/or an appetite increase. The MCH agonists can
CC also be used to treat disorders such as anorexia, acquired immune
CC deficiency syndrome (AIDS), wasting, cachexia and frail elderly. The MCH
CC antagonists can be used to facilitate weight loss, appetite decrease,
CC weight maintenance, cancer treatment, pain reduction, stress reduction
CC and/or treatment of sexual dysfunction. The present sequence is a human
CC MCH receptor variant cDNA.
XX
SQ Sequence 1269 BP; 234 A; 420 C; 347 G; 268 T; 0 other;
Alignment Scores:
Pred. No.: 1,98e-184 Length: 1269
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 22 Gaps: 0
US-09-885-478-2 (1-422) x AAD13654 (1-1269)
QY 1 MetSerValGlyAlaMetLysLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
Db 1 ATGTCAAGTGGAGCCATGAAGAGGAGTGGGAGGGCAGTTGGGCTTGAGGGCGGACG 60
QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
Db 61 GGCTGCCAGGCTACGAGGAAGACCCCTTCCCAACTGGGGGCTTGCGCTCCGGACAA 120
QY 41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGlyGlySerSerAlaArgLeu 60
Db 121 GGTGGCAGCGCTGAGAGCTGCCGACGCTGCGTGGTGGAGGGAGCTCAGCTCGTTG 180
QY 61 TrpGluGlnAlaThrGlyThrGlyTyrMetAspLeuGluAlaSerLeuLeuProThrGly 80
Db 181 TGGGAGCAGGCGACCGGCACTGGCTGATGAGACCTGGAAGCCTCGCTGCCACTGGT 240
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
Db 241 CCCAAGCGCCAGCAACACCTCTGATGGCCCCGATTAACCTCACTTCGGCAGGATCACCTCT 300
QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
Db 301 CGCAGGGGAGCATCTCTCATATCATCATCATCATGCTTCGGGTTCGGACCATCTGC 360
QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeu 140
Db 361 CTCCTGGGCATCATCGGAACCTCCACGGTCAATCTTCGGCGGTGTGAAGAACTCCAAGCTG 420
QY 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160
Db 421 CACTGTGCAACAACGTCCCGACACTCTTCATCATCAACCTCTCGGTAGATCTCTC 480
QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180
Db 481 TTYTCTCTGGGCATGCCCTTCATGATCCACAGCTCATGGGCAATGGGCTGTGGCACTTT 540
QY 181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
Db 541 GGGAGACCATGTGCACCCCTCATCATCAGGCCCATGGATGCCAATAGTCAAGTTCACGACACC 600
QY 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220
|||||

Db 601 TACATCCTGACCGCCATGGCCATGTGACCGCTACCTGGCCACTGTCACCCCATCTCTCC 660

QY 221 ThrIysPheArgIysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer 240

Db 661 ACGAAGTTCGGAGAGCCCTCTGTGGCCACCCCTGGTGATCTGCTCTGTGGCCCTCTCC 720

QY 241 PheIleSerIleThrProValTrpLeuTyraIaArgLeuIleProPheProGlyGlyAla 260

Db 721 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGA 780

QY 261 ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrrTrpPheThrLeuTyr 280

Db 781 GTGGGCTGGCGCATACGCCCTGGCCCAACCCAGACACTGACCTTACTGTGTACCCCTGTAC 840

QY 281 GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle 300

Db 841 CAGTTTTCCTGGCCCTTTGCCCTGCCCTTTTGTGTGCATCACAGCCGCATACGTAGAGATC 900

QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320

Db 901 CTGCAGCGCATGACGTCTCAGTGGCCCCGCCCTCCAGCGCAGCATCCGGCTCGCGAGCA 960

QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro 340

Db 961 AAGAGGGTGACCCGACAGCCATCGCCACTGTCTGTGCTTTGTGTGTGTGGGCACCC 1020

QY 341 TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360

Db 1021 TACTATGTGTACAGCTGACCCAGTTGTTCATCAGCCGCCGACCCCTCACCCTTGTCTAC 1080

QY 361 LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr 380

Db 1081 TTATACAATGGCGCATCAGCTTGGCTATGCCAACAGCTGCTCAACCCCTTGTGTAC 1140

QY 381 IleValLeuCysGlnThrPheArgIysArgLeuValLeuSerValLysProAlaAlaGln 400

Db 1141 ATCGTGTCTGTGAGAGCTTCCGCAACGGCTTGTCTGTGTGGTGAAGCCTGCAGCCCA 1200

QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGluSerIys 420

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QY 421 GlyThr 422

Db 1261 GGCACC 1266

RESULT 4

AAA91189

ID AAA91189 standard; DNA; 1269 BP.

XX

AC AAA91189;

XX

DT 08-MAY-2001 (first entry)

XX

DE Human MCH-R3 coding sequence.

XX

KW Human; melanin-concentrating hormone receptor; MCH-R1; MCH-R2; MCH-R3; weight loss; weight gain; cancer; pain; diabetes; stress; therapy;

KW sexual dysfunction; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1269

FT /*tag= a

FT /product= "MCH-R3"

XX

PN WO200105947-A1.

XX

PD 25-JAN-2001.

XX

PF 10-JUL-2000; 2000WO-US18733.

XX

PR 14-JUL-1999; 99US-0143706.

XX

PA (MERI) MERCK & CO INC.

XX

PI Howard AD;

XX

DR WPI: 2001-159528/16.

DR P-PSDB; AAY97670.

XX

PT Melanin-concentrating hormone receptor polypeptides for increasing or decreasing appetite, reducing stress and to screen for compounds that bind to the receptor -

PT

XX

PS Claim 7; Page 22; 43p; English.

XX

CC This sequence encodes a a melanin-concentrating hormone (MCH) receptor protein of the invention, designated MCH-R3. MCH receptor fragments and CC polypeptides are useful in assays to screen for compounds that bind to CC the MCH receptor and modulate the activity of the receptor. MCH Receptor CC activity is modulated to achieve weight loss, weight gain, to treat CC cancer (e.g. colon or breast), reduce pain, treat diabetes, reduce stress CC or treat sexual dysfunction. Nucleic acid coding for the MCH receptor can CC be used to cause an increase in appetite and to create a test system CC (e.g. a transgenic animal) for screening for compounds affecting MCH CC receptor expression. Inhibition of MCH receptor nucleic acid activity is CC useful to inhibit appetite or stress.

XX

SQ Sequence 1269 BP; 234 A; 420 C; 347 G; 268 T; 0 other;

Alignment Scores:

Pred. No.: 1.98e-184 Length: 1269

Score: 2207.00 Matches: 421

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.76% Mismatches: 0

Query Match: 99.77% Indels: 0

DB: 22 Gaps: 0

US-09-885-478-2 (1-422) x AAA91189 (1-1269)

QY 1 MetSerValGlyAlaMetLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20

Db 1 ATGTCAAGTGGAGCCCATGAAGAAGGAGTGGGAGGCGAGTGGGCTTGAGAGCGGCAGC 60

QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40

Db 61 GGCTGCCAGGCTACGAGAGAGACCCCTTCCCACTGCGGGCTTGCCGTCGCGAGCA 120

QY 41 GlyGlyArgArgTTrpArgLeuProGlnProAlaTrpValGluGlySerSerAlaArgLeu 60

Db 121 GGTGGCAGGCGCTGGAGGCTGCCCGACCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTTG 180

QY 61 TrpGluGlnAlaThrGlyThrGlyTyrPheMetAspLeuGluAlaSerLeuLeuProThrGly 80

Db 181 TGGAGCAGGCGCAGCCGCGACTGCGTGGATGACCTGGAAGCCTCGCTGCCCACTGGT 240

QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100

Db 241 CCCAACGCCAGCAACACCTCTGATGGCCCCGATTAACCTTCCGACAGATCACCTCT 300

QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120

Db 301 CGCAGCGGGAGCATCTCTCATCATCATCATCATCGCTTCGGGTTCGGCACCATCTGC 360

QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValAllyLysSerLysLeu 140

Db 361 CTCCTGGGCATATCGGGAAGTCCACGGTCAATCTTCGCGGTCTGAAGAAGTCCAAGCTG 420

QY 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160

Db 421 CACTGGTGCAACACGTCGCCGACATCTTCATCATCAACCTCTCGGTAGATCTCCTC 480

QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180

Db 481 TTTCCTCGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTT 540

QY 181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
|||||
Db 541 GGGAGACCATGTGCACCCCTCATCTACGGCCATGGATGCCAATAGTCAGTTCAACACGACAC 600

QY 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220
|||||
Db 601 TTACATCCGTGACCCCATGGCCATGTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCC 660

QY 221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer 240
|||||
Db 661 ACGAAGTTCGGAGACCCCTCTGTGGCCACCCCTGGATCTGCTCTGTGGCCCTCTCC 720

QY 241 PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla 260
|||||
Db 721 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCACAGAGTGA 780

QY 261 ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr 280
|||||
Db 781 GTGGGCTGGGGCATACGCCCTGCCCCAACCCAGACACTGACCTCTACTGTTCACCCCTGAC 840

QY 281 GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle 300
|||||
Db 841 CAGTTTTCCTGCGCTTTTGCCCTGCTTTGTGTGTCATCACAGCCGCGATACGTGAGGATC 900

QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
|||||
Db 901 CTGCAGCGCATGACGCTCTCAGTGGCCCCCGCTCCAGCGCAGCATCCGGCTGCGGACA 960

QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro 340
|||||
Db 961 AAGAGGGTGAGCCCGCACGCCATCGCCATCTGTCTGTCTTGTGTGTGGGACACC 1020

QY 341 TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
|||||
Db 1021 TACTATGTGTACAGCTGACCCAGTGTTCATCAGCCGCCGACCCCTCACTTGTCTAC 1080

QY 361 LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr 380
|||||
Db 1081 TTATACATGGCGGCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTGTGTAC 1140

QY 381 IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln 400
|||||
Db 1141 ATCGTGTCTGTGAGACGCTTCCCAACGCTTGTCTGTGTGTAAGCCCTGCAGCCACG 1200

QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGluSerLys 420
|||||
Db 1201 GGGCAGCTTGGCGGTGTACGAACGCTCAGACGGCTGACGAGAGGAGACAAAGCAAA 1260

QY 421 GlyThr 422
|||||
Db 1261 GGCACC 1266

RESULT 5
AAH47297
ID AAH47297 standard; cDNA; 1269 BP.
XX

AC AAH47297:

XX 30-NOV-2001 (first entry)

XX Human long form MCH1R cDNA.

XX Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion;
KW fluorescent polypeptide; orexigenic; anabolic; food intake; MCH1R; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1269
FT /tag= a

XX

PN WO200168706-A1.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-US08071.
XX
PR 15-MAR-2000; 2000US-0189698.
XX
PA (MERI) MERCK & CO INC.
XX
PI Marsh DJ;
XX
DR WPI; 2001-565791/63.
DR P-PSDB; AAB85894.

XX Fusion proteins comprising melanin concentrating hormone receptor
PT peptides and fluorescent proteins, useful for identifying appetite
PT stimulants -

XX Example 1; page 17-18; 71pp; English.

XX The invention provides melanin concentrating hormone (MCH) receptor
CC (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise
CC MCHR polypeptide regions from different species. The MCHR fusion protein
CC comprise MCHR polypeptide region and a fluorescent polypeptide region
CC joined directly, or via a linker, to the carboxy side of the MCHR
CC polypeptide region. The MCHR fusion proteins can be expressed by standard
CC recombinant methodology. MCH action promotes feeding (orexigenic) and up
CC regulation of MCH activity stimulates food intake. The present sequence
CC represents a human long form MCH1R cDNA.

XX Sequence 1269 BP; 234 A; 420 C; 347 G; 268 T; 0 other;

Alignment Scores:

Pred. No.: 1.98e-184 Length: 1269
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 22 Gaps: 0

US-09-885-478-2 (1-422) x AAH47297 (1-1269)

QY 1 MetSerValGlyAlaMetLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
|||||
Db 1 ATGTCACTGGGAGCCATGAGAAGAGGAGTGGGAGGGCAGTTGGGCTTGAGCGGCGACG 60

QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
|||||
Db 61 GGCTGCCAGGCTACGGAGGAAGACCCCTTCCCAACTGCGGGGCTTGGCGTCGGGACAA 120

QY 41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGluGlySerSerAlaArgLeu 60
|||||
Db 121 GGTGGCAGCGCTGGAGGCTGCCGACGCTGCGTGGGTGGAGGGGAGGCTCAGCTCGGTTG 180

QY 61 TrpGluAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly 80
|||||
Db 181 TGGGAGCAGCGCAGCCGACCTGGCTGATGGACCTGGAAGCCTGCTGCTGCCACTGGT 240

QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
|||||
Db 241 CCCAAGCGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTGGGAGGATCACTCT 300

QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
|||||
Db 301 CGCAGCGGGAGCATCTCTACATCAACATCATCATGCTTCGGGTGGCACCACATGTC 360

QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysSerLysLeu 140
|||||
Db 361 CTCCTGGGCATCATCGGAACTCCACGGTCATCTTGGCGGTCTGGAAGAAGTCCAAAGT 420

QY 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeu 160
|||||

Db 421 CACTGTGCAACAAGTCCCGACATCTTCATCATCAACCTCTCGGTAGATCTCCTC 480
QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180
Db 481 TTTCTCTCGGGCATGCCCTTCATGATGCACACGACTCATGGGCAATGGGTGTGGCAGCTTT 540
QY 181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
Db 541 GGGGAGACCATGTGCACCCCTCATGCAGGCCCATGGATGCCAATAGTCAATTCCACCAGCAC 600
QY 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220
Db 601 TACATCCTGACCCGCGCATGGCCATGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC 660
QY 221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer 240
Db 661 ACGAAGTTCGCGAAGCCCTCTGTGGCCACCCCTGGTGAATCTGCCTCCGTGGGCCCTCTCC 720
QY 241 PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla 260
Db 721 TTCAATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCACGAGAGGTGCA 780
QY 261 ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr 280
Db 781 GTGGGCTGGCGCATACGCCCTGCGCCAACCCAGACACTGACCTCTACTGTTCAACCTGTAC 840
QY 281 GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle 300
Db 841 CAGTTTTCCTGGCCTTGGCCTTGGCTTGTGTATCATCACAGCCGATACGTGAGGATC 900
QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
Db 901 CTGCAGCGCATGACGTCCTCAAGTGGCCCGCCGCTCCAGCGCAGCATCCGCGTGGGAGACA 960
QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro 340
Db 961 AAGAGGGTGACCCGACACAGCATGCCATCTGTGCTCTTCTTGTGTGCTGGCCACCC 1020
QY 341 TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
Db 1021 TACTATGTGCTACAGCTGACCCAGTGTTCATCAGCCCGCCGACCTCACCCTTTGTCTAC 1080
QY 361 LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr 380
Db 1081 TTAATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGACTGCCCTCAACCCCTTTGTGTAC 1140
QY 381 IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln 400
Db 1141 ATCGTCTCTGTGAGACGTTCCGCCAAACGCTTGCTCTGTGGTGAAGCCTGTCAGCCAG 1200
QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGlnSerLys 420
Db 1201 GGGCAGCTTCGCGCTGTCAACGCTCAGACGCGCTGACGAGAGAGACAGAAAGCAAA 1260
QY 421 GlyThr 422
Db 1261 GGCACC 1266
RESULT 6
ID AAA72918 standard; cDNA; 1275 BP.
AC AAA72918;
XX 22-NOV-2000 (first entry)
DE Human SLC-1 cDNA sequence SEQ ID NO:10.
XX
KW SLC-1; MHC; melanin concentrating hormone; screening; eating;
KW appetite stimulator; appetite regulator; period pain; atonic bleeding;
KW caesarean section; milk congestion; antiobestic agent; drug;
KW foetal asphyxia; cervical rupture; premature birth; uterine rupture;
KW Prader-Willi syndrome; anorectic; gynaecological; abortifaciant;

KW antoanaemia; anabolic; orphan G protein-couple receptor protein; ss.
XX
OS Homo sapiens.
XX
PN WO200040725-A1.
XX
PD 13-JUL-2000.
XX
PF 27-DEC-1999; 99WO-JP07336.
XX
PR 28-DEC-1998; 98JP-0374454.
PR 28-APR-1999; 99JP-0122688.
PR 02-SEP-1999; 99JP-0249300.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Mori M, Shimomura Y, Takekawa S, Sugo T, Ishibashi Y, Kitada C;
PI Suzuki N;
XX
DR WPI: 2000-475832/41.
DR P-PSDB; AAB12779.

Screening methods for compounds as SLC-1 (ant)agonists useful in the treatment of eating disorders and as preventives and remedies for e.g. atonic bleeding and Prader-Willi syndrome

Example 8; Page 110-111; 123pp; Japanese.

The present invention describes a method for screening components (I) or their salts that can alter the binding properties of melanin-concentrating hormone (MCH) or its derivative or salt to SLC-1 or its salt. Compounds identified by (I) are useful as SLC-1 (ant)agonists in eating disorders and as preventives and remedies for e.g. period pains, uterine recovery failure, caesarean section, artificial interruption of pregnancy, galactostosis, tonic uterine contraction, foetal asphyxia, CC rupture of uterus, cervical rupture, premature birth and Prader-Willi CC syndrome. The present sequence represents the human SLC-1 cDNA sequence, CC which is used in an example from the present invention.

XX SQ Sequence 1275 BP; 235 A; 420 C; 350 G; 270 T; 0 other;

Alignment Scores:
Pred. No.: 1.99e-184 Length: 1275
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 21 Gaps: 0

US-09-885-478-2 (1-422) x AAA72918 (1-1275)

QY 1 MetSerValGlyAlaMetLysIysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
Db 7 ATGTCAAGTGGGAGCCATGAAGAAGGAGAGTGGGAGGCGCAGTTGGCTTGAGGCGGCAGC 66
QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
Db 67 GCGTGGCAGGCTACGGAGGAGAGACCCCTTCCCAACTGCGGGGGCTTGCGCTCCGGACAA 126
QY 41 GlyGlyArgArgTyrPargLeuProGlnProAlaTrpValGlyGlySerSerAlaArgLeu 60
Db 127 GGTGGCAGGCGCTGAGGCTGCGCCGACGCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTTG 186
QY 61 TrpGluGlnAlaThrGlyThrGlyTyrMetAspLeuGluAlaSerLeuLeuProThrGly 80
Db 187 TGGGAGCAGCGGACCGGACCTGGATGGACCTGGAAGCCTCGCTGCCCACTGGT 246
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
Db 247 CCCAAGCGCAGCAACACCTGTGATGGCCCCGATACCTCACTTCGCGACGATCACCTCCT 306
QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120

Db 307 CGCAGCGGAGCATCTCCTACATCAACATCATGCGCTTCGGTGGCCACCATCTGC 366

QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysSerLysLeu 140

Db 367 CTCCTGGGCATCATCGGAACCTCCACGGTCACTCTCGCGGTGTAAGAAGTCCAAGCTG 426

QY 141 HistPcYsAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160

Db 427 CACTGGTGCAACACAGCTCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTC 486

QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180

Db 487 TTTCTCCTGGGCATGCGCTTCATGATCCACCACTCATGGGCAATGGGTGTGGCACTTT 546

QY 181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200

Db 547 GGGGAGACCATGTGCACCTCATCACGGCCATGATGCCAATAGTCAGTTCAACACGACACC 606

QY 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220

Db 607 TACATCCTGACCGCCATGCGCATGTGACCGCTACCTGAGCCACTGTCCACCCCATCTCTCC 666

QY 221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer 240

Db 667 ACGAAGTTCGCGAAGCCCTCTGTGGCCACCCCTGTGATCTGCCCTCTGTGGGCCCTCTCC 726

QY 241 PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla 260

Db 727 TTGATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGCA 786

QY 261 ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr 280

Db 787 GTGGGCTCGGGCATACGCCCTGCCCAACCCAGACACTGACCTTACTGTGTCACCCCTGTAC 846

QY 281 GlnPhePheLeuAlaPheAlaLeuProPheValIleThrAlaAlaTyrValArgIle 300

Db 847 CAGTTTTCCTGGCCTTGGCTGCTGCTTTTGTGTGTCATCACAGCCGCATACGTGAGGATC 906

QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320

Db 907 CTGCAAGCATGACGTCTCTCAGTGGCCCCCGCCTCCAGCGCAGCATCCGGGTGGGACA 966

QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro 340

Db 967 AAGAGGTGACCCCGCACAGCCATCGCCATCTGTCTGTCTTCTTGTGTGGGCCACCC 1026

QY 341 TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360

Db 1027 TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCGACCCCTCACCTTGTCTAC 1086

QY 361 LeuTyrAsnAlaAlaIleSerIleGlyTyrAlaAsnSerCysLeuAsnProPheValTyr 380

Db 1087 TTATACATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTGTGTAC 1146

QY 381 IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaIleGln 400

Db 1147 ATCGTCTCTGTGAGACGTTCCGCAACGCTTGGTCTGTGCGGTGAAGCCTGCAGCCACG 1206

QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGlnSerLys 420

Db 1207 GGGCAGCTTCGCGCTGTACAGCAACCTCAGACGGCTGACGAGAGAGACAGAAAGCAAA 1266

QY 421 GlyThr 422

Db 1267 GGCACC 1272

RESULT 7

AAF86229

ID AAF86229 standard; cDNA; 1275 BP.

XX

AC AAF86229;

XX

DT 05-JUL-2001 (first entry)

XX DE Human melanin concentrating hormone receptor (SLC-1) cDNA.

XX KW Melanin concentrating hormone; MCH; antagonist; diamine compound;

KW anorectic; antidiabetic; ophthalmological; neuroprotective; nephrotropic;

KW antiarteriosclerotic; antiarthritic; obesity; diabetes; arteriosclerosis;

KW arthritis; melanin concentrating hormone receptor; SLC-1; human; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 7..1275

FT /*tag= a

FT /product= "SLC-1"

FT /note= "Melanin concentrating hormone receptor"

XX WO200121169-A1.

XX PD 29-MAR-2001.

XX PF 19-SEP-2000; 2000WO-JP06376.

XX PR 20-SEP-1999; 99JP-0266278.

PR 17-JUL-2000; 2000JP-0221055.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Kato K, Mori M, Suzuki N, Shimomura Y, Takekawa S, Choh N;

XX DR WPI; 2001-328055/34.

DR P-PSDB; AAB81123.

XX PT Melanin concentrating hormone antagonists comprise new and known

PT diamine compounds for treating obesity

XX PS Examples; Page 271-273; 284pp; Japanese.

XX CC This invention relates to melanin concentrating hormone (MCH)

CC antagonists, comprising a diamine compound or its prodrug and/or salt.

CC use of the MCH antagonists can result in anorectic, antidiabetic,

CC ophthalmological, neuroprotective, nephrotropic, antiarteriosclerotic,

CC and antiarthritic activity. Melanin concentrating hormone (MCH)

CC antagonists can be used for treating obesity (e.g. exogenous obesity,

CC hypophyseal adiposity, hypothalamic obesity and hyperphagia) and

CC associated disorders such as diabetes, diabetic complications (such as

CC diabetic retinopathy, diabetic neuropathy and diabetic nephropathy),

CC arteriosclerosis and arthritis in the knees. The present sequence

CC represents human cDNA encoding melanin concentrating hormone receptor

CC (SLC-1). The SLC-1 cDNA is used in examples to demonstrate the use of the

CC antagonists of the invention.

XX SQ Sequence 1275 BP; 235 A; 420 C; 350 G; 270 T; 0 other;

Alignment Scores:

Pred. No.: 1.99e-184 Length: 1275

Score: 2207.00 Matches: 421

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.76% Mismatches: 0

Query Match: 99.77% Indels: 0

DB: 22 Gaps: 0

US-09-885-478-2 (1-422) x AAF86229 (1-1275)

QY 1 MetSerValGlyAlaMetLysLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20

Db 7 ATGTCAGTGGAGCCATGAAGAAGGAGTGGGAGGCGAGTTGGCTTGAGGCGGACGC 66

QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40

Db 67 GGCTGCCAGGCTACGAGGAAGACCCCTTCCCACTGCGGGGCTTGCCTCGGACAA 126

QY 41 GlyGlyArgArgTPrpArgLeuProGlnProAlaTrpValGlySerSerAlaArgLeu 60

Db 127 GGTGGCAGGCGCTGGAGGCTGCCGACGCTGCCGTGGTGGAGGGAGCTCAGCTCGGTTG 186
QY 61 TrpGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly 80
Db 187 TGGGAGCAGGCGACCGGCACTGCTGGATGGACCTGGAAGCCTCGCTGCGCCACTGGT 246
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
Db 247 CCCAAGCGCAGACACACCTCTGATGGCCCCGATAACCTCACTCGGCAGACGATCACCTCT 306
QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
Db 307 CGCAGCGGGAGCATCTCTCATCATCATCATGCTTCGGGTGTCGGACCACTCTGC 366
QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValAllyLysSerLysLeu 140
Db 367 CTCCTGGGCATCATCGGGAACCTCCACGGTCATCTTCGGGTCGTGAAGAAGTCCAACTG 426
QY 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160
Db 427 CACTGGTGCAACAACGCTCCCGACATCTTCATCATCAACCTCTCGGTAGATCTCTC 486
QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180
Db 487 TTTCTCTGGGCAATGCCCTTCATGATGATCAACAGCTCATGGGCAATGGGGGTGTGGCACTTT 546
QY 181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
Db 547 GGGGAGACCATGTGCACCCCTCATCACGGCCATGGATGCCAATATGTCAGTTCCACCAGACC 606
QY 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220
Db 607 TACATCTGACCCGCGCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC 666
QY 221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer 240
Db 667 ACGAAGTTCGGGAAGCCCTCTGTGGCCACCCCTGGTGAATCTGCTCTGTTGGGCCCTCTCC 726
QY 241 PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla 260
Db 727 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCACAGGAGGTGA 786
QY 261 ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr 280
Db 787 GTGGGCTGCGGCAATAGCCTGCCCCAACCCAGACACTGACCTTACTGTTACCCCTGTAC 846
QY 281 GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle 300
Db 847 CAGTTTTCCTGGCCTTGGCCCTGCTTGTGTGTCATCACAGCGCATACGTGAGATC 906
QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
Db 907 CTGCAGCGCATGACGTCTCAGTGGCCCCGCTCCAGCGCAGCATCCGGCTGGCGACA 966
QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro 340
Db 967 AAGAGGGTGACCCGCAACGCCATCGCCATCTGTCTTCTTGTGTGCTGGGCACCC 1026
QY 341 TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
Db 1027 TACTATGTGCTACAGCTGACCCAGTTGTCTCATCAGCCGCCCGACCTTGTGTAC 1086
QY 361 LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr 380
Db 1087 TTATACATGCGGCCATCAGCTTGGGTATGCCAACAGCTGCTCAACCCCTTGTGTAC 1146
QY 381 IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln 400
Db 1147 ATCGTGTCTGTGAGAGCTTCCGCAAAACGCTTGGTCTGTGGTGAACCTGACAGCCCA 1206
QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluArgThrGluSerLys 420
Db 1207 GGGCAGCTTGGCGCTGTACGAACAGCTCAGACGGCTGACGAGAGAGACAGAAAGCAAA 1266

QY 421 GlyThr 422
Db 1267 GGCACC 1272
RESULT 8
AAF86975
ID AAF86975 standard; cDNA; 1275 BP.
XX
AC AAF86975;
DT 06-JUL-2001 (first entry)
XX
DE Human SLC-1 coding sequence #1.
XX
KW Rat; human; SLC-1; MCH receptor; melanin-concentrating hormone;
KW obesity; diabetes; hypertension; arteriosclerosis; hyperphagia;
KW emotional disorder; reproductive disorder; memory disorder;
KW dementia; hormonal disorder; gonitis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..1275 /*tag= a /product= "SLC-1"
FT
XX
PN W0200121577-A2.
XX
PD 29-MAR-2001.
XX
PE 19-SEP-2000; 2000WO-JP06375.
XX
PR 20-SEP-1999; 99JP-0266298.
PR 16-DEC-1999; 99JP-0357889.
PR 20-APR-2000; 2000JP-0126272.
XX
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Kato K, Terauchi J, Mori M, Suzuki N, Shimomura Y, Takekawa S;
PI Ishihara Y;
XX
DR WPI; 2001-354775/37.
DR P-PSDB; AAB96871.
XX
PT New aromatic compounds are melanin concentrating hormone antagonists,
PT useful as anorectic agents, for treating or preventing obesity, also
PT memory or hormonal disorders or diabetes
XX
PS Examples; Page 357-358; 363pp; English.
XX
CC The present invention describes aromatic compounds capable of acting as
CC melanin-concentrating hormone (MCH) antagonists. Melanin-concentrating
CC hormone is an appetite control factor and antagonists were expected to be
CC useful as anti-obesity agents. They can be used in the treatment of
CC obesity, including malignant mastocytosis, exogenous, hyperinsular,
CC hypoplasmic, hypothyroid, hypothalamic, symptomatic, infantile, upper
CC body, alimentary, hypogonadal, simple and central obesity, systemic
CC mastocytosis and hypophyseal adiposity, hypertension, arteriosclerosis,
CC hyperphagia, emotional disorders, reproductive function disorders, memory
CC disorders, dementia, hormonal disorders, diabetes and gonitis. MCH binds
CC to the SLC-1 receptor. The present sequence is a version of the human
CC SLC-1 coding sequence given in the specification.
XX
SQ Sequence 1275 BP; 235 A; 420 C; 350 G; 270 T; 0 other;

Alignment Scores:
Pred. No.: 1.99e-184 Length: 1275
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 22 Gaps: 0

US-09-885-478-2 (1-422) x AAF86975 (1-1275)

QY	1	MeISerValGlyAlaMetLysLysGlyValGlyArgAlaValGlyLeuGlyGlySer	20
Db	7	ATGTCAAGTGGAGCCATGAAGAAGGAGTGGGAGAGGGCAGTTGGGCTTTGGAGCGGCACG	66
QY	21	GlyCysGlnAlaThrGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln	40
Db	67	GGCTGCAGGCGTACGAGGAAGAACCCCTTCCCAACTGCGGGGCTTGGCCTCCGGGACAA	126
QY	41	GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGlyGlySerSerAlaArgLeu	60
Db	127	GGTGGCAGGCGCTGGAGGCTGCCGAGCCTGCTGGGTGGAGGGAGCTCAGCTCGGTTG	186
QY	61	TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly	80
Db	187	TGGGAGCAGCGCAGCCGCACTGGCTGGATGGAAGCCCTCGCTGCGCCCACTGGT	246
QY	81	ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro	100
Db	247	CCCAACGCCAGCAACACCTCTGATGGCCCCGATAACTCACTTCGCGCAGATCACTCCT	306
QY	101	ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys	120
Db	307	CGCACGGGAGCATCTCTACATCAACATCATCATGCCCTCGGTGTTGCGGACCATCTGC	366
QY	121	LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysSerLysLeu	140
Db	367	CTCTGGGCATCATCGGGAACCTCCACGGTCACTTCGCGGTGAGAGAAGTCCAAGCTG	426
QY	141	HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu	160
Db	427	CACGTGGTCAACACAGTCCCGGACATCTTCATCATCAACCTCTCGGTAGTAGTCTCCTC	486
QY	161	PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe	180
Db	487	TTTCTCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGCTGTGGCATT	546
QY	181	GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerglnPheThrSerThr	200
Db	547	GGGGAGACCATGTGCACCCCTCATCAACGGCCATGGATGCAATAGTCAATTACACGACCC	606
QY	201	TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer	220
Db	607	TACATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC	666
QY	221	ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer	240
Db	667	ACGAAGTTCGGAAGCCCTGTGGGCCAACCTGGTGATCTGCCCTCTGTGGGCCCTTCC	726
QY	241	PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla	260
Db	727	TTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCACGAGAGTGCA	786
QY	261	ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr	280
Db	787	GTTGGGCTGGGGCATACGCCCTGCCAACCCAGACACTGACCCTTACTGGTTACACCCCTGAC	846
QY	281	GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle	300
Db	847	CAGTTTTCCTGGCCCTTTGGCCCTGCTTTTGTGTCATCACAGCCGCATACGTAGAGATC	906
QY	301	IeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr	320
Db	907	CTGCAGCGCATGACGTCTCAGTGGCCCCGCCCTCCAGCGCAGCATCCGGCTGGGACA	966
QY	321	LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro	340
Db	967	AAGAGGGTGACCCGACAGCCATCGCCATCTGTCTGTCTTCTTGTGTGCTGGGCACCC	1026
QY	341	TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr	360

Db	1027	TACTATGTGCTACAGCTGACCCAGTTGTTCATCAGCCGCCGACCCCTCACCCTTTGTCTAC	1086
QY	361	LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr	380
Db	1087	TTATACAATGCGGCATCATCAGCTTGGGCTATGCCAAACAGCTGCCTCAACCCCTTTGTGTAC	1146
QY	381	IleValLeuCysGluThrPheArgIlyAsrGluValLeuSerValIysProAlaIleGln	400
Db	1147	ATCGTGCTGTGTAGACGTTCCGCAAAAGCTTGGTCTGTGCTGGTGAAGCCTGCAGCCACAG	1206
QY	401	GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGluSerLys	420
Db	1207	GGGACAGCTTCGGCGCTGTACAGCAACGCTCAGACGCGCTGCAGAGAGAGACAGAAAGCAAA	1266
QY	421	GlyThr 422	
Db	1267	GGCACC 1272	
RESULT 9			
ABK10854			
ID	ABK10854	standard; DNA; 1275 BP.	
XX	AC	ABK10854;	
XX	DT	05-JUN-2002 (first entry)	
XX	DE	DNA encoding human melanin concentrating hormone receptor, SLC-1.	
XX	KW	G protein-coupled orphan; receptor; SLT; melanin-concentrating hormone;	
KW	KW	MCH; appetite-stimulating agent; obesity; malignant mastocytosis;	
KW	KW	exogenous obesity; hyperinsular obesity; sexual function disorder;	
KW	KW	overpowering intermittent pain; still born; uterus rupture;	
OS	OS	premature birth; Prader-Willi syndrome; SLC-1; human; gene; ds.	
XX	XX	Homo sapiens.	
FH	Key	Location/Qualifiers	
FT	CDS	7..1275	
FT		/*tag= a	
FT		/product= "SLC-1"	
FT		/note= "Melanin concentrating hormone receptor"	
XX	XX	WO200203070-A1.	
XX	PD	10-JAN-2002.	
XX	PF	04-JUL-2001; 2001WO-JP05809.	
XX	PR	05-JUL-2000; 2000JP-0208254.	
XX	PA	(TAKE) TAKEDA CHEM IND LTD.	
XX	PI	Mori M, Shimomura Y, Harada M, Sugo T, Shintani Y;	
XX	DR	WPI; 2002-164552/21.	
XX	DR	P-PSDB; AAU77541.	
PT	PT	Screening for compounds or salts which alter affinity of	
PT	PT	melanin-concentrating hormone with its receptor to provide agonists as	
PT	PT	appetite-stimulating agents and its antagonist for preventing or	
PT	PT	treating obesity, uses a protein or hormone	
XX	PS	Disclosure; Page 106-107; 112pp; Japanese.	
XX	CC	The invention describes a method of screening for compounds or their	
XX	CC	salts that can change affinity of melanin-concentrating hormone (MCH)	
XX	CC	with its G protein-coupled orphan receptor protein, SLT. The screened	
XX	CC	MCH receptor agonists are useful as appetite-stimulating agents and its	
XX	CC	antagonist for preventing or treating obesity e.g. malignant	
XX	CC	mastocytosis, exogenous obesity and hyperinsular obesity, and also	
XX	CC	for treating sexual function disorders, overpowering intermittent pains,	
XX	CC	still borns, uterus rupture, premature birth and Prader-Willi syndrome.	
XX	CC	This sequence encodes the human melanin concentrating hormone SLC-1,	

CC described in the invention.

XX Sequence 1275 BP; 235 A; 420 C; 350 G; 270 T; 0 other;

Alignment Scores:

Pred. No.: 1.99e-184 Length: 1275
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 24 Gaps: 0

US-09-885-478-2 (1-422) x ABK10854 (1-1275)

QY 1 MetSerValGlyAlaMetLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
Db 7 ATGTACGTGGAGCCATGAGAAGAGAGAGTGGGAGGGCAGTTGGCTTGGAGCGGACG 66
QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
Db 67 GGCTGCCAGGCTACGAGAGAAGACCCCTTCCCACTGCGGGCTTGGCTCCGGACAA 126
QY 41 GlyGlyArgArgTrrArgLeuProGlnProAlaTrrValGlyGlySerSerAlaArgLeu 60
Db 127 GGTGGCAGGCGCTGAGGCTGCCGACGCTGCGTGGGTGGAGGGAGCTCAGCTCGTTG 186
QY 61 TrrGluGlnAlaThrGlyThrGlyTrrMetAspLeuGluAlaSerLeuLeuProThrGly 80
Db 187 TGGAGCAGGCGACCGGACCTGGCTGGATGGACCTGGAAGCCTCGCTGCTGCCACTGGT 246
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
Db 247 CCCAAGCCAGCAACACACTCTGATGGCCCCGATTAACCTTCCGTCGACGATCACCTCTCT 306
QY 101 ArgThrGlySerIleSerTrrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
Db 307 CGCAGGGGAGCATCTCTACATCAACATCATCATGCTTCGGTGTTCGGCACCATCTGCTGC 366
QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeu 140
Db 367 CTCTGGGCATCATCGGGAAGCTCCACGGTCACTTTCGGGTGTAAGAGAAGTCCAAAGCTG 426
QY 141 HistrrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160
Db 427 CACTGGTGCACAACAGCTCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTCTC 486
QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrrPHisPhe 180
Db 487 TTTCTCTGGGCATGCCCTTCATGATCCACCAAGCTCATGGGCAATGGGTGTGGCACCTTT 546
QY 181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
Db 547 GGGGAGACCATGTGCACCTCATCACGGCCATGGATGCCAATAGTCAGTTCAACCAGCACCC 606
QY 201 TyrIleLeuThrAlaMetAlaIleAspArgTrrLeuAlaThrValHisProIleSerSer 220
Db 607 TACATCTTGACCGCCATGGCCATTGACCGCTGACCTGGCCACTGTCCACCCCATCTCTTCC 666
QY 221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrrPalalaLeuSer 240
Db 667 ACGAAGTTCGGGAAGCCCTGTGTGGCCACCCCTGGTGAATCTGCTCTGTGGGCCCTCTCC 726
QY 241 PheIleSerIleThrProValTrrPheuTrrPheuTrrPheuIleProPheProGlyGlyAla 260
Db 727 TTTATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGGTGCA 786
QY 261 ValGlyCysGlyIleArgLeuProAsnProAspTrrAspLeuTrrPrrPheThrLeuTyr 280
Db 787 GTGGGCTGGCGCATACGCTTGGCCCAACCCAGACACTGACCTTACTGTTCACCCCTGTAC 846
QY 281 GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle 300
Db 847 CAGTTTTCCTGGCCTTGGCCTTGGCCTTTCGTGTCATCACAGCCGCAATACGTGAGGATC 906

QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
Db 907 CTGCAGCGCATGACGTCTCAGTGGCCCCCGCCTCCCAAGCGCAGCATCCGGCTGGGACA 966
QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrrPalapro 340
Db 967 AAGAGGTGACCCCGCACAGCCATCGCCATCTGTCTGTCTTTGTGTGTGGCACACC 1026
QY 341 TyrTrrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
Db 1027 TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCCGCCGACCCCTCACCCTTGTCTAC 1086
QY 361 LeuTrrAsnAlaAlaIleSerLeuGlyTrrAlaAsnSerCysLeuAsnProPheValTyr 380
Db 1087 TTATACAATGCCGCCATCAGCTTGGGCTATGCCAACAGCTGCTCAACCCCTTGTGTAC 1146
QY 381 IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln 400
Db 1147 ATCGTCTCTGTGAGACGTTCCGCAACGCTTGTGCTGTGGTGAAGCCTGCAGCCACG 1206
QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGluSerLys 420
Db 1207 GGGCAGCTTCGGCTGTGCAGCAACGCTCAGACGGCTGACGAGAGAGACAGAAAGCAAA 1266
QY 421 GlyThr 422
Db 1267 GGCACC 1272

RESULT 10
ABA92411
ID ABA92411 standard; cDNA; 1275 BP.
XX AC ABA92411;
XX DT 14-MAR-2002 (first entry)
XX DE Human SLC-1 encoding cDNA SEQ ID NO:8.
XX KW Human; SLC-1; melanin concentrating hormone antagonist; obesity;
KW anorectic; antidiabetic; hypotensive; antiarteriosclerotic;
KW diabetes; hypertension; arteriosclerosis; ss.
XX OS Homo sapiens.
XX FH Key
FH CDS Location/Qualifiers
FT 7..1275 /*tag= a
FT /product= "SLC-1"
XX PN WO200182925-A1.
XX PD 08-NOV-2001.
XX PF 26-APR-2001; 2001WO-JP03614.
XX PR 28-APR-2000; 2000JP-0134295.
PR 13-DEC-2000; 2000JP-0384897.
XX PA (TAKE) TAKEDA CHEM IND LTD.
XX PI Ishihara Y, Suzuki N, Takekawa S;
XX DR WPI; 2002-075131/10.
DR P-PSDB; ABB04941.
XX PT Melanin aggregating hormone antagonist for treating obesity -
XX PS Example; Page 209-210; 223pp; Japanese.
XX CC The present invention describes a melanin aggregating hormone antagonist
CC (I). (I) has anorectic, antidiabetic, antiarteriosclerotic and
CC hypotensive. (I) can be used in the treatment and prevention of obesity.

CC It may be combined with treatments for diabetes, hypertension or
arteriosclerosis. The present sequence encodes human SLC-1, which is
used the exemplification of the present invention.

XX Sequence 1275 BP; 235 A; 420 C; 350 G; 270 T; 0 other;

Alignment Scores:

Pred. No.:	1.99e-184	Length:	1275
Score:	2207.00	Matches:	421
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.76%	Mismatches:	0
Query Match:	99.77%	Indels:	0
DB:	24	Gaps:	0

US-09-885-478-2 (1-422) x ABA92411 (1-1275)

QY	1	MetSerValGlyAlaMetLysLysGlyValGlyArgAlaValGlyLeuGlyGlySer	20
DB	7	ATGTCAGTGGAGCCATGAAGAAGGAGTGGGAGGCGAGTGGCTTGAGGCGGACGC	66
QY	21	GlyCysGlnAlaThrGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln	40
DB	67	GGCTGCCAGGCTACGGAGGAAGACCCCTTCCCAACTGCGGGGCTTGCGGACAA	126
QY	41	GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGlyGlySerSerAlaArgLeu	60
DB	127	GGTGGCAGGGCGTGAGGCTGCCGAGCCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTTG	186
QY	61	TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly	80
DB	187	TGGGAGCAGGCGACCGGCACTGGCTGGATGAGCTGGAAGCCTCGCTGCTGCCACTG	246
QY	81	ProAsnAlaSerAsnTrpSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro	100
DB	247	CCCAACGCCAGCAACACCTCTGATGGCCCCGATTAACCTCACTTCGGCAGATCACCTCT	306
QY	101	ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys	120
DB	307	CGCAGCGGGAGCATCTCCTACATCAACATCATGCTTCGGTGTTCGGACCATCTGC	366
QY	121	LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeu	140
DB	367	CTCCTGGGCATCATCGGAACTCCACGGTCACTTCGCGGTCGTGAAGAAATCCAAAGCTG	426
QY	141	HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu	160
DB	427	CACCTGGTGCACAACAACGTCCTCCGACATCTCATCATCAACCTCTCGTAGTGAATCTCCTC	486
QY	161	PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe	180
DB	487	TTTCTCTCTGGGCATGCCCCCTTCATGATCCACACGCTCATGGGCAATGGGCTGTGGCACTTT	546
QY	181	GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr	200
DB	547	GGGAGACCATGTGCACCCCTCATCAACGGCCATGGATGCCAATAAGTCAATCACACGACAC	606
QY	201	TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer	220
DB	607	TACATCCTGACCGCCATGGCCATGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC	666
QY	221	ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer	240
DB	667	ACGAAGTTCGGGAAGCCCTCTGTGGCCACCCCTGGTGAATGCTCCTCGTGGGCCCTCTCC	726
QY	241	PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla	260
DB	727	TTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGGTGCA	786
QY	261	ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr	280
DB	787	GTGGGCTGGCGCATACGCTGCCCAACCCAGACACTGACCTTACTGTTCAACCTGTAC	846
QY	281	GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle	300

DB	847	CAGTTTTCCTGGCCCTTGCCCTTGCCCTTTGTGGTCATCACAGCCGCATACGTGAGGATC	906
QY	301	LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr	320
DB	907	CTGCAGCGCATGAGCTCCTCAGTGTGGCCCCCGCTCCACAGCGACGATCCGGCTGCGGACA	966
QY	321	LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro	340
DB	967	AAGAGGGTGAACCCGACAGCCATCGCCATCTGCTGTCTTCTTGTGTGCTGGACACC	1026
QY	341	TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr	360
DB	1027	TACTATGTGTACAGCTGACCCAGTTGTCATCAAGCCGCCGACCTCACCCTTGTCTAC	1086
QY	361	LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr	380
DB	1087	TTATACAATGCGGCCATCAAGCTTGGCTATGCCAACAAGCTGCCTCAACCCCTTGTGTAC	1146
QY	381	IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln	400
DB	1147	ATCGTGCTCTGTGAGACGTTCCGCAACGCTTGTCCTGTGGTGAAGCCTGCAGCCACG	1206
QY	401	GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGlnSerLys	420
DB	1207	GGGCAAGCTTGGCGCTGTCAACAAGCTCAGACGGCTGACGAGAGAGACAGAAAGCAAA	1266
QY	421	GlyThr 422	
DB	1267	GGCACC 1272	
RESULT 11			
AAI69442			
ID	AAI69442 standard; DNA; 1275 BP.		
XX	AAI69442;		
AC			
XX			
DT	28-FEB-2002 (first entry)		
XX			
DE	Human SLC-1 cDNA.		
XX			
KW	SLC-1; melanin-concentrating hormone antagonist; anorectic; depression;		
KW	antidiabetic; hypotensive; antiarteriosclerotic; antilipemic; obesity;		
KW	antiarthritic; antidepressant; tranquilizer; malignant mastocytosis;		
KW	hypophyseal adiposity; hypothyroid obesity; hyperphagia; diabetes;		
KW	hypertension; arteriosclerosis; hyperlipidaemia; arthritis; anxiety;		
XX	human; ss.		
OS	Homo sapiens.		
XX			
FH	Key		
FT	CDS		
FT	7.1275		
FT	/*tag= a		
FT	/product= "SLC-1"		
XX	WO200187834-A1.		
PN			
XX			
PD	22-NOV-2001.		
XX			
PF	15-MAY-2001; 2001WO-JP04015.		
XX			
PR	16-MAY-2000; 2000JP-0148674.		
XX			
PR	13-APR-2001; 2001JP-0116219.		
XX			
PA	(TAKE) TAKEDA CHEM IND LTD.		
XX			
PI	Ishihara Y, Terauchi J, Suzuki N, Takekawa S, Aso K;		
XX			
DR	WPI; 2002-055668/07.		
DR	P-PSDB; AAG80611.		
XX			
PT	Use of new and known amine derivatives as melanin concentrating hormone		
PT	antagonists for treating e.g. obesity, diabetes, hypertension and		

PT arteriosclerosis -
XX
PS Disclosure; Page 251-252; 283pp; Japanese.
XX
CC This invention describes a novel use of an amine derivative (I) as a
CC melanin concentrating hormone antagonist which has anorectic,
CC antidiabetic, hypotensive, antiarteriosclerotic, antilipemic,
CC antiarthritic, antidepressant and tranquilliser activity. The products of
CC the invention can be used as melanin concentrating hormone antagonists
CC for treating and preventing obesity (including malignant mastocytosis,
CC hypophyseal adiposity, hypothyroid obesity, infantile obesity and
CC hyperphagia), diabetes, hypertension and arteriosclerosis as well as
CC diabetic complications, hyperlipidaemia, arthritis, depression and
CC anxiety. This sequence encodes the human melanin-concentrating hormone
CC SLC-1 gene described in the method of the invention.
XX
SQ Sequence 1275 BP; 235 A; 420 C; 350 G; 270 T; 0 other;

Alignment Scores:
Pred. No.: 1.99e-184 Length: 1275
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 24 Gaps: 0

US-09-885-478-2 (1-422) x AAI69442 (1-1275)
QY 1 MetSerValGlyAlaMetLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
Db 7 ATGTCAGTGGAGCCATGAAGAAGGAGTGGGAGGGCAGTTGGGCTTGAGAGCGGCACG 66
QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
Db 67 GGCTGCCAGGCTACGAGAGAACCCCTTCCCACTGCGGGGCTTGCGCTCCGGGACAA 126
QY 41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGlyGlySerSeraIaArgLeu 60
Db 127 GGTGGCAGGGCGCTGGAGGCTGCGCAGCCTGCGTGGTGGAGGGGAGCTCAGCTCGGTTG 186
QY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly 80
Db 187 TGGGAGCAGGCGACCGCACTGGCTGATGAGCTGAAGCCCTCGCTGCCCACTGCT 246
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
Db 247 CCCAACGCGCAGCAACACCTCTGATGGCCCCGATTAACCTCACTTCGCAGATCACCTCCT 306
QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
Db 307 CGCACGGGAGCATCTCTACATCAACATCATGCTTCGGTGTTCGGCACCATCTCTGC 366
QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeu 140
Db 367 CTCCTGGGCATCATCGGGAACCTCACCGGTCACTTCGCGGTGAAGATCCAAAGCTG 426
QY 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160
Db 427 CACTGGTGCAACAACGTCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTCCTC 486
QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180
Db 487 TTTCTCCTGGGCATGCCCTTCATGATCCACGACTCATGGGCAATGGGTGTGGCACTTT 546
QY 181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
Db 547 GGGGAGACCATGTGCACCTCATCAAGGCGCATGGATGCCAATAGTCAGTTCACCGACACC 606
QY 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220
Db 607 TACATCCTGACCGCGCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCC 666
QY 221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer 240

Db 667 ACGAAGTTCCGGAAGCCCTCTGTGGCCACCCCTGGTGAATCTGCCCTCCTGTGGGCCCTCTCC 726
QY 241 PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla 260
Db 727 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCACGAGGTGCA 786
QY 261 ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr 280
Db 787 GTGGGCTGGCGCATACGCCCTTGCCCAACCCAGACACTGACCTTACTGTTCACCCCTGTAC 846
QY 281 GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle 300
Db 847 CAGTTTTCCTGGCCTTTTGCCCTTGCCCTTTGTGTCATCACAGCCGCATACGTGAGGATC 906
QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
Db 907 CTGCAGCGCAWGAGCTCCTCAGTGGCCCCCGCCCTCCAGCGCAGCATCCGGCTGCGACA 966
QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro 340
Db 967 AAGAGGGTGACCCGCACAGCCATCGCCATCTGTCTGTCTTCTTGTGTGCTGGGCACCC 1026
QY 341 TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
Db 1027 TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCGCCCTCACCTTTGTCTAC 1086
QY 361 LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysIleAsnProPheValTyr 380
Db 1087 TTATACAATGCCGCCATCAGCTTGGGCTATGCCAACAGCTGCTCAACCCCTTGTGTAC 1146
QY 381 IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln 400
Db 1147 ATCGTGTCTGTGAGACGTTCCGCAACGCTTGGTCTGTGGTGAAGCCGTGCAGCCCA 1206
QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGluSerLys 420
Db 1207 GGGCAGCTTTCGCGCTGTGAGCAACGCTCAGACGCGTGAAGAGAGAGACAGAAAGCAA 1266
QY 421 GlyThr 422
Db 1267 GGCACC 1272

RESULT 12
AA72924
ID AAA72924 standard; cDNA; 1283 BP.
XX
AC AAA72924;
XX
XX
DT 22-NOV-2000 (first entry)
XX
DE Human SLC-1 (L) cDNA sequence SEQ ID NO:17.
XX
KW SLC-1; MHC; melanin concentrating hormone; screening; eating;
KW appetite stimulator; appetite regulator; period pain; atonic bleeding;
KW caesarean section; milk congestion; antioberstic agent; drug;
KW foetal asphyxia; cervical rupture; premature birth; uterine rupture;
KW Prader-Willi syndrome; anorectic; gynaecological; abortifaciant;
KW antoanaemia; anabolic; orphan G protein-couple receptor protein; ss.
XX
OS Homo sapiens.
XX
PN WO200040725-A1.
XX
PD 13-JUL-2000.
XX
PF 27-DEC-1999; 99WO-JP07336.
XX
PR 28-DEC-1998; 98JP-0374454.
PR 28-APR-1999; 99JP-0122688.
PR 02-SEP-1999; 99JP-0249300.
XX
PA (TAKE) TAKEDA CHEM IND LTD.

XX Mori M, Shimomura Y, Takekawa S, Sugo T, Ishibashi Y, Kitada C;
PI Suzuki N;
XX WPI: 2000-475832/41.
DR
XX Screening methods for compounds as SLC-1 (ant)agonists useful in the
PT treatment of eating disorders and as preventives and remedies for e.g.
PT atonic bleeding and Prader-Willi syndrome -
XX
PS Example 11; page 115-116; 123pp; Japanese.
XX
CC The present invention describes a method for screening components (I) or
CC their salts that can alter the binding properties of melanin-
CC concentrating hormone (MCH) or its derivative or salt to SLC-1 or its
CC salt. Compounds identified by (I) are useful as SLC-1 (ant)agonists in
CC eating disorders and as preventives and remedies for e.g. period pains,
CC uterine recovery failure, caesarean section, artificial interruption of
CC pregnancy, galactostosis, tonic uterine contraction, foetal asphyxia,
CC rupture of uterus, cervical rupture, premature birth and Prader-Willi
CC syndrome. The present sequence represents a human SLC-1 cDNA sequence,
CC which is used in an example from the present invention.
XX
SQ Sequence 1283 BP; 238 A; 423 C; 350 G; 272 T; 0 other;

Alignment Scores:
Pred. No.: 2.01e-184 Length: 1283
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 21 Gaps: 0

US-09-885-478-2 (1-422) x AAA72924 (1-1283)

QY 1 MetSerValGlyAlaMetIySgLyValGlyArgAlaValGlyLeuGlyGlySer 20
DB 8 ATGTCACTGGGAGCCATGAAAGAGGAGTGGGAGGGCAGTTGGCTTGAGCGGCAGC 67
QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
DB 68 GGCTGCCAGGCTACGGAGGAAGACCCCTTCCCAACTGCGGGCTTGCGCTCCGGAGCAA 127
QY 41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGluGlySerSerAlaArgLeu 60
DB 128 GGTGGCAGCGCTGGAGGCTGCCGAGCCTGCGTGGGTGGAGGGGAGGCTCAGCTCGGTTG 187
QY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly 80
DB 188 TGGAGCAGCGCAGACCGGACCTGCTGATGGAGCCTGGAACCTCGCTGCGCCACTGGT 247
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
DB 248 CCCAACGCCAGCAACACCTGTGATGGCCCCGATAACTCACTTCGGCAGGATCACTCCT 307
QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
DB 308 CGCACGGGGAGCATCTCTACATCAACATCATCATGCTTCGTTGTCGGACCACTGCG 367
QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValIySsSerIySleu 140
DB 368 CTCCTGGGCATCATCGGGAACCTCCACGGTCACTTCGCGGGTGTGAAGAAGTCCAGCTG 427
QY 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160
DB 428 CACTGGTGCAACAACGTCCCGACACTTCATCATCAACCTCTCGGTAGTAGATCTCTC 487
QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180
DB 488 TTTCTCTGGGCATGCCCTTCATGATCCACACGCTCATGGGCAATGGGTTGTGGCACTTT 547
QY 181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200

DB 548 GGGAGACCATGTGCACCCCTCATTCACGGCCATGGAATGCCAATAGTCAGTTTCACGACACC 607
QY 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220
DB 608 TACATCCTGACCGCCATGGCCATTTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC 667
QY 221 ThrIySPheArgIySProSerValAlaThrIleuValIleCysIleuLeuTrpAlaLeuSer 240
DB 668 ACGAGTTCGGAAGCCCTCTGTGGCCACCCCTGGTGAATCTGCCTCTGTGGGCCCTCTCC 727
QY 241 PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla 260
DB 728 TTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGCA 787
QY 261 ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr 280
DB 788 GTGGCTGGCGCATACGCGCTGCCCAACCCAGACACTGACCTTACTGGTTCACTGTAC 847
QY 281 GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle 300
DB 848 CAGTTTTCCTGGCCTTTGCTTGCCTTTTGTGTGATCATCAGCCGATACGTAGAGATC 907
QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
DB 908 CTGCAGCGCAWAGACGTCTCCTAGTGGCCCCCGCCCTCCAGCGCAGCATCCGGCTGGGACA 967
QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro 340
DB 968 AAGAGGTTGACCCCGCACAGCCATCGCCATCTGTCTGTCTTGTGTGTGGCACC 1027
QY 341 TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
DB 1028 TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCCGCCGACCCCTCACCCTTGTCTAC 1087
QY 361 LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr 380
DB 1088 TTATACATATCGGCCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTGTGTAC 1147
QY 381 IleValLeuCysGluThrPheArgIySArgLeuValLeuSerValIySProAlaIaGln 400
DB 1148 ATCGTGTCTGTGAGACGTTCCGCCAACGCTTGGTCTGTGCTGGAAGCCTGCAGCCAG 1207
QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGluSerIyS 420
DB 1208 GGGCAGCTTGGCGCTGTCAAGCAACGCTCAGACGGCTGACGAGAGAGACAGAAAGCAA 1267
QY 421 GlyThr 422
DB 1268 GGCACC 1273
RESULT 13
AAF86235
ID AAF86235 standard; cDNA; 1283 BP.
XX
AC AAF86235;
XX
DT 05-JUL-2001 (first entry)
XX
DE Human melanin concentrating hormone receptor (L) (SLC-1 L) related cDNA.
XX
KW Melanin concentrating hormone; MCH; antagonist; diamine compound;
KW anorectic; antidiabetic; ophthalmological; neuroprotective; nephrotropic;
KW antiarteriosclerotic; antiarthritic; obesity; diabetes; arteriosclerosis;
KW arthritis; melanin concentrating hormone receptor; SLC-1; human; ss.
XX Homo sapiens.
XX
OS
PN WO200121169-A1.
XX
XX 29-MAR-2001.
PD
XX
PF 19-SEP-2000; 2000WO-JF06376.
XX

PR 20-SEP-1999; 99JP-0266278.
PR 17-JUL-2000; 2000JP-0221055.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Kato K, Mori M, Suzuki N, Shimomura Y, Takekawa S, Choh N;
XX
DR WPI; 2001-328055/34.
XX
PT Melanin concentrating hormone antagonists comprise new and known
PT diamine compounds for treating obesity -
XX
PS Examples; Page 275-276; 284pp; Japanese.
XX
CC This invention relates to melanin concentrating hormone (MCH)
CC antagonists, comprising a diamine compound or its prodrug and/or salt.
CC Use of the MCH antagonists can result in anorectic, antidiabetic,
CC ophthalmological, neuroprotective, nephrotropic, antiarteriosclerotic,
CC and antiarthritic activity. Melanin concentrating hormone (MCH)
CC antagonists can be used for treating obesity (e.g. exogenous obesity,
CC hypophyseal adiposity, hypothalamic obesity and hyperphagia) and
CC associated disorders such as diabetes, diabetic complications (such as
CC diabetic retinopathy, diabetic neuropathy and diabetic nephropathy),
CC arteriosclerosis and arthritis in the knees. The present sequence
CC represents cDNA related to human melanin concentrating hormone receptor
CC (SLC-1). The sequence is used in examples demonstrating the use of the
CC antagonists of the invention.
XX
SQ Sequence 1283 BP; 238 A; 423 C; 350 G; 272 T; 0 other;

Alignment Scores:
Pred. No.: 2.01e-184 Length: 1283
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 22 Gaps: 0

US-09-885-478-2 (1-422) x AAF86235 (1-1283)

QY 1 MetSerValGlyAlaMetLysLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
Db 8 ATGTCA GTGGAGCCATGAAGAAGGAGTGGGAGGCGCAGTTGGGCTTGGAGGGCGCAGC 67
QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
Db 68 GGCTGCCAGGCTACGAGGAAGACCCCTTCCCAACTGCGGGCTTGCCTCCGGACAA 127
QY 41 GlyGlyArgArgTArgLeuProGlnProAlaTArgValGlyGlySerSerAlaArgLeu 60
Db 128 GGTGGCAGGCGCTGGAGGCTGCCGACCTGGGTGGGTGGAGGGGAGCTCAGCTCGGTG 187
QY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly 80
Db 188 TGGGAGCAGGCGGACCTGGCTGATGGCCCGATTAACCTCCTCCTGCTGCCCCACTGGT 247
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
Db 248 CCCAAGCCAGCAACACCTCTGATGGCCCGATTAACCTCCTCCTGCGGACGATCACCCTCT 307
QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
Db 308 CGCAGCGGGAGACATCTCTACATCAACATCATATGCTTCGGTTCGGCAGCATCTGC 367
QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValAlaLysLysSerLysLeu 140
Db 368 CTCCTGGGCATCATCGGGAACCTCCACGGTCACTTCGCGGTGTGAAGAAGTCCAAAGCTG 427
QY 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValAlaAspLeuLeu 160
Db 428 CACTGGGTGCAACAACGTCGCCGACATCTTCATCATCAACCTTCGGTAGATCTCCTC 487
QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180

Db 488 TTTCTCCTGGGCATGCCCTTCATGATGCCACCAGCTCATGGGCAATGGGTGTGGCACTTT 547
QY 181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
Db 548 GGGAGAGACCATGTGCACCCCTCATCATCAGGCCCATGTGATGCCAATAGTCAAGTCCAGCACC 607
QY 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220
Db 608 TACATCCTGACCCGCATATGGCCATGTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCC 667
QY 221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer 240
Db 668 ACGAAGTTCGGAAAGCCCTGTGTGGCCACCCTGGTATCTGCCCTGTGGCCCTCTCC 727
QY 241 PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla 260
Db 728 TTCATCAGCATACACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGCA 787
QY 261 ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr 280
Db 788 GTGGGCTGGGATACGCGCTGCGCCACACAGACACTGACCTTACTGTTCAACCTGTAC 847
QY 281 GlnPhePheLeuAlaPheAlaLeuProPheValIleThrAlaAlaTyrValArgIle 300
Db 848 CAGTTTTCCTGGCCTTTGGCCCTGTGCTTTGTGTGTCATCACAGCCGATACGTGAGGATC 907
QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
Db 908 CTGCAGCGCATGACGTCTCAGTGGCCCCCGCTCCACGCGCAGCATCCGGCTGCGGACA 967
QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro 340
Db 968 AAGAGGTGACCCGACAGCCATCGCATCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1027
QY 341 TyrTrpValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
Db 1028 TACTATGTGTACAGCTGACCCAGTGTTCATCAGCCGCGCCGACCCCTCACCCTTGTCTAC 1087
QY 361 LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr 380
Db 1088 TTATACAATGGGGCCATCAGCTTGGGCTATGCCAACAAGCTGCTCAACCCCTTGTGTAC 1147
QY 381 IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln 400
Db 1148 ATCGTGTCTGTGAGAGCGTCCGCAACGCTTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1207
QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGluSerLys 420
Db 1208 GGGCAGCTTCGGGCTGTCAAGCAACGCTCAGACGCGCTGACGAGAGAGACAGAAACAA 1267
QY 421 GlyThr 422
Db 1268 GGCACC 1273

RESULT 14
AAF86981
ID AAF86981 standard; cDNA; 1283 BP.
XX
XX AAF86981;
AC
XX
DT 06-JUL-2001 (first entry)
XX
DE Human SLC-1 coding sequence #3.
XX
XX Rat; human; SLC-1; MCH receptor; melanin-concentrating hormone;
KW obesity; diabetes; hypertension; arteriosclerosis; hyperphagia;
KW emotional disorder; reproductive disorder; memory disorder;
KW dementia; hormonal disorder; gonitis; ss.
XX
OS Homo sapiens.
XX
PN WO200121577-A2.

XX 29-MAR-2001.
PD
XX
PF 19-SEP-2000; 2000WO-JP06375.
XX
PR 20-SEP-1999; 99JP-0266298.
PR 16-DEC-1999; 99JP-0357889.
PR 20-APR-2000; 2000JP-0126272.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Kato K, Terauchi J, Mori M, Suzuki N, Shimomura Y, Takekawa S;
PI Ishihara Y;
XX WPI; 2001-354775/37.
DR
XX
PT New aromatic compounds are melanin concentrating hormone antagonists,
PT useful as anorectic agents, for treating or preventing obesity, also
PT memory or hormonal disorders or diabetes
XX
PS Examples; Page 362-363; 363pp; English.
XX
CC The present invention describes aromatic compounds capable of acting as
CC melanin-concentrating hormone (MCH) antagonists. Melanin-concentrating
CC hormone is an appetite control factor and antagonists were expected to be
CC useful as anti-obesity agents. They can be used in the treatment of
CC obesity, including malignant mastocytosis, exogenous, hyperinsular,
CC hypoplasmic, hypothyroid, hypothalamic, symptomatic, infantile, upper
CC body, alimentary, hypogonadal, simple and central obesity, systemic
CC mastocytosis and hypophyseal adiposity, hypertension, arteriosclerosis,
CC hyperphagia, emotional disorders, reproductive function disorders, memory
CC disorders, dementia, hormonal disorders, diabetes and gonitis. MCH binds
CC to the SLC-1 receptor. The present sequence is a version of the human
CC SLC-1 coding sequence given in the specification.
XX
SQ Sequence 1283 BP; 238 A; 423 C; 350 G; 272 T; 0 other;

Alignment Scores:
Pred. No.: 2.01e-184 Length: 1283
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 22 Gaps: 0

US-09-885-478-2 (1-422) x AAF86981 (1-1283)
QY 1 MetSerValGlyAlaMetLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
DB 8 ATGTCACTGGAGCCATGAAGAAGAGTGGGAGGCGAGTTGGCTTGAGCGGCAGC 67
QY 21 GlyCysGlnAlaThrGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
DB 68 GGCTGCCAGGCTACGAGAGAACCCCTTCCCACTGCGGGCTTGCGCTCGGAGCAA 127
QY 41 GlyGlyArgArgTyrPargLeuProGlnProAlaTyrValGlyGlySerSerAlaArgLeu 60
DB 128 GGTGGCAGCGCTGGAGGCTGCCGACGCTGCGTGGTGAAGGGAGCTCAGCTCGGTTG 187
QY 61 TyrGluGlnAlaThrGlyThrGlyTyrMetAspLeuGluAlaSerLeuLeuProThrGly 80
DB 188 TGGGAGCAGCGCAGCCGCTGCTGATGAGCTGAGCCTGGAAGCCTCGCTGCCCACTGGT 247
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
DB 248 CCCAAGCCAGCAACACCTCTGATGGCCCCGATAACCTCAGTTGGCAGATCACTCCT 307
QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
DB 308 CGCACGGGGAGCATCTCTACATCAACATCATGCTTCGCTGGTGTGGCACCATCTGC 367
QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeu 140

DB 368 CTCCTGGGCATCATCGGGAACCTCCAGGCTCATCTTCGGCGGTGTAAGAAGTCCAAGCTG 427
QY 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160
DB 428 CACTGGTGCAACAACGTCGCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTCC 487
QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTyrPheIsphe 180
DB 488 TTTCTCTGGGCAATGCCCTTCATGATCCACAGCTCATGGGCAATGGGGTGTGGCACTTT 547
QY 181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
DB 548 GGGGAGACCATGTGCACCCCTCATCACGGCCATGGATGCCAATAGTCAGTTCAACAGCACC 607
QY 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220
DB 608 TACATCCTGACCCGCAATGGCCATTGACCGGTACCTGGCCACTGTCCACCCCATCTTCC 667
QY 221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrrPalaLeuSer 240
DB 668 ACGAAGTTCGGAAGCCCTCTGTGGCCACCCTGGTGAATCTGCCCTCCTGGGGCCCTCTCC 727
QY 241 PheIleSerIleThrProValTrrPleuTyrAlaArgLeuIleProPheProGlyGlyAla 260
DB 728 TTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCCTTCCAGAGGTGCA 787
QY 261 ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrrPheThrLeuTyr 280
DB 788 GTGGGCTGGCGCATACGCGTCCCAACCCAGACACTGAACCTCTACTGTGTTACCCCTGTAC 847
QY 281 GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle 300
DB 848 CAGTTTTCCTGGCCTTGGCCCTGCTTTGTGTGTCATCACAGCCGATACGTGAGGATC 907
QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
DB 908 CTGCAGCGCATGACGTCTCTAGTGGCCCCCGCCCTCCAGCGAGCATCCGGCTGGGACA 967
QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrrPalaPro 340
DB 968 AAGAGGCTGACCCCGCACAGCCATCGCCATCTGTGTGTCTTGTGTGTGGCCACCC 1027
QY 341 TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
DB 1028 TACTATGTCTTACAGCTGACCCAGTTGTTCATCAGCCGCCGACCCCTCACCTTGTCTAC 1087
QY 361 LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr 380
DB 1088 TTATACATGCGGCCATCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTGTGTAC 1147
QY 381 IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaIleGln 400
DB 1148 ATCGTCTCTGTGAGACGTTCCGCAACGCTTGGTCTGTGCTGGAAGCCTGCAGCCAG 1207
QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGluSerLys 420
DB 1208 GGGCAGCTTGGCGCTGTGAGCAACGCTCAGACGGCTGACGAGAGAGACAGAAGCAAA 1267
QY 421 GlyThr 422
DB 1268 GGCACC 1273

RESULT 15
ABA92417
ID ABA92417 standard; cDNA; 1283 BP.
XX
AC ABA92417;
XX
DT 14-MAR-2002 (first entry)
XX
DE Human SLC-1 (L) nucleotide sequence SEQ ID NO:15.
XX
KW Human; SLC-1; melanin concentrating hormone antagonist; obesity;

KM anorectic; antidiabetic; hypotensive; antiarteriosclerotic;
KW diabetes; hypertension; arteriosclerosis; ss.
XX Homo sapiens.
XX WO200182925-A1.
XX
XX 08-NOV-2001.
XX
XX 26-APR-2001; 2001WO-JP03614.
XX
XX 28-APR-2000; 2000JP-0134295.
XX 13-DEC-2000; 2000JP-0384897.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX Ishihara Y, Suzuki N, Takekawa S;
XX WPI; 2002-075131/10.
XX
XX Melanin aggregating hormone antagonist for treating obesity
XX
XX Example; page 214-215; 223pp; Japanese.
XX
XX The present invention describes a melanin aggregating hormone antagonist
XX (I). (I) has anorectic, antidiabetic, antiarteriosclerotic and
XX hypotensive. (I) can be used in the treatment and prevention of obesity.
XX It may be combined with treatments for diabetes, hypertension or
XX arteriosclerosis. The present sequence represents a human SLC-1 (L) cDNA
XX sequence, which is used in the exemplification of the present invention.
XX
XX Sequence 1283 BP; 238 A; 423 C; 350 G; 272 T; 0 other:

Alignment Scores:
Pred. No.: 2.01e-184 Length: 1283
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 24 Gaps: 0

US-09-885-478-2 (1-422) x ABA92417 (1-1283)

QY 1 MetSerValGlyAlaMetLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
DB 8 ATGTCAAGTGGAGCCATGAAGAAGGAGTGGGAGGCGAGTTGGCTTGAGGCGGAGC 67
QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
DB 68 GGCTGCAGGCTACGAGAGAACCCCTTCCCACTGGCGGGCTTGGCTCCGGACAA 127
QY 41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGlyGlySerSerAlaArgLeu 60
DB 128 GGTGGCAGGCGCTGAGAGCTGCCGACCTGCGTGGGTGAGGGAGCGTCACTCGTGTG 187
QY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly 80
DB 188 TGGGAGCAGGCGACCGGACCTGGATGAGACCTGGAAGCCTCGCTGCTGCCACTGGT 247
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
DB 248 CCCAACGCCAGACACACCTGATGGCCCCGATACTCACTTCGGCAGGATCACTCTCT 307
QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
DB 308 CGCAGCGGGAGCATCTCTCTACTCAACATCATCATGCTTCGTTGCGCACCATCTCTGC 367
QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeu 140
DB 368 CTCTGGGCATCATCGGGAAGTCCACGGTCACTTCGCGGTGAGAGAACTCCAAGCTG 427
QY 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160

DB 428 CACTGGTGCAACAACGTCGCCGACATCTTCATCATCAACCTCTCGGTAGATCTCCTC 487
QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180
DB 488 TTTCTCTGGGCAATGCCCTTCATGATTCACCAAGCTCATGGGCAATGGGTGTGGCACTTT 547
QY 181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
DB 548 GGGGAGACCATGTGCACCCCTCAATCACGGCCATGATGCCAATAGTCAATTACACGACACC 607
QY 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220
DB 608 TACATCTGACCGCATGGCCATGGCCATGGACGCTACCTGGCCACTGTCCACCCCATCTTCC 667
QY 221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer 240
DB 668 ACGAAGTTCGGAGGCCCTCTGTGGCCACCCCTGTGATCTGCTCTCTGGGCCCTCTCC 727
QY 241 PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla 260
DB 728 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCACGAGGTGCA 787
QY 261 ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr 280
DB 788 GTGGGCTGGCGCATACGCTGTGCCCAACACAGACACTGACCTCTACTGGTTACACCTGTAC 847
QY 281 GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle 300
DB 848 CAGTTTTCCTGGCCTTTGCCCTTGCCCTTTGTGTGTCATCACAGCCGATACGTGAGGATC 907
QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
DB 908 CTGCAGCGCATGACGCTCTCAGTGGCCCCGCCCTCCACAGCGACGATCCGGCTGGGACA 967
QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro 340
DB 968 AAGAGGGTGACCCGACAGACCATGCGCATCTGTCTGTCTTCTTTGTGTGGTGGGACCC 1027
QY 341 TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
DB 1028 TACTATGTGCTACAGCTGACCCAGTTGTTCATCACGCCGCCGACCCCTCACCTTGTCTAC 1087
QY 361 LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr 380
DB 1088 TTATACAATGCGGCATCAGCTTGGGCTATGCCAACAGAGCTGCTCAACCCCTTGTGTAC 1147
QY 381 IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln 400
DB 1148 ATCGTGTCTGTGAGACGTTCCGCAACGCTTGGTCTGTGCTGTGAAGCTGCACCCAG 1207
QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGluSerLys 420
DB 1208 GGGCAGCTTCCGCGTGTCAAGCAACGCTCAGACGGCTGACGAGGAGAGACAGAAACAAA 1267
QY 421 GlyThr 422
DB 1268 GGCACC 1273

Search completed: February 19, 2003, 12:13:42
Job time : 298 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 11:07:07 ; Search time 3647 Seconds
(without alignments)
3367.531 Million cell updates/sec

Title: US-09-885-478-2
Perfect score: 2212
Sequence: 1 MSVGAMKKGVGRAVGLGGG.....LRVSNAGTADERTESKGT 422

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09885478/runat_13022003_105051_12766/app_query.fasta_1.583
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09885478.@CGN.1.1.2425_@runat_13022003_105051_12766 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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2: gb_htg:*
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13: gb_un:*
14: gb_vt:*
15: em_ba:*
16: em_fun:*
17: em_in:*
18: em_hum:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
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37: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2212	100.0	1269	AR169785	AR169785 Sequence
2	2212	100.0	2042	BC001736	BC001736 Homo sapi
3	2212	100.0	2042	BC021146	BC021146 Homo sapi
4	2207	99.8	1275	BD013168	BD013168 MCH recep
5	2207	99.8	1275	AB063174	AB063174 Homo sapi
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8	2207	99.8	1283	BD006655	Bd006655 MCH recep
9	2164	97.8	1385	AX174768	AX174768 Sequence
10	2000	90.4	1444	AF513988	AF513988 Macaca mu
11	2000	90.4	3488	AR202509	AR202509 Sequence
12	1971	89.1	122557	HS229A8	Z86090 Human DNA s
13	1824	82.5	1074	BD013173	BD013173 MCH recep
14	1824	82.5	1074	BD006654	Bd006654 MCH recep
15	1824	82.5	2133	AX280965	AX280965 Sequence
16	1819	82.2	1062	AX280767	AX280767 Sequence
17	1818	82.2	1062	AX280727	AX280727 Sequence
18	1818	82.2	1062	AX280759	AX280759 Sequence
19	1817	82.1	1062	AX280763	AX280763 Sequence
20	1814	82.0	1062	AX280743	AX280743 Sequence
21	1814	82.0	1062	AX280751	AX280751 Sequence
22	1813	82.0	1062	AX280739	AX280739 Sequence
23	1812	81.9	1062	AX280731	AX280731 Sequence
24	1811	81.9	1062	AX280747	AX280747 Sequence
25	1811	81.9	1062	AX280755	AX280755 Sequence
26	1809	81.8	1062	AY078245	AY078245 Macaca mu
27	1795	81.1	1062	AY112898	AY112898 Mustela p
28	1783	80.6	1214	AR169786	AR169786 Sequence
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37	1708	77.2	1877	HSU71092	U71092 Homo sapien
38	1692	76.5	1316	AR096459	AR096459 Sequence
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40	1662	75.1	128125	AC127953	AC127953 Rattus no
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ALIGNMENTS

RESULT 1

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LOCUS Sequence 1 from patent US 6291195.
DEFINITION ARI69785
ACCESSION ARI69785
VERSION ARI69785.1 GI:17907693
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1269)
AUTHORS Salon,J.A., Laz,T.M., Nagorny,R. and Wilson,A.E.
TITLE DNA encoding a human melanin concentrating hormone receptor (MCH1)
and uses thereof
JOURNAL Patent: US 6291195-A 1 18-SEP-2001;
FEATURES location/Qualifiers
source 1..1269
/organism="unknown"
BASE COUNT 234 a 419 c 347 g 269 t
ORIGIN
Alignment Scores:
Pred. No.: 5.13e-149 length: 1269
Score: 2212.00 Matches: 422
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-885-478-2 (1-422) x ARI69785 (1-1269)
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Db 61 GGCTGCCAGGCTACGAGAGAGACCCCTTCCCGACTGCGGGCTTGCGCTCCGGGACAA 120
QY 41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGluGlySerSerAlaArgLeu 60
Db 121 GGTGGCAGGCGCTGGAGGCTGCCGACGCTGCGTGGGTGGAGGGGAGGCTCAGCTCGGTTG 180
QY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly 80
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QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTyrHisPhe 180
Db 481 TTTCCTCTGGGCATGCCCTTCATATCAACACGATCATGGGCAATGGGCTGTGGCACTTT 540
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QY 221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer 240
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QY 381 IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln 400
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Db 1261 GGCACC 1266
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BC001736 2042 bp mRNA linear PRI 12-JUL-2001
LOCUS
DEFINITION Homo sapiens, Similar to G protein-coupled receptor 24, clone
MGC:3221 IMAGE:3503484, mRNA, complete cds.
ACCESSION BC001736
VERSION BC001736.1 GI:12804624
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 2042)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (16-JAN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butlerfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lisa Prabh, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 6 Row: 1 Column: 16.

FEATURES
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BASE COUNT 454 a 600 c 565 g 423 t
ORIGIN

Alignment Scores:
Pred. No.: 9.38e-149 Length: 2042
Score: 2212.00 Matches: 422
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-885-478-2 (1-422) x BC001736 (1-2042)

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QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
Db 274 GGCTGCCAGGCTACGGAGGAAGACCCCTTCCGCACTGCGGGCTTGCGCTCGGACAA 333
QY 41 GlyGlyArgArgTTrpArgLeuProGlnProAlaTrpValGlyGlySerSeraLaargLeu 60
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QY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly 80
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QY 101 ArgThrGlySerIleSerTrpIleAsnIleIleMetProSerValPheGlyThrIleCys 120
Db 514 CGCAGGGGAGCATCTCTACATCAACATCATATGCTTCGTTGGTGGCACCACATCTGC 573
QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValIySLySerIySleu 140
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Db 574 CTCCTGGGCATCATCGGGAACCTCCACGGTCACTCTTCGGGTGTAAGAAAGTCCAAGCTG 633
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QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGluSerLys 420
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QY 421 GlyThr 422
Db 1474 GGCACC 1479
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BC021146
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DEFINITION Homo sapiens, clone MGC:32129 IMAGE:4890530, mRNA, complete cds.
ACCESSION BC021146
VERSION BC021146.1 GI:18088973
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

REFERENCE 1 (bases 1 to 2042)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabps-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lissa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 40 Row: n Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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Source Location/Qualifiers

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LSVKPAAQGLRAVNSNAQTAEERTESKGT"

CDS
BASE COUNT 454 a 600 c 565 g 423 t
ORIGIN

Alignment Scores:
Pred. No.: 9.38e-149 Length: 2042
Score: 2212.00 Matches: 422
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-885-478-2 (1-422) x BC021146 (1-2042)

QY 1 MetSerValGlyAlaMetLysLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
Db 214 ATGTCAAGTGGAGCATGAAGAGGAGTGGGAGGCGAGTTGGCTTGAGGCGGCAGC 273
QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
Db 274 GGCTGCCAGGCTTACGAGAGAACCCCTTCCGACTGGGGGCTTGCGCTCCGGGACAA 333

QY 41 GlyGlyArgArgTyrParGleuProGlnProAlaTrpValGluGlySerSerAlaArgLeu 60
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DEFINITION MCH receptor antagonist.
ACCESSION BD013168
VERSION BD013168.1 GI:22093357
KEYWORDS WO 0121169-A/7.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1275)
AUTHORS Kato,K., Mori,M., Suzuki,N., Shimomura,Y., Takekawa,S. and Cho,N.
TITLE MCH receptor antagonist
JOURNAL Patent: WO 0121169-A 7 29-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD,KANEYOSHI KATO,MASAKI MORI,NOBUHIRO
SUZUKI, YUKIO SHIMOMURA,SHIRO TAKEKAWA,NOBUO CHO
COMMENT OS Homo sapiens (human)
PN WO 0121169-A/7
PD 29-MAR-2001
PE 19-SEP-2000 WO 2000JP006376
PR 20-SEP-1999 JP 99P 266278,17-JUL-2000 JP 00P 221055 PI
KANEYOSHI KATO,MASAKI MORI,NOBUHIRO SUZUKI,YUKIO SHIMOMURA PI
,SHIRO TAKEKAWA,
PI NOBUO CHO
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LOCUS AB063174 1275 bp mRNA linear PRI 16-JUN-2001
DEFINITION Homo sapiens SLC-1 mRNA for somatostatin receptor-like protein,
complete cds.
ACCESSION AB063174
VERSION AB063174.1 GI:14475646
KEYWORDS
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Shimomura,Y., Mori,M., Sugo,T., Ishibashi,Y., Abe,M., Kurokawa,T.,
Onda,H., Nishimura,O., Sumino,Y. and Fujino,M.
TITLE Isolation and identification of melanin-concentrating hormone as
the endogenous ligand of the SLC-1 receptor
JOURNAL Biochem. Biophys. Res. Commun. 261 (3), 622-626 (1999)
MEDLINE 99373129
REFERENCE 2 (bases 1 to 1275)
AUTHORS Sugo,T. and Mori,M.
TITLE Direct Submission
JOURNAL Submitted (13-JUN-2001) Tsukasa Sugo, Takeda Chemical Industries,
Ltd., Discovery Research Laboratories I, Pharmaceutical Research
Division; Wadai 10, Tsukuba, Ibaraki 300-4247, Japan
(E-mail:Sugo_Tsukasa@takeda.co.jp, Tel:81-298-64-5010(ex.5010),
Fax:81-298-64-5000)

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BASE COUNT 235 a 420 c 350 g 270 t
ORIGIN

Alignment Scores:
Pred. No.: 1.17e-148 Length: 1275
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 9 Gaps: 0

US-09-885-478-2 (1-422) x AB063174 (1-1275)

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XX BD006649.1

DT 08-FEB-2002 (Rel. 70, Created)

DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)

DE MCH receptor antagonist.

KW JP 03075319-T/7.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

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RP 1-1275

RA Kato K., Mori M., Suzuki N., Shimomura Y., Takeka S., Cho N.;

RT "MCH receptor antagonist";

RL Patent number JP03075319-T/7, 16-FEB-2001.

RL TAKEDA CHEMICAL INDUSTRIES LTD.

OS Homo sapiens (human)

PN JP 03075319-T/7

PD 16-FEB-2001

PF 19-SEP-2000 JP 2000006376

CC PR 20-SEP-1999 JP 99P 266278, 17-JUL-2000 JP 00P 221055

CC PI KANEYOSHI KATO, MASAOKI MORI, NOBUHIRO SUZUKI, YUKIO SHIMOMURA,

CC PI SHIRO TAKEKAWA,

CC PI NOBUO CHO

CC PC A61K31/137, A61K31/27, A61K31/4035, A61K31/44, A61K31/445,

CC PC A61K31/4453,

CC PC A61K31/472, A61P43/00, A61P31/04, C07D211/14, C07D211/18,

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QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGlnGluArgThrGlnSerLys 420

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LOCUS BD013174 1283 bp DNA linear PAT 02-AUG-2002
DEFINITION MCH receptor antagonist.
ACCESSION BD013174
VERSION BD013174.1 GI:22093363
KEYWORDS WO 0121169-A/13.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1283)
AUTHORS Kato,K., Mori,M., Suzuki,N., Shimomura,Y., Takekawa,S. and Cho,N.
TITLE MCH receptor antagonist
JOURNAL Patent: WO 0121169-A 13 29-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD,KANEYOSHI KATO,MASAKI MORI,NOBUHIRO
SUZUKI, YUKIO SHIMOMURA,SHIRO TAKEKAWA,NOBUO CHO
COMMENT OS Homo sapiens (human)
PN WO 0121169-A/13
PD 29-MAR-2001
PF 19-SEP-2000 WO 2000JP006376
PR 20-SEP-1999 JP 99P 266278,17-JUL-2000 JP 00P 221055 PI
KANEYOSHI KATO,MASAKI MORI,NOBUHIRO SUZUKI,YUKIO SHIMOMURA PI
,SHIRO TAKEKAWA,
PI NOBUO CHO
PC A61K31/137,A61K31/27,A61K31/4035,A61K31/44,A61K31/445, PC
A61K31/4453,
PC A61K31/472,A61P43/00,A61P31/04,C07D211/14,C07D211/18 PC
,C07D211/46,C07D211/58,
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Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
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QY 41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGluGlySerSerAlaArgLeu 60
Db 128 GGTGGCAGGCGCTGAGAGCTGCCGACGCTGCGTGGTGAGGGGAGAGCTCAGCTCGGTTG 187
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Db 248 CCCAACGCCAGCAACACCTCTGTATGGCCCCGATAACCTCACTTCGGCAGGATCACCTCTCT 307
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Db 308 CGCACGGGAGACATCTCCTACATCAACATCATCATGCTTGGGTGTTCCGCACCATCTGC 367
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Db 368 CTCCTGGCATCATCGGGAACCTCCACGGTCACTCTTCGGGGTGTGAAGAAGTCCAAAGCTG 427
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QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
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ID BD006655 standard; DNA; HUM; 1283 BP.

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XX AC BD006655;
XX SV BD006655.1
XX DT 08-FEB-2002 (Rel. 70, Created)
DT DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)
XX MCH receptor antagonist.
DE JP 03075319-T/13.
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX [1]
RN Kato K., Mori M., Suzuki N., Shimomura Y., Takeka S., Cho N.;
RP 1-1283
RA "MCH receptor antagonist";
RT Patent number JP03075319-T/13, 16-FEB-2001.
RL TAKEDA CHEMICAL INDUSTRIES LTD. .
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CC PI KANEYOSHI KATO,MASAKI MORI,NOBUHIRO SUZUKI,YUKIO SHIMOMURA,
CC PI SHIRO TAKEKAWA,
CC PI NOBUO CHO
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Alignment Scores:
Pred. No.: 1.18e-148 Length: 1283
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
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DEFINITION Sequence 1 from Patent WO0143759.
ACCESSION AX174768
VERSION AX174768.1 GI:14598289
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1385)
AUTHORS Campbell,C.A., Hadjingham,S.J., Harrison,D.C. and Hervieu,G.J.
TITLE New use
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SMITHKLINE BEECHAM PLC (GB)
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QY 191 MetAspAlaAsnSerGlnPheThrSerThrTyrIleLeuThrAlaMetAlaIleAspArg 210
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ACCESSION AF513988
VERSION AF513988
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SOURCE rhesus monkey.
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
REFERENCE
1 (bases 1 to 1444)
AUTHORS Tan,C.P., Sano,H., Iwaasa,H., Pan,J., Sailer,A., Hreniuk,D.L.,
Feighner,S.D., Palyha,O.C., Figueroa,D.J., Austin,C.P., Jiang,M.M.,
Yu,H., Ito,J., Ito,M., Ito,M., Guan,X.M., Kanatani,A., Van der
Ploeg,L.H.T. and Howard,A.D.
TITLE Melanin-Concentrating Hormone Receptor Subtypes 1 and 2: Species
Specific Gene Expression
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1444)
AUTHORS Tan,C.P., Sano,H., Iwaasa,H., Pan,J., Sailer,A., Hreniuk,D.L.,
Feighner,S.D., Palyha,O.C., Figueroa,D.J., Austin,C.P., Jiang,M.M.,
Yu,H., Ito,J., Ito,M., Ito,M., Guan,X.M., Kanatani,A., Van der
Ploeg,L.H.T. and Howard,A.D.
TITLE Direct Submission
JOURNAL Submitted (21-MAY-2002) Metabolic Disorders, Merck & Co., Box 2000


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QY      135 ValLysLysSerLysLeuHisTrpCysAsnAsnValProAspIlePheIleIleAsnLeu 154
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QY      195 SerGlnPheThrSerThrTyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThr 214
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QY      215 ValHisProIleSerSerThrLysPheArgLysProSerValAlaThrLeuValIleCys 234
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Db      662 CCCTTCCAGGAGGTGCAGTGGCCCTGCCGCATCCGCTTGCCCAACCCGGACACTGACCTT 721
QY      275  TyrTrpPheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuProPheValValIleThr 294
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QY      295  AlaAlaTyrValArgIleLeuGlnArgMetThrSerSerValAlaProAlaSerGlnArg 314
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QY      315  SerIleArgLeuArgThrLysArgValThrArgThrAlaIleAlaIleCysLeuValPhe 334
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QY      335  PheValCysTrpAlaProTyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgPro 354
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QY      355  ThrLeuThrPheValTyrLeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCys 374
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QY      375  LeuAsnProPheValTyrIleValLeuCysGluThrPheArgLysArgLeuValLeuSer 394
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AR202509
LOCUS      AR202509      3488 bp      DNA
DEFINITION Sequence 1 from patent US 6362326.
ACCESSION  AR202509
VERSION    AR202509.1  GI:20257048
KEYWORDS
SOURCE
ORGANISM  Unknown.
REFERENCE  1 (bases 1 to 3488)
AUTHORS  Sathe,G., Ellis,C.E., Halsey,W. and Bergsma,D.
TITLE    11 cby genomic sequence
JOURNAL  Patent: US 6362326-A 1 26-MAR-2002;
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Score:          2000.00      Matches:      422
Percent Similarity: 51.09%      Conservative: 0
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US-09-885-478-2 (1-422) x AR202509 (1-3488)
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Db 689 GGTGGCAGGCGCTGAGGCTGCCCGCAGCTGCTGGGTGAGGGGAGCTCAGCTCGGTTG 748
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QY 217 ProIleSerSerThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeu 236
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QY 397 ProAlaAlaGlnGlyGlnleuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArg 416
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Db 2969 CCTGCAGCCAGGGGACGCTTCGCCCTGTACGACACGCTCAGACGGCTGACGAGAGAGAG 3028

QY 417 ThrGluSerLysGlyThr 422
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RESULT 12
HS229A8 122557 bp DNA linear PRI 14-JAN-2000
LOCUS
DEFINITION Human DNA sequence from clone 229A8 on chromosome 22q13. Contains
an RPL4 (60S Ribosomal Protein L4) and a GAPD (Liver Glyceraldehyde
3-phosphate Dehydrogenase (EC 1.2.1.12)) pseudogene, the gene for
SLC1 (G Protein-Coupled Receptor GPR24, 7 transmembrane receptor
(rhodopsin family) member), ESTs, an STR, GSSs, genomic marker
D2S279, a ca repeat polymorphism and a putative Cpg Island,
complete sequence.
286090
286090.10 GI:4972260
HTG: ca repeat polymorphism: Cpg Island; D2S279; GAPD; GPR24;
ribosomal protein L4; RPL4; SLC1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 122557)
Lloyd,D.
REFERENCE Direct Submission
AUTHORS Submitted (19-AUG-1999) Sanger Centre, Hinxton, Cambridgeshire,
TITLE CBI0 ISA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone
JOURNAL requests: clonerequest@sanger.ac.uk
COMMENT On Jun 2, 1999 this sequence version replaced gi:4938278.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
This sequence was generated from part of bacterial clone contigs of
human chromosome 22, constructed by the Sanger Centre Chromosome 22
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr22
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence is
the entire insert of clone 229A8. The true right end of clone
591N18 (AL031594) is at 28405 in this sequence. The start of this
sequence overlaps with the end of sequence 298048.
229A8 is from the human BAC library described in U-J. Kim et al.
(1996) Genomics 34, 213-218. VECTOR: pBAC108L.
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2580. .3144
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2609. .2611
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/replace="tgt"
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Em:AF104410; match: ESTs: Em:AI619775 Em:AA632727
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US-09-885-478-2 (1-422) x HS229A8 (1-122557)
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LOCUS MCH receptor antagonist.
DEFINITION BD013173
ACCESSION BD013173
VERSION BD013173.1 GI:22093362
KEYWORDS WO 0121169-A/12.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1074)
REFERENCE Kato,K., Mori,M., Suzuki,N., Shimomura,Y., Takekawa,S. and Cho,N.
AUTHORS MCH receptor antagonist
TITLE Patent: WO 0121169-A 12 29-MAR-2001;
JOURNAL TAKEDA CHEMICAL INDUSTRIES LTD, KANEYOSHI KATO, MASAOKI MORI, NOBUHIRO
SUZUKI, YUKIO SHIMOMURA, SHIRO TAKEKAWA, NOBUO CHO
COMMENT OS Homo sapiens (human)
PN WO 0121169-A/12
PD 29-MAR-2001
PF 19-SEP-2000 WO 2000JP006376
PR 20-SEP-1999 JP 99P 266278,17-JUL-2000 JP 00P 221055 PI
KANEYOSHI KATO, MASAOKI MORI, NOBUHIRO SUZUKI, YUKIO SHIMOMURA PI
, SHIRO TAKEKAWA,
PI NOBUO CHO
PC A61K31/137, A61K31/27, A61K31/4035, A61K31/44, A61K31/445, PC
A61K31/4453,
PC A61K31/472, A61P43/00, A61P31/04, C07D211/14, C07D211/18 PC
, C07D211/46, C07D211/58,
PC C07D211/70, C07D401/12, C07D405/12, C07D409/12, C07D417/12 CC
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QY 110 IleIleMetProSerValPheGlyThrIleCysLeuLeuGlyIleIleGlyAsnSerThr 129
Db 127 ATCATCATGCCCTTCGGTGTTCGGCACCATCTGCCCTCTGGGCATCATCGGGAATCCACG 186
QY 130 ValIlePheAlaValValLysLysSerLysLeuHistPrcysAsnAsnValProAspIle 149
Db 187 GTCATCTTCGGCGTCGTGAAGAAGTCCAAGCTGCACCTGGTGCAACAACGTCCTCCCGACATC 246
QY 150 PheIleIleAsnLeuSerValValAspLeuLeuPheLeuLeuGlyMetProPheMetIle 169
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QY 170 HisGlnLeuMetGlyAsnGlyValTrrPheHisPheGlyGluThrMetCysThrLeuIleThr 189
Db 307 CACCAGCTCATGGGCAATGGGGTGTGGCACCATTGGGGAGACCATGTGCACCCCTCATCAGC 366
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QY 230 ThrLeuValIleCysLeuLeuTrrPalalaLeuSerPheIleSerIleThrProValTrrPleu 249
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QY 270 ProAspThrAspLeuTyrTrrPheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuPro 289
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QY 370 TyrAlaAsnSerCysLeuAsnProPheValTyrIleValLeuCysGluThrPheArgLys 389
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QY 390 ArgLeuValLeuSerValLysProAlaAlaGlnGlyGlnLeuArgAlaValSerAsnAla 409
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QY 410 GlnThrAlaAspGluGluArgThrGluSerLysGlyThr 422
Db 1027 CAGACGGCTGACGAGAGAGACAGAAAGCAAAAGGCACC 1065
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AX280965

LOCUS AX280965 2133 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 588 from Patent WO0177172.
ACCESSION AX280965
VERSION AX280965.1 GI:16608240
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Lehmann-Bruinsma,K., Liaw,C.W. and Lin,I.L.
TITLE Non-endogenous, constitutively activated known g protein-coupled
JOURNAL Patent: WO 0177172-A 588 18-OCT-2001;
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source 1. 2133
BASE COUNT 513 a 609 c 543 g 468 t
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Score: 1824.00 Matches: 353
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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QY 110 IleIleMetProSerValPheGlyThrIleCysLeuLeuGlyIleIleGlyAsnSerThr 129
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QY 130 ValIlePheAlaValValLysLysSerLysLeuHistPrcysAsnAsnValProAspIle 149
Db 181 GTCATCTTCGGCGTGTGAAGAAGTCCAAGCTGCACCTGGTGTGCAACAACGTCCTCCGACATC 240
QY 150 PheIleIleAsnLeuSerValValAspLeuLeuPheLeuLeuGlyMetProPheMetIle 169
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QY 170 HisGlnLeuMetGlyAsnGlyValTrrPheHisPheGlyGluThrMetCysThrLeuIleThr 189
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QY	310	ProAlaSerGlnArgSerIleArgLeuArgThrLysArgValThrArgThrAlaIleAla	329
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Search completed: February 19, 2003, 13:15:08
Job time : 3686 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:50:31 ; Search time 33.4921 Seconds
(without alignments)
1678.958 Million cell updates/sec

Title: US-09-885-478-2
Perfect score: 2212
Sequence: 1 MSVGMKKGVGRAVGLGGGS.....LRVSNAGTADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 segs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2212	100.0	422	21	AAB13436	Human MCH1 recepto
2	2212	100.0	422	23	AAU75853	Human melanin conc
3	2207	99.8	422	21	AAB12779	Human SLC-1 protei
4	2207	99.8	422	22	AAE07330	Human melanin-conc
5	2207	99.8	422	22	AAB81123	Human melanin conc
6	2207	99.8	422	22	AAB96871	Human SLC-1. Homo
7	2207	99.8	422	22	AAV97668	Human MCH-R3 prote
8	2207	99.8	422	22	AAB85894	Human long form MC
9	2207	99.8	422	23	AAU77541	Human melanin conc
10	2207	99.8	422	23	ABB04941	Human SLC-1 protei

11	2207	99.8	422	23	AAG80611	Human SLC-1 protei
12	2206	99.7	422	21	AAB13440	Mutant human MCH1
13	2206	99.7	422	23	AAU75857	Human melanin conc
14	2200	99.5	422	21	AAB13441	Mutant human MCH1
15	2200	99.5	422	23	AAU75858	Human melanin conc
16	2197	99.3	422	22	AAB85998	Human long form/mo
17	2197	99.3	673	22	AAB85907	Human long form/mo
18	2184	98.7	417	22	AAE07329	Human melanin-conc
19	2184	98.7	417	22	AAV97669	Human MCH-R2 prote
20	1824	82.5	353	19	AAW61370	Human 11CB splice
21	1824	82.5	353	20	AAV16570	Amino acid sequenc
22	1824	82.5	353	21	AAB13442	Truncated human MC
23	1824	82.5	353	21	AAV90258	Human 11cby protei
24	1824	82.5	353	22	AAE07328	Human melanin-conc
25	1824	82.5	353	22	AAE04747	Human 11CBY protei
26	1824	82.5	353	22	AAV97668	Human short form M
27	1824	82.5	353	22	AAB85895	Human short form M
28	1824	82.5	353	23	AAU76893	Human melanin conc
29	1824	82.5	353	23	AAU75859	Human short form M
30	1824	82.5	709	22	AAB56396	Human melanin conc
31	1819	82.2	353	22	AAB56307	TSHR-Gs-alpha fusi
32	1818	82.2	353	22	ABB56297	Non-endogenous hum
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34	1817	82.1	353	22	ABB56306	Non-endogenous hum
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36	1814	82.0	353	22	ABB56303	Non-endogenous hum
37	1814	82.0	353	22	AAB85897	Human short form/m
38	1814	82.0	604	22	AAB85906	Human short form/m
39	1813	82.0	353	22	ABB56300	Non-endogenous hum
40	1812	81.9	353	22	ABB56298	Non-endogenous hum
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42	1811	81.9	353	22	ABB56304	Non-endogenous hum
43	1808	81.7	353	21	AAV57284	Human GPCR protein
44	1781	80.5	353	23	AAU76892	Dog melanin-concen
45	1763	79.7	353	21	AAB12778	Rat SLC-1 protein

ALIGNMENTS

RESULT 1	
AAB13436	
ID AAB13436	standard; Protein; 422 AA.
AC AAB13436;	
XX	
DT 17-NOV-2000	(first entry)
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DE Human MCH1	receptor.
XX	
KW Human; MCH1	receptor; melanin concentrating hormone; neuroregulator;
KW G-protein	coupled; PEXU.HR-TU231; feeding; water balance;
KW energy	metabolism; arousal; attention; memory; cognitive function;
KW psychiatric	disorder; stress; sexual activity; hormone disorder;
KW hypertension;	diabetes; cardiovascular; gastrointestinal;
KW electrolyte	balance; respiratory; asthma; reproductive function;
KW immune;	endocrine; musculoskeletal; Alzheimer's disease;
KW sensory	modulation; transmission; motor coordination;
KW Parkinson's	disease; olfaction; urinary; depression; pain;
KW schizophrenia;	morphine tolerance; opiate addiction; migraine.
XX	
OS Homo sapiens.	
XX	
FH	
FT Region	Location/Qualifiers
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FT	149..169
FT	/label= Transmembrane_region_2
FT	193..208
FT	/label= Transmembrane_region_3
FT	228..262
FT	/label= Transmembrane_region_4
FT	274..301
FT	Region

FT /label= Transmembrane_region_5
FT Region 323..349
FT /label= Transmembrane_region_6
FT Region 358..383
FT /label= Transmembrane_region_7
XX WO200039279-A2.
XX
XX 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US31169.
XX
XX 31-DEC-1998; 98US-0224426.
XX
XX (SYNA-) SYNAPTIC PHARM CORP.
XX
XX Salon JA, Laz TM, Nagorny R, Wilson AE;
XX
XX WPI; 2000-548644/50.
XX N-PSDB; AAA63240.
XX
XX Novel nucleic acid encoding human melanin concentrating hormone
PT receptor useful for treating cardiovascular disorders, hypertension and
PT diabetes, whose mutant form is activated by melanin concentrating
PT hormone -
XX
XX Claim 7; Fig 2; 173pp; English.
XX
XX Neuroregulators modulate communication in the nervous system. Melanin
CC concentrating hormone 1 (MCH) is one such neuroregulator. MCH may serve
CC as an integrative neuropeptide, involved in stress response, feeding
CC regulation and sexual activity. Also, MCH is thought to participate in
CC water balance regulation, energy metabolism, general arousal/attention
CC state, memory and cognitive functions and psychiatric disorders. The
CC present sequence is the human MCH1 receptor. The present sequence is a
CC G-protein coupled receptor and has 7 transmembrane regions. MCH1 receptor
CC may be used in the therapy for a variety of disorders: steroid or
CC pituitary hormone disorder, epinephrine release disorder,
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder e.g. Alzheimer's disease, sensory modulation and
CC transmission disorder, motor coordination disorder, sensory integration
CC disorder, dopaminergic function disorder e.g. Parkinson's disease,
CC olfaction disorder, sympathetic innervation disorder, depression, stress,
CC fluid-imbalance disorder, urinary disorder e.g. urinary incontinence,
CC seizure, pain, psychotic behaviour e.g. schizophrenia, morphine
CC tolerance, opiate addiction or migraine. The coding sequence for the
CC present protein is also contained in plasmid pEX1.HR-TL231 (ATCC 203197).
XX
XX Sequence 422 AA;
SQ

Query Match 100.0%; Score 2212; DB 21; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.2e-223;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVGRAVGLGGSGQATEEDPLPDCGACAPGGGRRWRLLPQPAWVEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSGQATEEDPLPDCGACAPGGGRRWRLLPQPAWVEGSSARL 60

QY 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTASGSPRTGSISYINIIIMPSVFGTIC 120
Db 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTASGSPRTGSISYINIIIMPSVFGTIC 120

QY 121 LGGIIGNSTVIFAAYVKKSKLHWCNVDPDIFITNLVVDLLFLGLGMPFMIHQLMGNGVWHF 180
Db 121 LGGIIGNSTVIFAAYVKKSKLHWCNVDPDIFITNLVVDLLFLGLGMPFMIHQLMGNGVWHF 180

QY 181 GETMCTLITAMDANSQFTSTYILLTAMAIDRYLATVHPISSTKFRKPSVATLVICLIMALS 240
Db 181 GETMCTLITAMDANSQFTSTYILLTAMAIDRYLATVHPISSTKFRKPSVATLVICLIMALS 240

QY 241 FISTPFWLYARLIPEPGAVCGIRLPNPDTLWFTLYQFLAFALPFVVITAAVRI 300
Db 241 FISTPFWLYARLIPEPGAVCGIRLPNPDTLWFTLYQFLAFALPFVVITAAVRI 300

QY 301 LQRMSSVAPASQRSIRLTRKRYTRTAIAICLVFVCWAPYYVLQTLQSLISRPTLFVY 360
Db 301 LQRMSSVAPASQRSIRLTRKRYTRTAIAICLVFVCWAPYYVLQTLQSLISRPTLFVY 360

QY 361 LYNAISLGYANSCLPFVYIYLCETFRKRLVLSVKPAQGQLRAVSNAGTADERTESK 420
Db 361 LYNAISLGYANSCLPFVYIYLCETFRKRLVLSVKPAQGQLRAVSNAGTADERTESK 420

QY 421 GT 422
Db 421 GT 422

RESULT 2
AAU75853
ID AAU75853 standard; Protein; 422 AA.
XX
XX AAU75853;
XX
XX 08-MAY-2002 (first entry)
XX
XX Human melanin concentrating hormone receptor, MCH1.
XX
XX Human; melanin concentrating hormone receptor; MCH1;
KW steroid hormone disorder; pituitary hormone disorder;
KW epinephrine release disorder; gastrointestinal disorder;
KW cardiovascular disorder; hypertension; diabetes; respiratory disorder;
KW asthma; reproductive function disorder; immune disorder;
KW musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
KW memory disorder; motor coordination disorder; obesity; eating disorder;
KW dopaminergic function disorder; pain; psychosis; opiate addiction;
KW affective disorder; migraine; transgenic.
XX
XX Homo sapiens.
XX OS
XX PN WO200202744-A2.
XX PD 10-JAN-2002.
XX PF 05-JUL-2001; 2001WO-US21350.
XX PR 05-JUL-2000; 2000US-0610635.
XX PA (SYNA-) SYNAPTIC PHARM CORP.
XX PI Salon JA, Laz TM, Nagorny R, Wilson AE;
XX DR WPI; 2002-164532/21.
XX DR N-PSDB; ABK14548.
XX
XX Purified human melanin concentrating hormone receptor protein and
PT polynucleotides for screening modulator useful for treating memory
PT disorder, sensory modulation and transmission disorder, motor
PT coordination disorder -
XX
XX Example; Fig 2; 524pp; English.
XX
XX The invention relates to a purified human melanin concentrating hormone
CC (MCH1) receptor protein and its encoding nucleic acid (or mutant
CC activated by MCH or its analogue or homologue). Also included are
CC expression vectors, probes, transformed insect cells, antisense
CC oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting
CC the binding of the antibody to MCH1, a transgenic animal expressing the
CC protein, or a homologous knockout or antisense complementary to the MCH1
CC nucleic acid, ant/agonists of MCH1, and methods of isolating chemical
CC compounds which activate MCH1. The protein, nucleic acid, antibody,
CC ant/agonists and compound are useful for diagnosing and treating a
CC steroid or pituitary hormone disorder, an epinephrine release disorder, a
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance

CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder, sensory modulation and transmission disorder, motor
CC coordination disorder, sensory integration disorder, motor integration
CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder,
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC represents human MCH1.

XX
SQ Sequence 422 AA;

Query Match 100.0%; Score 2212; DB 23; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.2e-223;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGGGRRWRLLPQPAWVEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGGGRRWRLLPQPAWVEGSSARL 60
QY 61 WEQATGTGWMDLASLLPTGPNASNTSDGPDNLTSAGSPPTGTSISYINIMPSVFGTIC 120
Db 61 WEQATGTGWMDLASLLPTGPNASNTSDGPDNLTSAGSPPTGTSISYINIMPSVFGTIC 120
QY 121 LGGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQMGVWHF 180
Db 121 LGGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQMGVWHF 180
QY 181 GETMCTLITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240
Db 181 GETMCTLITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240
QY 241 FISITPVMLYARLIPEPPGAVGCGIRLPNPDLDLYWFTLYQFLAFALPFVVITAAYVRI 300
Db 241 FISITPVMLYARLIPEPPGAVGCGIRLPNPDLDLYWFTLYQFLAFALPFVVITAAYVRI 300
QY 301 LQRMSSVAPASQRSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVY 360
Db 301 LQRMSSVAPASQRSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVY 360
QY 361 LYNAAISLGYANSCNLPFVYIVLCETFRKRLVLSVKPAAQGOLRAVSNAGTADERTESK 420
Db 361 LYNAAISLGYANSCNLPFVYIVLCETFRKRLVLSVKPAAQGOLRAVSNAGTADERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 3
AAB12779
ID AAB12779 standard; Protein; 422 AA.

XX
AC AAB12779;

DT 22-NOV-2000 (first entry)

XX
DE Human SLC-1 protein sequence SEQ ID NO:11.

XX
KW SLC-1; MHC; melanin concentrating hormone; screening; eating;
KW appetite stimulator; appetite regulator; period pain; atonic bleeding;
KW caesarean section; milk congestion; antiobestic agent; drug;
KW foetal asphyxia; cervical rupture; premature birth; uterine rupture;
KW Prader-Willi syndrome; anorectic; gynaecological; abortifaciant;
KW antoanaemia; anabolic; orphan G protein-couple receptor protein.

OS Homo sapiens.

XX
PN WO200040725-A1.

XX
PD 13-JUL-2000.

XX
PF 27-DEC-1999; 99WO-JP07336.
XX
PR 28-DEC-1998; 98JP-0374454.
PR 28-APR-1999; 99JP-0122688.
PR 02-SEP-1999; 99JP-0249300.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Mori M, Shimomura Y, Takekawa S, Sugo T, Ishibashi Y, Kitada C;
PI Suzuki N;
XX
DR WPI; 2000-475832/41.
DR N-PSDB; AAA72918.

PT Screening methods for compounds as SLC-1 (ant)agonists useful in the
PT treatment of eating disorders and as preventives and remedies for e.g.
PT atonic bleeding and Prader-Willi syndrome
XX
PS Claim 6; Page 111-113; 123pp; Japanese.

CC The present invention describes a method for screening components (I) or
CC their salts that can alter the binding properties of melanin-
CC concentrating hormone (MCH) or its derivative or salt to SLC-1 or its
CC salt. Compounds identified by (I) are useful as SLC-1 (ant)agonists in
CC eating disorders and as preventives and remedies for e.g. period pains,
CC uterine recovery failure, caesarean section, artificial interruption of
CC pregnancy, galactostosis, tonic uterine contraction, foetal asphyxia,
CC rupture of uterus, cervical rupture, premature birth and Prader-Willi
CC syndrome. The present sequence represents the human SLC-1 protein
CC sequence, which is used in an example from the present invention.

XX
SQ Sequence 422 AA;

Query Match 99.8%; Score 2207; DB 21; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-223;
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGGGRRWRLLPQPAWVEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGGGRRWRLLPQPAWVEGSSARL 60
QY 61 WEQATGTGWMDLASLLPTGPNASNTSDGPDNLTSAGSPPTGTSISYINIMPSVFGTIC 120
Db 61 WEQATGTGWMDLASLLPTGPNASNTSDGPDNLTSAGSPPTGTSISYINIMPSVFGTIC 120
QY 121 LGGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQMGVWHF 180
Db 121 LGGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQMGVWHF 180
QY 181 GETMCTLITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240
Db 181 GETMCTLITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240
QY 241 FISITPVMLYARLIPEPPGAVGCGIRLPNPDLDLYWFTLYQFLAFALPFVVITAAYVRI 300
Db 241 FISITPVMLYARLIPEPPGAVGCGIRLPNPDLDLYWFTLYQFLAFALPFVVITAAYVRI 300
QY 301 LQRMSSVAPASQRSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVY 360
Db 301 LQRMSSVAPASQRSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVY 360
QY 361 LYNAAISLGYANSCNLPFVYIVLCETFRKRLVLSVKPAAQGOLRAVSNAGTADERTESK 420
Db 361 LYNAAISLGYANSCNLPFVYIVLCETFRKRLVLSVKPAAQGOLRAVSNAGTADERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 4
AAE07330

ID AAE07330 standard; Protein; 422 AA.
XX AAE07330;
AC
XX 06-NOV-2001 (first entry)
DT
XX
DE Human melanin-concentrating hormone receptor variant #3.
XX
XX Human; melanin-concentrating hormone; MCH analogue; signal transduction;
KW appetite; therapy; anorexia; acquired immune deficiency syndrome; AIDS;
KW wasting; cachexia; frail elderly; weight maintenance; cancer; anorectic;
KW pain reduction; stress reduction; sexual dysfunction; variant.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200157070-A1.
XX
XX 09-AUG-2001.
XX
XX 01-FEB-2001; 2001WO-US03293.
XX
XX 03-FEB-2000; 2000US-0179967.
XX
XX (MERI) MERCK & CO INC.
XX
XX Bednarek M;
XX
XX WPI; 2001-483416/52.
DR N-PSDB; AAD13654.
XX
XX Novel peptide encoding a melanin-concentrating hormone analog useful
PT for increasing weight or appetite -
XX
XX
PS Disclosure; Page 35-36; 66pp; English.
XX
XX The present invention relates to truncated melanin-concentrating hormone
CC (MCH) analogues active at the MCH receptor. The truncated MCH analogues
CC are optionally modified peptide derivatives of mammalian MCH. The MCH
CC analogues can bind to the MCH receptor and bring about signal
CC transduction. The MCH agonists can be used to facilitate a weight gain,
CC maintenance of weight and/or an appetite increase. The MCH agonists can
CC also be used to treat disorders such as anorexia, acquired immune
CC deficiency syndrome (AIDS), wasting, cachexia and frail elderly. The MCH
CC antagonists can be used to facilitate weight loss, appetite decrease,
CC weight maintenance, cancer treatment, pain reduction, stress reduction
CC and/or treatment of sexual dysfunction. The present sequence is a human
CC MCH receptor variant.
XX
SQ Sequence 422 AA;

Query Match 99.8%; Score 2207; DB 22; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-223;
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 241 FISITPWLVARLIPFGAVGCGIRLPNPDLDYWFTLYQFFLAFALEFVVITAAVRI 300
QY 301 LQMTSSVAPASQSRIRLTKRVTRTAIAICLVEFCWAPYYVLQLTQLSISRPTLTFVY 360
Db 301 LQMTSSVAPASQSRIRLTKRVTRTAIAICLVEFCWAPYYVLQLTQLSISRPTLTFVY 360
QY 361 LYNAAISLGYANSCLNPFYIIVLCETFRKRLVLSVKPAAGQLRAVSNQTADEERTESK 420
Db 361 LYNAAISLGYANSCLNPFYIIVLCETFRKRLVLSVKPAAGQLRAVSNQTADEERTESK 420
QY 421 GT 422
Db 421 GT 422
Db 421 GT 422

RESULT 5
AAB81123
ID AAB81123 standard; Protein; 422 AA.
XX
XX AAB81123;
XX
XX 05-JUL-2001 (first entry)
XX
XX
DE Human melanin concentrating hormone receptor (SLC-1).
XX
KW Melanin concentrating hormone; MCH; antagonist; diamine compound;
KW anorectic; antidiabetic; ophthalmological; neuroprotective; nephrotropic;
KW antiarteriosclerotic; antiarthritic; obesity; diabetes; arteriosclerosis;
KW arthritis; melanin concentrating hormone receptor; SLC-1; human.
XX
OS Homo sapiens.
XX
XX WO200121169-A1.
XX
XX 29-MAR-2001.
XX
XX 19-SEP-2000; 2000WO-JP06376.
XX
XX 20-SEP-1999; 99JP-0266278.
XX
XX 17-JUL-2000; 2000JP-0221055.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Kato K, Mori M, Suzuki N, Shimomura Y, Takekawa S, Choh N;
XX
XX WPI; 2001-328055/34.
XX
XX N-PSDB; AAF86229.
XX
XX Melanin concentrating hormone antagonists comprise new and known
PT diamine compounds for treating obesity -
XX
XX
PS Examples; Page 271-273; 284pp; Japanese.
XX
XX This invention relates to melanin concentrating hormone (MCH)
CC antagonists, comprising a diamine compound or its prodrug and/or salt.
CC Use of the MCH antagonists can result in anorectic, antidiabetic,
CC ophthalmological, neuroprotective, nephrotropic, antiarteriosclerotic,
CC and antiarthritic activity. Melanin concentrating hormone (MCH)
CC antagonists can be used for treating obesity (e.g. exogenous obesity,
CC hypophyseal adiposity, hypothalamic obesity and hyperphagia) and
CC associated disorders such as diabetes, diabetic neuropathy and diabetic nephropathy),
CC arteriosclerosis and arthritis in the knees. The present sequence
CC represents the human melanin concentrating hormone receptor (SLC-1). The
CC SLC-1 cDNA is used in examples to demonstrate the use of the antagonists
XX of the invention.
XX
SQ Sequence 422 AA;

Query Match 99.8%; Score 2207; DB 22; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-223;
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSVGMKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGGGRMRRLPQPAWEGSSARL	60
Db	1	MSVGMKKGVGRAVGLGGSGCQATEEDPLPNCGACAPGGGRMRRLPQPAWEGSSARL	60
QY	61	WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSAGSPPTGISISYINIIMPSVEGTIC	120
Db	61	WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSAGSPPTGISISYINIIMPSVEGTIC	120
QY	121	LLGIIGNSTVIFAIVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHOLMGNGVWHF	180
Db	121	LLGIIGNSTVIFAIVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHOLMGNGVWHF	180
QY	181	GETMCTLTAMDANSQFTSTYILTAMADRYLATVHPISSTFKRRKPSVATLVICLMAALS	240
Db	181	GETMCTLTAMDANSQFTSTYILTAMADRYLATVHPISSTFKRRKPSVATLVICLMAALS	240
QY	241	FISITPVMLYARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFALPFVVITAAYRI	300
Db	241	FISITPVMLYARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFALPFVVITAAYRI	300
QY	301	LQRMSSVAPASQORSIRLRTKRVTRTAIAICLVFVWCWAPIYVQLTQLSISRPTLFVY	360
Db	301	LQRMSSVAPASQORSIRLRTKRVTRTAIAICLVFVWCWAPIYVQLTQLSISRPTLFVY	360
QY	361	LYNNAISLGANSCLNPFVYIVLCETFRKRLVLSVKPAAQGGOLRAVSNAQTADEERTESK	420
Db	361	LYNNAISLGANSCLNPFVYIVLCETFRKRLVLSVKPAAQGGOLRAVSNAQTADEERTESK	420
QY	421	GT 422	
Db	421	GT 422	

RESULT 6
AAB96871
ID AAB96871 standard; Protein; 422 AA.
XX
AC AAB96871;
XX
DT 06-JUL-2001 (first entry)
XX
DE Human SLC-1.
XX
KW Rat; human; SLC-1; MCH receptor; melanin-concentrating hormone;
KW obesity; diabetes; hypertension; arteriosclerosis; hyperphagia;
KW emotional disorder; reproductive disorder; memory disorder;
KW dementia; hormonal disorder; gonitis.
XX
OS Homo sapiens.
XX
PN WO200121577-A2.
XX
PD 29-MAR-2001.
XX
PF 19-SEP-2000; 2000WO-JP06375.
XX
PR 20-SEP-1999; 99JP-0266298.
PR 16-DEC-1999; 99JP-0357889.
PR 20-APR-2000; 2000JP-0126272.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Kato K, Terauchi J, Mori M, Suzuki N, Shimomura Y, Takekawa S;
PI Ishihara Y;
XX
DR MPI; 2001-354775/37.
DR N-PSDB; AAF86975.
XX
PT New aromatic compounds are melanin concentrating hormone antagonists,
PT useful as anorectic agents, for treating or preventing obesity, also
PT memory or hormonal disorders or diabetes -
XX
PS Examples; Page 358-360; 363pp; English.

XX The present invention describes aromatic compounds capable of acting as
CC melanin-concentrating hormone (MCH) antagonists. Melanin-concentrating
CC hormone is an appetite control factor and antagonists were expected to be
CC useful as anti-obesity agents. They can be used in the treatment of
CC obesity, including malignant mastocytosis, exogenous, hyperinsular,
CC hypoplastic, hypothyroid, hypothalamic, symptomatic, infantile, upper
CC body, alimentary, hypogonadal, simple and central obesity, systemic
CC mastocytosis and hypophyseal adiposity, hypertension, arteriosclerosis,
CC hyperphagia, emotional disorders, reproductive function disorders, memory
CC disorders, dementia, hormonal disorders, diabetes and gonitis. MCH binds
CC to the SLC-1 receptor. The present sequence is the human SLC-1 protein
CC sequence.
XX
SQ Sequence 422 AA;

Query Match	99.8%;	Score 2207;	DB 22;	Length 422;
Best Local Similarity	99.8%;	Pred. No. 3.9e-223;		
Matches 421; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	MSVGMKKGVGAVGLGGSGCQATEEDPLPDCACAPGCGRRRRLPOPAMEGSSARL	60
Dd	1	MSVGAMKKGVRAGVLGGSGCQATEEDPLPNCAGACAPGCGRRRRLPOPAMEGSSARL	60
QY	61	WEQATGTGWMDIEASLLPTGPNASNTSDGPDNLTSAGSPPRGISISYINIMPSVEGTIC	120
Dd	61	WEQATGTGWMDIEASLLPTGPNASNTSDGPDNLTSAGSPPRGISISYINIMPSVEGTIC	120
QY	121	LLGIIGNSTVFPAVVKSKSLHMCNNVPDIFIINLSVDLLFLGMPEMIHQLMGNVWHF	180
Dd	121	LLGIIGNSTVFPAVVKSKSLHMCNNVPDIFIINLSVDLLFLGMPEMIHQLMGNVWHF	180
QY	181	GETMCTLTITAMDANSQFTSTYILTAMAIDRYLATVHPISSTRKRKPSVATLVICLMAWS	240
Dd	181	GETMCTLTITAMDANSQFTSTYILTAMAIDRYLATVHPISSTRKRKPSVATLVICLMAWS	240
QY	241	FISITPWMLYARLIPFGGAVGCGIRLPNDTDLYWFTLYQFFLAFAFPVVITAAYRI	300
Dd	241	FISITPWMLYARLIPFGGAVGCGIRLPNDTDLYWFTLYQFFLAFAFPVVITAAYRI	300
QY	301	LQRMSSVAPASQRSIRLRTKRVTRTAIAICLVFEVCWAPYYVLQTLQSISRPTLFVY	360
Dd	301	LQRMSSVAPASQRSIRLRTKRVTRTAIAICLVFEVCWAPYYVLQTLQSISRPTLFVY	360
QY	361	LYNAAISLGIANCLNPFVIIVLCETFRKRLVLSVKKPAAQGQLRAVSNAQTADDERTESK	420
Dd	361	LYNAAISLGIANCLNPFVIIVLCETFRKRLVLSVKKPAAQGQLRAVSNAQTADDERTESK	420
QY	421	GT 422	
Dd	421	GT 422	

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RESULT 7
AA97670
ID      AA97670 standard; Protein; 422 AA.
XX
AC      AA97670;
XX
DT      08-MAY-2001 (first entry)
XX
DE      Human MCH-R3 protein sequence.
XX
KW      Human; melanin-concentrating hormone receptor; MCH-R1; MCH-R2; MCH-R3;;
KW      weight loss; weight gain; cancer; pain; diabetes; stress; therapy;
KW      sexual dysfunction.
XX
OS      Homo sapiens.
XX
PN      WO200105947-A1.
XX
PD      25-JAN-2001.
XX

```

PF 10-JUL-2000; 2000WO-US18733.
XX
PR 14-JUL-1999; 99US-0143706.
XX
PA (MERI) MERCK & CO INC.
XX
PI Howard AD;
XX
DR WPI; 2001-159528/16.
DR N-PSDB; AAA91189, AAA91192.
XX
PT Melanin-concentrating hormone receptor polypeptides for increasing or
PT decreasing appetite, reducing stress and to screen for compounds that
PT bind to the receptor -
XX
PS Claim 21; Page 23; 43pp; English.
XX
CC This sequence is a melanin-concentrating hormone (MCH) receptor
CC protein of the invention, designated MCH-R3. MCH receptor fragments and
CC polypeptides are useful in assays to screen for compounds that bind to
CC the MCH receptor and modulate the activity of the receptor. MCH Receptor
CC activity is modulated to achieve weight loss, weight gain, to treat
CC cancer (e.g. colon or breast), reduce pain, treat diabetes, reduce stress
CC or treat sexual dysfunction. Nucleic acid coding for the MCH receptor can
CC be used to cause an increase in appetite and to create a test system
CC (e.g. a transgenic animal) for screening for compounds affecting MCH
CC receptor expression. Inhibition of MCH receptor nucleic acid activity is
CC useful to inhibit appetite or stress.
XX
SQ Sequence 422 AA;

Query Match 99.8%; Score 2207; DB 22; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-223;
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDGACAPGGGRRWRLPQPAWEGSSARL 60
1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPNCGACAPGGGRRWRLPQPAWEGSSARL 60
Db
QY 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIIMPSVFGTIC 120
61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIIMPSVFGTIC 120
Db
QY 121 LGGIIGNSTVIFA VVKSKSLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
121 LGGIIGNSTVIFA VVKSKSLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
Db
QY 121 LGGIIGNSTVIFA VVKSKSLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
121 LGGIIGNSTVIFA VVKSKSLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
Db
QY 181 GETMCTLITAMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLWALS 240
181 GETMCTLITAMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLWALS 240
Db
QY 241 FISITPVMLYARLIPFPGAVGCGIRLPNDTDLWFTLYQFFLAFALEPVVITAAYVRI 300
241 FISITPVMLYARLIPFPGAVGCGIRLPNDTDLWFTLYQFFLAFALEPVVITAAYVRI 300
Db
QY 301 LQMTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
301 LQMTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
Db
QY 361 LYNAAISLGYANSCNPFVYIVLCETFRKRLVSVKPAAGQLRAVSNAGTADERTESK 420
361 LYNAAISLGYANSCNPFVYIVLCETFRKRLVSVKPAAGQLRAVSNAGTADERTESK 420
Db
QY 421 GT 422
421 GT 422
Db 421 GT 422
421 GT 422

RESULT 8
AAB85894
ID AAB85894 standard; Protein; 422 AA.
XX
AC AAB85894;

XX
DT 30-NOV-2001 (first entry)
XX
DE Human long form MCH1R sequence.
XX
KW Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion;
KW fluorescent polypeptide; orexigenic; anabolic; food intake; MCH1R.
XX
OS Homo sapiens.
XX
PN WO200168706-A1.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-US08071.
XX
PR 15-MAR-2000; 2000US-0189698.
XX
PA (MERI) MERCK & CO INC.
XX
PI Marsh DJ;
XX
DR WPI; 2001-565791/63.
DR N-PSDB; AAH47297.
XX
PT Fusion proteins comprising melanin concentrating hormone receptor
PT peptides and fluorescent proteins, useful for identifying appetite
PT stimulants -
XX
PS Claim 1; Page 12-13; 71pp; English.
XX
CC The invention provides melanin concentrating hormone (MCH) receptor
CC (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise
CC MCHR polypeptide regions from different species. The MCHR fusion protein
CC comprise MCHR polypeptide region and a fluorescent polypeptide region
CC joined directly, or via a linker, to the carboxy side of the MCHR
CC polypeptide region. The MCHR fusion proteins can be expressed by standard
CC recombinant methodology. MCH action promotes feeding (orexigenic) and up
CC regulation of MCH activity stimulates food intake. The present sequence
CC represents a human long form MCHR protein sequence.
XX
SQ Sequence 422 AA;

Query Match 99.8%; Score 2207; DB 22; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-223;
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDGACAPGGGRRWRLPQPAWEGSSARL 60
1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPNCGACAPGGGRRWRLPQPAWEGSSARL 60
Db
QY 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIIMPSVFGTIC 120
61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIIMPSVFGTIC 120
Db
QY 121 LGGIIGNSTVIFA VVKSKSLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
121 LGGIIGNSTVIFA VVKSKSLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
Db
QY 121 LGGIIGNSTVIFA VVKSKSLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
121 LGGIIGNSTVIFA VVKSKSLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
Db
QY 181 GETMCTLITAMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLWALS 240
181 GETMCTLITAMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLWALS 240
Db
QY 241 FISITPVMLYARLIPFPGAVGCGIRLPNDTDLWFTLYQFFLAFALEPVVITAAYVRI 300
241 FISITPVMLYARLIPFPGAVGCGIRLPNDTDLWFTLYQFFLAFALEPVVITAAYVRI 300
Db
QY 301 LQMTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
301 LQMTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
Db
QY 361 LYNAAISLGYANSCNPFVYIVLCETFRKRLVSVKPAAGQLRAVSNAGTADERTESK 420
361 LYNAAISLGYANSCNPFVYIVLCETFRKRLVSVKPAAGQLRAVSNAGTADERTESK 420

Db 361 LYNNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAOGQLRAVSNAQTADERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 9
AAU77541
ID AAU77541 standard; Protein; 422 AA.
XX
AC AAU77541;
XX
DT 05-JUN-2002 (first entry)
XX

DE Human melanin concentrating hormone receptor, SLC-1.
XX
KW G protein-coupled orphan; receptor; SLC; melanin-concentrating hormone;
KW MCH; appetite-stimulating agent; obesity; malignant mastocytosis;
KW exogenous obesity; hyperinsular obesity; sexual function disorder;
KW overpowering intermittent pain; still born; uterus rupture;
KW premature birth; Prader-Willi syndrome; SLC-1; human.
XX

OS Homo sapiens.
XX
PN WO200203070-A1.
XX
PD 10-JAN-2002.
XX
PF 04-JUL-2001; 2001WO-JP05809.
XX
PR 05-JUL-2000; 2000JP-0208254.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Mori M, Shimomura Y, Harada M, Sugo T, Shintani Y;
XX
DR WPI; 2002-164552/21.
DR N-PSDB; ABK10854.
XX

PT Screening for compounds or salts which alter affinity of
PT melanin-concentrating hormone with its receptor to provide agonists as
PT appetite-stimulating agents and its antagonist for preventing or
PT treating obesity, uses a protein or hormone -

PS Disclosure; Page 103-105; 112pp; Japanese.

XX
CC The invention describes a method of screening for compounds or their
CC salts that can change affinity of melanin-concentrating hormone (MCH)
CC with its G protein-coupled orphan receptor protein, SLC. The screened
CC MCH receptor agonists are useful as appetite-stimulating agents and its
CC antagonist for preventing or treating obesity e.g. malignant
CC mastocytosis, exogenous obesity and hyperinsular obesity, and also
CC for treating sexual function disorders, overpowering intermittent pains,
CC still borns, uterus rupture, premature birth and Prader-Willi syndrome.
CC This is the amino acid sequence of the human melanin concentrating
CC hormone SLC-1, described in the invention.

XX
SQ Sequence 422 AA;

Query Match 99.8%; Score 2207; DB 23; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-223;
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVGRAVGLGGSGQATEEDPLPDCGACAPGGGRRRLPQPAWVEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSGQATEEDPLPNCGACAPGGGRRRLPQPAWVEGSSARL 60
QY 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSAGSPRTGISISYINIIMPSVFGTIC 120
Db 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSAGSPRTGISISYINIIMPSVFGTIC 120
QY 121 LGLIGNSTVIFA VVKSKLHWCNNVPDIFIINLSVVDLFLGLGMPFIHQLMGNGVWHF 180

Db 121 LGLIGNSTVIFA VVKSKLHWCNNVPDIFIINLSVVDLFLGLGMPFIHQLMGNGVWHF 180
QY 181 GETMCTLITAMDANSQFTSTYILTAMAI DRYLATVHPISSTKFRKPSVATLVICLTMALS 240
Db 181 GETMCTLITAMDANSQFTSTYILTAMAI DRYLATVHPISSTKFRKPSVATLVICLTMALS 240
QY 241 FISTPFWLYARLIPFGAVGCGIRLPNPDLDYWFLLYQFFLAFALPFWVITAAYVRI 300
Db 241 FISTPFWLYARLIPFGAVGCGIRLPNPDLDYWFLLYQFFLAFALPFWVITAAYVRI 300
QY 301 LQRMSSVAPASQRSIRLTRKRVTRTAIACLVFVCWAPYVYLQTLQLSISRPTLTFVY 360
Db 301 LQRMSSVAPASQRSIRLTRKRVTRTAIACLVFVCWAPYVYLQTLQLSISRPTLTFVY 360
QY 361 LYNNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAOGQLRAVSNAQTADERTESK 420
Db 361 LYNNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAOGQLRAVSNAQTADERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 10
ABB04941
ID ABB04941 standard; Protein; 422 AA.
XX
AC ABB04941;
XX
DT 14-MAR-2002 (first entry)
XX
DE Human SLC-1 protein SEQ ID NO:9.
XX
KW Human; SLC-1; melanin concentrating hormone antagonist; obesity;
KW anorectic; antidiabetic; hypotensive; antiarteriosclerotic;
KW diabetes; hypertension; arteriosclerosis.
XX
OS Homo sapiens.
XX
PN WO200182925-A1.
XX
PD 08-NOV-2001.
XX
PF 26-APR-2001; 2001WO-JP03614.
XX
PR 28-APR-2000; 2000JP-0134295.
XX
PR 13-DEC-2000; 2000JP-0384897.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Ishihara Y, Suzuki N, Takekawa S;
XX
DR WPI; 2002-075131/10.
DR N-PSDB; ABA92411.
XX

PT Melanin aggregating hormone antagonist for treating obesity -
PT Example; Page 210-212; 223pp; Japanese.

XX
CC The present invention describes a melanin aggregating hormone antagonist
CC (I). (I) has anorectic, antidiabetic, antiarteriosclerotic and
CC hypotensive. (I) can be used in the treatment and prevention of obesity.
CC It may be combined with treatments for diabetes, hypertension or
CC arteriosclerosis. The present sequence represents human SLC-1, which is
CC used the exemplification of the present invention.

SQ Sequence 422 AA;
Query Match 99.8%; Score 2207; DB 23; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-223;
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDGCACAPGQGGRRWRLPQPAWEGSSARL 60
|||||
Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPNCGACAPGQGGRRWRLPQPAWEGSSARL 60
OY 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPPRGTGISYINIMPSVEGTIC 120
|||||
Db 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPPRGTGISYINIMPSVEGTIC 120
OY 121 LGGIGNSTVIFAVVKKSKLHMCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
|||||
Db 121 LGGIGNSTVIFAVVKKSKLHMCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
OY 181 GETMCTLITAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAL 240
|||||
Db 181 GETMCTLITAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAL 240
OY 241 FISITPVWLYARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFAFPFVITAAVYRI 300
|||||
Db 241 FISITPVWLYARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFAFPFVITAAVYRI 300
OY 301 LQRMSSVAPASQRSIRLRTKRVTRTAIAICLVFVWCWAPYVVLQTLQLSISRPTLFVY 360
|||||
Db 301 LQRMSSVAPASQRSIRLRTKRVTRTAIAICLVFVWCWAPYVVLQTLQLSISRPTLFVY 360
OY 361 LYNAAISLGYANSCLNPFYIVLCETFRKRLVLSVKPAQGGQLRAVSNAGTADERTESK 420
|||||
Db 361 LYNAAISLGYANSCLNPFYIVLCETFRKRLVLSVKPAQGGQLRAVSNAGTADERTESK 420
OY 421 GT 422
||
Db 421 GT 422
RESULT 11
AAG80611
ID AAG80611 standard; Protein: 422 AA.
XX AAG80611;
AC
XX 28-FEB-2002 (first entry)
DT XX
DE Human SLC-1 protein.
XX
KW SLC-1; melanin-concentrating hormone antagonist; anorectic; depression;
KW antidiabetic; hypotensive; antiarteriosclerotic; antilipemic; obesity;
KW antiarthritic; antidepressant; tranquiliser; malignant mastocytosis;
KW hypophyseal adiposity; hypothyroid obesity; hyperphagia; diabetes;
KW hypertension; arteriosclerosis; hyperlipidaemia; arthritis; anxiety;
KW human.
XX
OS Homo sapiens.
XX
PN WO200187834-A1.
XX
PD 22-NOV-2001.
XX
PF 15-MAY-2001; 2001WO-JP04015.
XX
PR 16-MAY-2000; 2000JP-0148674.
PR 13-APR-2001; 2001JP-0116219.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Ishihara Y, Terauchi J, Suzuki N, Takekawa S, Aso K;
XX
XX WPI; 2002-055668/07.
DR N-PSDB; AAI69442.
XX
PT Use of new and known amine derivatives as melanin concentrating hormone
PT antagonists for treating e.g. obesity, diabetes, hypertension and
PT arteriosclerosis -
XX
PS Disclosure; Page 252-254; 283pp; Japanese.

XX This invention describes a novel use of an amine derivative (I) as a
CC melanin concentrating hormone antagonist which has anorectic,
CC antidiabetic, hypotensive, antiarteriosclerotic, antilipemic,
CC antiarthritic, antidepressant and tranquiliser activity. The products of
CC the invention can be used as melanin concentrating hormone antagonists
CC for treating and preventing obesity (including malignant mastocytosis,
CC hypophyseal adiposity, hypothyroid obesity, infantile obesity and
CC hyperphagia), diabetes, hypertension and arteriosclerosis as well as
CC diabetic complications, hyperlipidaemia, arthritis, depression and
CC anxiety. This sequence represents the human melanin-concentrating hormone
CC SLC-1 gene described in the method of the invention.
XX
SQ Sequence 422 AA;
Query Match 99.8%; Score 2207; DB 23; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-223;
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDGCACAPGQGGRRWRLPQPAWEGSSARL 60
|||||
Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPNCGACAPGQGGRRWRLPQPAWEGSSARL 60
OY 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPPRGTGISYINIMPSVEGTIC 120
|||||
Db 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPPRGTGISYINIMPSVEGTIC 120
OY 121 LGGIGNSTVIFAVVKKSKLHMCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
|||||
Db 121 LGGIGNSTVIFAVVKKSKLHMCNNVPDIFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
OY 181 GETMCTLITAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAL 240
|||||
Db 181 GETMCTLITAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAL 240
OY 241 FISITPVWLYARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFAFPFVITAAVYRI 300
|||||
Db 241 FISITPVWLYARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFAFPFVITAAVYRI 300
OY 301 LQRMSSVAPASQRSIRLRTKRVTRTAIAICLVFVWCWAPYVVLQTLQLSISRPTLFVY 360
|||||
Db 301 LQRMSSVAPASQRSIRLRTKRVTRTAIAICLVFVWCWAPYVVLQTLQLSISRPTLFVY 360
OY 361 LYNAAISLGYANSCLNPFYIVLCETFRKRLVLSVKPAQGGQLRAVSNAGTADERTESK 420
|||||
Db 361 LYNAAISLGYANSCLNPFYIVLCETFRKRLVLSVKPAQGGQLRAVSNAGTADERTESK 420
OY 421 GT 422
||
Db 421 GT 422
RESULT 12
AAB13440
ID AAB13440 standard; Protein: 422 AA.
XX AAB13440;
AC
XX 17-NOV-2000 (first entry)
DT XX
DE Mutant human MCH1 receptor encoded by plasmid R106.
XX
KW Human; MCH1 receptor; melanin concentrating hormone; neuroregulator;
KW G-protein coupled; feeding; water balance; energy metabolism; arousal;
KW attention; memory; cognitive function; psychiatric disorder; stress;
KW sexual activity; hormone disorder; hypertension; diabetes;
KW cardiovascular; gastrointestinal; electrolyte balance; musculoskeletal;
KW asthma; reproductive function; immune; endocrine; transmission;
KW Alzheimer's disease; sensory modulation; transmissiion;
KW motor coordination; Parkinson's disease; olfaction; urinary; depression;
KW seizure; pain; schizophrenia; morphine tolerance; opiate addiction;
KW migraine; mutant; mutein.
XX

OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 70
FT /note= "Wild-type Met substituted by Ala"
XX
PN WO200039279-A2.
XX PD 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US31169.
XX PR 31-DEC-1998; 98US-0224426.
XX PA (SYNA-) SYNAPTIC PHARM CORP.
XX PI Salon JA, Laz TM, Nagorny R, Wilson AE;
XX DR WPI; 2000-548644/50.
XX
PT Novel nucleic acid encoding human melanin concentrating hormone
PT receptor useful for treating cardiovascular disorders, hypertension and
PT diabetes, whose mutant form is activated by melanin concentrating
PT hormone -
XX
XX Claim 8; Fig 13; 173pp; English.
XX
CC Neuroregulators modulate communication in the nervous system. Melanin
CC concentrating hormone 1 (MCH1) is one such neuroregulator. MCH may serve
CC as an integrative neuropeptide, involved in stress response, feeding
CC regulation and sexual activity. Also, MCH is thought to participate in
CC water balance regulation, energy metabolism, general arousal/ attention
CC state, memory and cognitive functions and psychiatric disorders. The
CC present sequence is the mutant human MCH1 receptor encoded by plasmid
CC R106. The present sequence is a G-protein coupled receptor. MCH1 receptor
CC may be used in the therapy for a variety of disorders: steroid or
CC pituitary hormone disorder, epinephrine release disorder,
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder e.g. Alzheimer's disease, sensory modulation and
CC transmission disorder, motor coordination disorder, sensory intergration
CC disorder, dopaminergic function disorder e.g. Parkinson's disease,
CC olfaction disorder, sympathetic innervation disorder, depression, stress,
CC fluid-imbalance disorder, urinary disorder e.g. urinary incontinence,
CC seizure, pain, psychotic behaviour e.g. schizophrenia, morphine
CC tolerance, opiate addiction or migraine.
XX
XX Sequence 422 AA;
SQ

Query Match 99.7%; Score 2206; DB 21; Length 422;
Best Local Similarity 99.8%; Pred. No. 5e-223;
Matches 421; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDGACAPGGGRRWRLLPQPAWEGSSARL 60
DB 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDGACAPGGGRRWRLLPQPAWEGSSARL 60
QY 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTASGSPRRTGSISYINIIMPSVFGTIC 120
DB 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTASGSPRRTGSISYINIIMPSVFGTIC 120
QY 121 LLAGINSTVIFAVVKKSKLHCNNVPDIFILNSVVDLFLGMPFMHQLMGNGVWHF 180
DB 121 LLAGINSTVIFAVVKKSKLHCNNVPDIFILNSVVDLFLGMPFMHQLMGNGVWHF 180
QY 181 GETMCTLTAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLWALS 240
DB 181 GETMCTLTAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLWALS 240
QY 241 FISITPWLARLIPFPGAVGCGIRLPNPDPDLWFTLYQFFLAFLPFVVTAAVYRI 300

DB 241 FISITPWLARLIPFPGAVGCGIRLPNPDPDLWFTLYQFFLAFLPFVVTAAVYRI 300
QY 301 LQMTSSVAPASQSRIRLRTKRYTRTAIAICLVFVCWAPYVYLQLTQLSISRPTLFVY 360
DB 301 LQMTSSVAPASQSRIRLRTKRYTRTAIAICLVFVCWAPYVYLQLTQLSISRPTLFVY 360
QY 361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKRAAQQLRAVSNQTADEERTESK 420
DB 361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKRAAQQLRAVSNQTADEERTESK 420
QY 421 GT 422
DB 421 GT 422

RESULT 13
AAU75857
ID AAU75857 standard; Protein: 422 AA.
XX
XX AAU75857;
AC
XX
XX 08-MAY-2002 (first entry)
DT
DE Human melanin concentrating hormone receptor, MCH1, R106 mutant.
XX
XX Human; melanin concentrating hormone receptor; MCH1; R106;
KW steroid hormone disorder; pituitary hormone disorder;
KW epinephrine release disorder; gastrointestinal disorder; mutein;
KW cardiovascular disorder; hypertension; diabetes; respiratory disorder;
KW asthma; reproductive function disorder; immune disorder; mutant;
KW musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
KW memory disorder; motor coordination disorder; obesity; eating disorder;
KW dopaminergic function disorder; pain; psychosis; opiate addiction;
KW affective disorder; migraine; transgenic.
XX
XX Homo sapiens.
OS Synthetic.
OS
FH Key Location/Qualifiers
FT Misc-difference 70
FT /note= "Wild-type Met substituted by Ala"
XX
XX WO200202744-A2.
XX 10-JAN-2002.
PD
XX
XX 05-JUL-2001; 2001WO-US21350.
PF
XX
XX 05-JUL-2000; 2000US-0610635.
PR
XX
XX (SYNA-) SYNAPTIC PHARM CORP.
PA
XX
XX Salon JA, Laz TM, Nagorny R, Wilson AE;
PI
XX
XX WPI; 2002-164532/21.
DR
XX
XX Purified human melanin concentrating hormone receptor protein and
PT polynucleotides for screening modulator useful for treating memory
PT disorder, sensory modulation and transmission disorder, motor
PT coordination disorder -
XX
PS Claim 8; Fig 13; 524pp; English.
XX
XX The invention relates to a purified human melanin concentrating hormone
CC (MCH1) receptor protein and its encoding nucleic acid (or mutant
CC activated by MCH or its analogue or homologue). Also included are
CC expression vectors, probes, transformed insect cells, antisense
CC oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting
CC the binding of the antibody to MCH1, a transgenic animal expressing the
CC protein, or a homologous knockout or antisense complementary to the MCH1
CC nucleic acid, ant/agonists of MCH1, and methods of isolating chemical
CC compounds which activate MCH1. The protein, nucleic acid, antibody,

CC ant/agonists and compound are useful for diagnosing and treating a
CC steroid or pituitary hormone disorder, an epinephrine release disorder, a
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder, sensory modulation and transmission disorder, motor
CC coordination disorder, sensory integration disorder, motor integration
CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder,
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC represents human MCH1 mutant encoded by plasmid R106, which has a
CC methionine residue mutated to alanine in order to investigate the true
CC start codon of MCH1.

XX
SQ Sequence 422 AA;

Query Match 99.7%; Score 2206; DB 23; Length 422;
Best Local Similarity 99.8%; Pred. No. 5e-223;
Matches 421; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVRAVGLGGSGCCQATEEDLPDCGACAPGGGRRWRLLPQPAWEGSSARL 60
Db 1 MSVGAMKKGVRAVGLGGSGCCQATEEDLPDCGACAPGGGRRWRLLPQPAWEGSSARL 60
QY 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSAGSPRTGTSISYINIMPSVFGTIC 120
Db 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSAGSPRTGTSISYINIMPSVFGTIC 120
QY 121 LIGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPMIHQLMGNGVWHF 180
Db 121 LIGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPMIHQLMGNGVWHF 180
QY 181 GETMCTLITAMDANSOFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVCLIMALS 240
Db 181 GETMCTLITAMDANSOFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVCLIMALS 240
QY 241 FISTPFWLYARLIPFGGAVGCGIRLPNDJDLWFTLYOFPLAFALPFVVTAAVYRI 300
Db 241 FISTPFWLYARLIPFGGAVGCGIRLPNDJDLWFTLYOFPLAFALPFVVTAAVYRI 300
QY 301 LQRMSSVAPASQSRISIRTKRVRTATAICLVEFCWAPYVVLQTLQSLISRPLTFVY 360
Db 301 LQRMSSVAPASQSRISIRTKRVRTATAICLVEFCWAPYVVLQTLQSLISRPLTFVY 360
QY 361 LYNAAISLGYANSCLNPFVIVLCETFRKRLVLSVKPAAGQGLRAVSNAGTADERTESK 420
Db 361 LYNAAISLGYANSCLNPFVIVLCETFRKRLVLSVKPAAGQGLRAVSNAGTADERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 14
AAB13441
ID AAB13441 standard; Protein; 422 AA.
XX
AC AAB13441;
XX
DT 17-NOV-2000 (first entry)
XX
DE Mutant human MCH1 receptor encoded by plasmid R114.
XX
KW Human; MCH1 receptor; melanin concentrating hormone; neuroregulator;
KW G-protein coupled; feeding; water balance; energy metabolism; arousal;
KW attention; memory; cognitive function; psychiatric disorder; stress;
KW sexual activity; hormone disorder; hypertension; diabetes;
KW cardiovascular; gastrointestinal; electrolyte balance; respiratory;
KW asthma; reproductive function; immune; endocrine; musculoskeletal;
KW Alzheimer's disease; sensory modulation; transmission;

KW motor coordination; Parkinson's disease; olfaction; urinary; depression;
KW seizure; pain; schizophrenia; morphine tolerance; opiate addiction;
KW migraine; mutant; mutein.
XX Homo sapiens.
OS Synthetic.
XX
FH Key location/Qualifiers
FT Misc-difference 6 /note= "Wild-type Met substituted by Ala"
FT Misc-difference 70 /note= "Wild-type Met substituted by Ala"
FT
XX
PN MO200039279-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US31169.
XX
PR 31-DEC-1998; 98US-0224426.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Salon JA, Laz TM, Nagorny R, Wilson AE;
XX WPI; 2000-548644/50.
XX
PT Novel nucleic acid encoding human melanin concentrating hormone
PT receptor useful for treating cardiovascular disorders, hypertension and
PT diabetes, whose mutant form is activated by melanin concentrating
PT hormone -
XX
PS Claim 9; Fig 14; 173pp; English.

CC Neuroregulators modulate communication in the nervous system. Melanin
CC concentrating hormone 1 (MCH1) is one such neuroregulator. MCH may serve
CC as an integrative neuropeptide, involved in stress response, feeding
CC regulation and sexual activity. Also, MCH is thought to participate in
CC water balance regulation, energy metabolism, general arousal/ attention
CC state, memory and cognitive functions and psychiatric disorders. The
CC present sequence is the mutant human MCH1 receptor encoded by plasmid
CC R114. The present sequence is a G-protein coupled receptor. MCH1 receptor
CC may be used in the therapy for a variety of disorders: steroid or
CC pituitary hormone disorder, epinephrine release disorder,
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder e.g. Alzheimer's disease, sensory modulation and
CC transmission disorder, motor coordination disorder, sensory integration
CC disorder, dopaminergic function disorder e.g. Parkinson's disease,
CC olfaction disorder, sympathetic innervation disorder, depression, stress,
CC fluid-imbalance disorder, urinary disorder e.g. urinary incontinence,
CC seizure, pain, psychotic behaviour e.g. schizophrenia, morphine
CC tolerance, opiate addiction or migraine.

SQ Sequence 422 AA;

Query Match 99.5%; Score 2200; DB 21; Length 422;
Best Local Similarity 99.5%; Pred. No. 2.1e-222;
Matches 420; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVRAVGLGGSGCCQATEEDLPDCGACAPGGGRRWRLLPQPAWEGSSARL 60
Db 1 MSVGAMKKGVRAVGLGGSGCCQATEEDLPDCGACAPGGGRRWRLLPQPAWEGSSARL 60
QY 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSAGSPRTGTSISYINIMPSVFGTIC 120
Db 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSAGSPRTGTSISYINIMPSVFGTIC 120
QY 121 LIGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPMIHQLMGNGVWHF 180
Db 121 LIGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPMIHQLMGNGVWHF 180

QY 181 GETMCTLTITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240
181 GETMCTLTITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240
QY 241 FISTPVMYLARLIPFGGAVGCGIRLNPDPDLWFTLYQFFLAFALPFWVITAAYVRI 300
241 FISTPVMYLARLIPFGGAVGCGIRLNPDPDLWFTLYQFFLAFALPFWVITAAYVRI 300
Db 241 FISTPVMYLARLIPFGGAVGCGIRLNPDPDLWFTLYQFFLAFALPFWVITAAYVRI 300
QY 301 LQMTSSVAPASQSRIRLTKRVRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
301 LQMTSSVAPASQSRIRLTKRVRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
Db 301 LQMTSSVAPASQSRIRLTKRVRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
QY 361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
QY 421 GT 422
421 GT 422
Db 421 GT 422
RESULT 15
AAU75858
ID AAU75858 standard; Protein; 422 AA.
AC AAU75858;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human melanin concentrating hormone receptor, MCH1, R114 mutant.
XX
KW Human; melanin concentrating hormone receptor; MCH1; R114;
KW steroid hormone disorder; pituitary hormone disorder;
KW epinephrine release disorder; gastrointestinal disorder; mutein;
KW cardiovascular disorder; hypertension; diabetes; respiratory disorder;
KW asthma; reproductive function disorder; immune disorder; mutant;
KW musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
KW memory disorder; motor coordination disorder; obesity; eating disorder;
KW dopaminergic function disorder; pain; psychosis; opiate addiction;
KW affective disorder; migraine; transgenic.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 6 /note= "Wild-type Met substituted by Ala"
FT Misc-difference 70 /note= "Wild-type Met substituted by Ala"
FT
XX
PN WO200202744-A2.
XX
PD 10-JAN-2002.
XX
PF 05-JUL-2001; 2001WO-US21350.
XX
PR 05-JUL-2000; 2000US-0610635.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Salon JA, Laz TM, Nagorny R, Wilson AE;
XX
DR WPI; 2002-164532/21.
XX
PT Purified human melanin concentrating hormone receptor protein and
PT polynucleotides for screening modulator useful for treating memory
PT disorder, sensory modulation and transmission disorder, motor
PT coordination disorder -
XX
PS Claim 9; Fig 14; 524pp; English.
XX
CC The invention relates to a purified human melanin concentrating hormone

CC (MCH1) receptor protein and its encoding nucleic acid (or mutant
CC activated by MCH or its analogue or homologue). Also included are
CC expression vectors, probes, transformed insect cells, antisense
CC oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting
CC the binding of the antibody to MCH1, a transgenic animal expressing the
CC protein, or a homologous knockout or antisense complementary to the MCH1
CC nucleic acid, ant/agonists of MCH1, and methods of isolating chemical
CC compounds which activate MCH1. The protein, nucleic acid, antibody,
CC ant/agonists and compound are useful for diagnosing and treating a
CC steroid or pituitary hormone disorder, an epinephrine release disorder, a
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder, sensory modulation and transmission disorder, motor
CC coordination disorder, sensory integration disorder, motor integration
CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder,
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC represents human MCH1 mutant encoded by plasmid R114, which has a
CC methionine residue mutated to alanine in order to investigate the true
CC start codon of MCH1.
XX
SQ Sequence 422 AA;
QY 1 MSVGAMKKGVRAGVLGGSGCQATEEDPLPDGACAPGGGRWRRLPQPAWEGSSARL 60
1 MSVGAMKKGVRAGVLGGSGCQATEEDPLPDGACAPGGGRWRRLPQPAWEGSSARL 60
Db 1 MSVGAMKKGVRAGVLGGSGCQATEEDPLPDGACAPGGGRWRRLPQPAWEGSSARL 60
QY 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTIC 120
61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTIC 120
Db 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTIC 120
QY 121 LLIIGNSTVIFAVVKKSKLHMCNNVPDIFIINLSYVDLLELLGMPFMHQLMGNVWHF 180
121 LLIIGNSTVIFAVVKKSKLHMCNNVPDIFIINLSYVDLLELLGMPFMHQLMGNVWHF 180
Db 121 LLIIGNSTVIFAVVKKSKLHMCNNVPDIFIINLSYVDLLELLGMPFMHQLMGNVWHF 180
QY 181 GETMCTLTITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240
181 GETMCTLTITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240
Db 181 GETMCTLTITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240
QY 241 FISTPVMYLARLIPFGGAVGCGIRLNPDPDLWFTLYQFFLAFALPFWVITAAYVRI 300
241 FISTPVMYLARLIPFGGAVGCGIRLNPDPDLWFTLYQFFLAFALPFWVITAAYVRI 300
Db 241 FISTPVMYLARLIPFGGAVGCGIRLNPDPDLWFTLYQFFLAFALPFWVITAAYVRI 300
QY 301 LQMTSSVAPASQSRIRLTKRVRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
301 LQMTSSVAPASQSRIRLTKRVRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
Db 301 LQMTSSVAPASQSRIRLTKRVRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
QY 361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
Db 361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
QY 421 GT 422
421 GT 422
Db 421 GT 422

Search completed: February 13, 2003, 13:58:00
Job time : 35.4921 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:55:16 ; Search time 24.477 Seconds
(without alignments)
2971.547 Million cell updates/sec

Title: US-09-885-478-28

Perfect score: 1824
Sequence: 1 MDLEASLLPTGPNASNTSDG.....LRAVSNAGTADERTESKGT 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1824	100.0	422	4 Q96S47	Q96S47 homo sapien
2	1824	100.0	422	4 Q9BV08	Q9BV08 homo sapien
3	601	32.9	121	6 Q9MZ01	Q9MZ01 sus scrofa
4	565.5	31.0	340	4 Q969V1	Q969V1 homo sapien
5	559.5	30.7	340	4 Q9BXA8	Q9BXA8 homo sapien
6	559.5	30.7	340	6 Q8SQ54	Q8SQ54 macaca fasc
7	522	28.6	370	13 Q8UWL5	Q8UWL5 fugu rubrip
8	521.5	28.6	346	4 Q96GE0	Q96GE0 homo sapien
9	515.5	28.3	356	4 Q96TF2	Q96TF2 homo sapien
10	512.5	28.1	346	11 Q91Y73	Q91Y73 mus musculu
11	502.5	27.5	367	13 Q9PVG0	Q9PVG0 carassius a
12	499.5	27.4	367	13 Q9PVF9	Q9PVF9 carassius a
13	494.5	27.1	346	6 Q95KS6	Q95KS6 ovls arles
14	491	26.9	315	6 Q9GKP7	Q9GKP7 sus scrofa
15	486.5	26.7	380	13 Q9DGQ6	Q9DGQ6 carassius a
16	469	25.7	390	13 Q8QGQ4	Q8QGQ4 carassius a

17	456	25.0	385	11 Q9JK40	Q9JK40 mus musculu
18	444	24.3	454	4 Q9H573	Q9H573 homo sapien
19	442.5	24.3	390	11 Q8VI71	Q8VI71 mus musculu
20	442.5	24.3	391	11 Q8VI70	Q8VI70 mus musculu
21	442.5	24.3	393	11 Q9R1M0	Q9R1M0 mus musculu
22	442.5	24.3	401	11 Q9R1L9	Q9R1L9 mus musculu
23	442.5	24.3	409	11 Q8VI69	Q8VI69 mus musculu
24	442.5	24.3	438	11 Q9R0D1	Q9R0D1 mus musculu
25	442.5	24.3	444	11 Q9J1Y1	Q9J1Y1 mus musculu
26	439	24.1	400	6 Q95M54	Q95M54 macaca fasc
27	435	23.8	383	13 Q42324	Q42324 catostomus
28	422	23.1	384	13 Q98UH1	Q98UH1 brachydanio
29	419.5	23.0	377	13 Q98U14	Q98U14 brachydanio
30	407	22.3	373	13 Q57585	Q57585 brachydanio
31	402.5	22.1	272	4 Q9BWH1	Q9BWH1 homo sapien
32	393.5	21.6	451	5 Q9VWQ1	Q9VWQ1 drosophila
33	388	21.3	362	11 Q9J1N4	Q9J1N4 rattus norv
34	388	21.3	362	11 Q8VI74	Q8VI74 mus musculu
35	373	20.4	380	5 Q9NEV2	Q9NEV2 lymnaea sta
36	370.5	20.3	393	5 Q9VWQ0	Q9VWQ0 drosophila
37	367	20.1	291	11 Q91Z24	Q91Z24 mus musculu
38	367	20.1	325	11 Q8VIN4	Q8VIN4 mus musculu
39	367	20.1	330	11 Q8VI1P1	Q8VI1P1 mus musculu
40	367	20.1	370	11 Q8VI1P0	Q8VI1P0 mus musculu
41	366	20.1	380	5 Q9NEV1	Q9NEV1 lymnaea sta
42	364.5	20.0	380	5 Q9NEV3	Q9NEV3 lymnaea sta
43	363	19.9	380	5 Q9NEV0	Q9NEV0 lymnaea sta
44	361.5	19.8	359	13 Q9PVY7	Q9PVY7 anguilla an
45	361	19.8	423	5 Q964D4	Q964D4 periplaneta

ALIGNMENTS

RESULT 1
ID Q96S47 PRELIMINARY; PRT; 422 AA.
AC Q96S47;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Somatostatin receptor-like protein.
GN SLC-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sugo T., Mori M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99373129; PubMed=10441476;
RA Shimomura Y., Mori M., Sugo T., Ishibashi Y., Abe M., Kurokawa T.,
RA Onda H., Nishimura O., Sumino Y., Fujino M.;
RT "Isolation and identification of melanin-concentrating hormone as the
RT endogenous ligand of the SLC-1 receptor."
RL Biochem. Biophys. Res. Commun. 261:622-626(1999).
DR EMBL; AB063174; BAB60890.1; -;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00011; 7tm_1; 1.
DR PRINTS; PRO1559; DUFFYANTGEN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 422 AA; 45962 MW; 3986919A18183818 CRC64;

Query Match 100.0%; Score 1824; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLEASLLPTGPNASNTSDGPDNLTSGAGSPRTGSSISYINIIIMPSVFGTICLIGIGNST 60
|||||

Db 70 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGISYINILIMPSVEGTICLLIGINST 129
QY 61 VIFAIVKKSKLHWCNNVPDIFITINLSVDDLFLGLMPFMIHOLMGNGVMHGEETMCTLIT 120
Db 130 VIFAIVKKSKLHWCNNVPDIFITINLSVDDLFLGLMPFMIHOLMGNGVMHGEETMCTLIT 189
QY 121 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVAITVICLLMALSFSISTPVWL 180
Db 190 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVAITVICLLMALSFSISTPVWL 249
QY 181 YARLIPFPGAVGCGIRLPNPDITLWFTLYQFFLAFALPFAVITAAYVRILQRMSSVA 240
Db 250 YARLIPFPGAVGCGIRLPNPDITLWFTLYQFFLAFALPFAVITAAYVRILQRMSSVA 309
QY 241 PASQSRIRLRKRVTRTAIAICLVFVCWAPYVYLQLTQLSISRPITLTFVLYNAAISLG 300
Db 310 PASQSRIRLRKRVTRTAIAICLVFVCWAPYVYLQLTQLSISRPITLTFVLYNAAISLG 369
QY 301 YANSCLNPFVYIYLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 353
Db 370 YANSCLNPFVYIYLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 422

RESULT 2

Q9BV08 PRELIMINARY; PRT; 422 AA.
AC Q9BV08;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Similar to G protein-coupled receptor 24 (Hypothetical 46.0 kda protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC001736; AAH01736.1; -.
DR EMBL; BC021146; AAH21146.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01559; DUFFYANTIGEN.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS50262; G_PROTEIN_RECEPT_F1_2; 1.
KW Receptor; Hypothetical protein.
SQ SEQUENCE 422 AA; 45963 MW; 86A9F398B5D5F397 CRC64;

Query Match 100.0%; Score 1824; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGISYINILIMPSVEGTICLLIGINST 60
Db 70 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGISYINILIMPSVEGTICLLIGINST 129
QY 61 VIFAIVKKSKLHWCNNVPDIFITINLSVDDLFLGLMPFMIHOLMGNGVMHGEETMCTLIT 120
Db 130 VIFAIVKKSKLHWCNNVPDIFITINLSVDDLFLGLMPFMIHOLMGNGVMHGEETMCTLIT 189
QY 121 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVAITVICLLMALSFSISTPVWL 180
Db 190 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVAITVICLLMALSFSISTPVWL 249
QY 181 YARLIPFPGAVGCGIRLPNPDITLWFTLYQFFLAFALPFAVITAAYVRILQRMSSVA 240

|||||
Db 250 YARLIPFPGAVGCGIRLPNPDITLWFTLYQFFLAFALPFAVITAAYVRILQRMSSVA 309
QY 241 PASQSRIRLRKRVTRTAIAICLVFVCWAPYVYLQLTQLSISRPITLTFVLYNAAISLG 300
Db 310 PASQSRIRLRKRVTRTAIAICLVFVCWAPYVYLQLTQLSISRPITLTFVLYNAAISLG 369
QY 301 YANSCLNPFVYIYLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 353
Db 370 YANSCLNPFVYIYLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 422

RESULT 3

Q9MZ01 PRELIMINARY; PRT; 121 AA.
AC Q9MZ01;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE Melanin-concentrating hormone receptor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN; HYPOTHALAMUS;
RA Matteri R.L.;
RT "Sus scrofa melanin-concentrating hormone (MCH) receptor."
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF273611; AAF81827.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS50262; G_PROTEIN_RECEPT_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13583 MW; 884D8268B6F9F010 CRC64;

Query Match 32.9%; Score 601; DB 6; Length 121;
Best Local Similarity 99.2%; Pred. No. 1.1e-48;
Matches 120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 225 TAAAYVRILQRMSSVAPASQSRIRLRKRVTRTAIAICLVFVCWAPYVYLQLTQLSISR 284
Db 1 TAAAYVRILQRMSSVAPASQSRIRLRKRVTRTAIAICLVFVCWAPYVYLQLTQLSISR 60
QY 285 PTLTFVLYNAAISLGYANSCINPFVYIYLCETFRKRLVSVKPAAGQLRAVSNAQTAD 344
Db 61 PTLTFVLYNAAISLGYANSCINPFVYIYLCETFRKRLVSVKPAAGQLRAVSNAQTAE 120
QY 345 E 345
Db 121 E 121

RESULT 4

Q969V1 PRELIMINARY; PRT; 340 AA.
AC Q969V1;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE G protein-coupled receptor (Melanin-concentrating hormone 2 receptor) (Melanin-concentrating hormone receptor MCH-R2) (GPRV17).
GN SLT OR GPRV17.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurama T., Matsumoto S., Takasaki J., Terai K., Matsumoto M.,
RA Kamohara M., Saito T., Soga T., Saito Y., Oda T., Masuno Y.,
RA Furuichi K.;
RT "Molecular characterization of a novel melanin-concentrating hormone
RT receptor : Evidence of its expression in lateral hypothalamus.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB058850; BAB87843.1; -.
SQ SEQUENCE 340 AA; 38769 MW; BD22CF1972332439 CRC64;

Query Match	30.7%;	Score 559.5;	DB 6;	Length 340;
Best Local Similarity	36.7%;	Pred. No. 2.9e-44;		
Matches 112; Conservative	60;	Mismatches 122;	Indels 11;	Gaps 4;

[illegible]

RESULT 7	Q8UWL5	PRELIMINARY;	PRT;	370 AA.
ID	Q8UWL5	PRELIMINARY;	PRT;	370 AA.
AC	Q8UWL5;			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Somatostatin receptor 2.			
GN	SSTR2.			
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;			
OC	Tetraodontidae; Takifugu.			
OX	NCBI_TaxID=31033;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21564205; PubMed=11707075;			
RA	Bagheri-Fam S., Ferraz C., Demaille J., Scherer G., Pfeifer D.;			
RT	"Comparative Genomics of the SOX9 Region in Human and Fugu rubripes";			
RT	Conservative of Short Regulatory Sequence Elements within Large			
RT	Intergenic Regions.";			
RL	Genomics 78:73-82(2001).			
DR	EMBL; AF329945; AAL32173.1; -.			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRRHODPSN.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.			
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.			
KW	Receptor.			
SQ	SEQUENCE 370 AA; 41364 MW; 420BB12F204946B6 CRC64;			

Query Match	28.6%	Score 522;	DB 13;	Length 370;
Best Local Similarity	33.0%	Pred. No. 1e-40;		
Matches 122; Conservative	75;	Mismatches 131;	Indels 42;	Gaps 11;

[illegible]

RESULT 8			
Q96GE0			
ID	Q96GE0	PRELIMINARY;	PRT; 346 AA.
AC	Q96GE0;		
DT	01-DEC-2001	(TREMBLrel. 19, Created)	
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)	
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)	
DE	Unknown (Protein for IMAGE:3354783) (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euthera; Primates; Carnivora; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RA	TISSUE=EYE;		
RA	Strausberg R.;		
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC009522; AAH09522.1; -.		
DR	InterPro: IPR000276; GPCR_Rhodpsn.		
DR	Pfam: PF00001; 7tm_1; 1.		
DR	PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.		
DR	PROSITE: PS50262; G_PROTEIN_RECIP_F1_2; 1.		
FT	NON_TER 1 1		
SO	SEQUENCE 346 AA; 38790 MW; EA073A6CC05FEB72 CRC64;		

Query Match	28.6%;	Score 521.5;	DB 4;	Length 346;
Best Local Similarity	31.7%;	Pred. No. 1.1e-40;		
Matches 110; Conservative	73;	Mismatches 125;	Indels 39;	Gaps 7;

```

OY      13 NASNTSDGPDMLTSAGSPPRGTGISTINIIMPSVEFGTICLGIIGNSTVIFAAVYKSKLH  72
      | | : : | | | | : : : : : : : : : : : : : : : : : : : : : :
Db      6 NTSNQTEPYDILTS-----NAVLTEIFYEVCICIGCNFLVYVILRYAKM-  51

OY      73 WCNNVPDIFIINLSVVDLFLGMPF-----MIHQLMGNGVWHFEGETMCTLTAMDANS  126
      : : : : : : : : | | : : : : : : : : : : : : : : : : : : : : : :
Db      52 --KTITNIVILNLAIADLEFMLGLPELMAQVALVH-----WPEGKAICRVVMYFDGIN  102

OY      127 QFTSTYILPAMAIDRYLATVHPISSTFKRKPVSATLVICLLMALSFISITPVMYLARLIP  186
      | | | : : : | | | | | | | | | | | | : : : : : : : : : : : :
Db      103 QFTSIFCLTVNSIDRYLAVVHPIKSAKRRRPRTAKMITMAWGVSLVILPIMITYAGLRS  162

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OY 187 FPGAVGCGIRLPNDTDLY-WFTLYQFLAFALPEVVITAAYRILOQRTSSVAPASQR 245
DB 163 NQWGRSSCTINWPGESGAWYTGFIITYFILGLFVPLTIICLCYFIITIKVSSGIRVGSS 222
OY 246 SIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQLSIS-RPTLTFVLYNNAISLGYANS 304
DB 223 KRKKSEKKVTRMVSIVAVFIFCWLPEYIFNVSSVSMAISPTPALKGMFDFVVLITYANS 282
OY 305 CLNPFVYIVLCETFRKRLVLSVKPAPAOGLRAVSNAGTADERTESK 351
DB 283 CANPILYAFLSDNFKK-----SFQNVLCVLKVSGETDGRSDSK 321

RESULT 9
O96TF2 PRELIMINARY; PRT; 356 AA.
AC O96TF2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Somatostatin receptor 2B.
GN SSTR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20084417; PubMed=10619399;
RA Petersen S., Rasch A.C., Presch S., Beil F.U., Schulte H.M.;
RT "Genomic structure and transcriptional regulation of the human
somatostatin receptor type 2.";
RL Mol. Cell. Endocrinol. 157:75-85(1999).
RL EMBL; AF184174; AAF42810.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 356 AA; 40006 MW; D10FA237FAED61F3 CRC64;

Query Match 28.3%; Score 515.5; DB 4; Length 356;
Best Local Similarity 31.0%; Pred. No. 4.1e-40;
Matches 110; Conservative 77; Mismatches 123; Indels 45; Gaps 9;

OY 2 DLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLIGNSTV 61
DB 20 DLNGSVST--NTSNQTEPYDLS-----NAVLTFYFVVCVGLCGNTLV 64
OY 62 IFAVVKKSKLHWCNNVPDIFITINLSVVDLLFLGMPF-----MIHQLMGNGVWHFGETM 115
DB 65 IYVILRYAKM--KTITNIIYLNLAIADLFMLGLPFLAMQVALVH-----WPFCKAI 114
OY 116 CTLITAMDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLWALSFSIS 175
DB 115 CRVVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRPRPTAKMITMAVWGVSLLVI 174
OY 176 TPVWLYARLIPEPGAVGCGIRLPNDTDLY-WFTLYQFLAFALPEVVITAAYRILOQ 234
DB 175 LPIMITYAGLRSNQWGRSSCTINWPGESGAWYTGFIITYFILGLFVPLTIICLCYLFITIK 234
OY 235 MTSSVAPASQSRIRLTKRVTRTAIAICLVFVCWAPYVVLQTLQLSIS-RPTLTFVLY 293
DB 235 VKSSGIRVGSSKRKKSEKVTMVSIVAVFIFCWLPEYIFNVSSVSMAISPTPALKGMF 294
OY 294 NAAISLGYANSCLNPFYIVLCETFRK--RLVLSVKPAPAOGLRAVSNAGTAD 345
DB 295 DFVVVLITYANSCANPILYAFLSDNFKKSFQNVLCVKA-----DNSKSGEE 340

RESULT 10
O91Y73 PRELIMINARY; PRT; 346 AA.
ID O91Y73

AC O91Y73;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Somatostatin receptor type 2.
GN SSTR2 OR SST2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=LIVER;
RX MEDLINE=21201198; PubMed=11278805;
RA Puente E., Saint-Laurent N., Torrisani J., Furet C., Schally A.V.,
RA Vaysse N., Buscail L., Susini C.;
RT "Transcriptional Activation of Mouse sst2 Somatostatin Receptor
Promoter by Transforming Growth Factor-beta. Involvement of Smad4.";
RL J. Biol. Chem. 276:13461-13468(2001).
RL EMBL; AF008914; AAD01420.1; -.
DR MGD; MGI:98328; Ssstr2.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 346 AA; 38586 MW; D7A20AEC1371C400 CRC64;

Query Match 28.1%; Score 512.5; DB 11; Length 346;
Best Local Similarity 31.3%; Pred. No. 7.5e-40;
Matches 111; Conservative 75; Mismatches 126; Indels 43; Gaps 9;

OY 2 DLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLIGNSTV 61
DB 20 DLNGSLGPS--NGSNQTEPYDMS-----NAVLTFYFVVCVGLCGNTLV 64
OY 62 IFAVVKKSKLHWCNNVPDIFITINLSVVDLLFLGMPF-----MIHQLMGNGVWHFGETM 115
DB 65 IYVILRYAKM--KTITNIIYLNLAIADLFMLGLPFLAMQVALVH-----WPFCKAI 114
OY 116 CTLITAMDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLWALSFSIS 175
DB 115 CRVVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRPRPTAKMINVAVWCVSLLVI 174
OY 176 TPVWLYARLIPEPGAVGCGIRLPNDTDLY-WFTLYQFLAFALPEVVITAAYRILOQ 234
DB 175 LPIMITYAGLRSNQWGRSSCTINWPGESGAWYTGFIITYAFILGLFVPLTIICLCYLFITIK 234
OY 235 MTSSVAPASQSRIRLTKRVTRTAIAICLVFVCWAPYVVLQTLQLSIS-RPTLTFVLY 293
DB 235 VKSSGIRVGSSKRKKSEKVTMVSIVAVFIFCWLPEYIFNVSSVSVAISPTPALKGMF 294
OY 294 NAAISLGYANSCLNPFYIVLCETFRKL--VLSVKPAPAOGLRAVSNAGTAD 346
DB 295 DFVVVLITYANSCANPILYAFLSDNFKKSFQNVLCVKA-----DNSQGAED 341

RESULT 11
O9PVG0 PRELIMINARY; PRT; 367 AA.
AC O9PVG0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Somatostatin receptor type 1 subtype A.
GN SST1A.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.

```
RC TISSUE=BRAIN;
RX MEDLINE=20005543; PubMed=10537151;
RA Lin X., Janovick J.A., Brothers S., Conn P.M., Peter R.E.;
RT "Molecular cloning and expression of two type one somatostatin
  receptors in goldfish brain.";
RL Endocrinology 140:5211-5219(1999).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF097726; AAF08613.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 367 AA; 41658 MW; BE85E6C26C103614 CRC64;

Query Match      27.5%; Score 502.5; DB 13; Length 367;
Best Local Similarity 30.1%; Pred. No. 7e-39;
Matches 97; Conservative 80; Mismatches 120; Indels 25; Gaps 6;

QY 2 DLEASLPTGPNASNTSDGPDNLTSGSPRTGSSISYINIIMPSVFGTICLLGIIGNSTV 61
   :||| | :||| | :||| | :||| | :||| | :||| | :||| | :||| | :||| |
Db 9 NLEDGLYLINFSSNETHNGDSHGSSA-----IFISFYSVCLVGLCGNSMV 55

QY 62 IFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQMGNGVWHFGETMCTLITA 121
   | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 56 IYVIFRYAKMKKTATN---IYILNLAIADLMLSVPLVTSSLLHH-WPFGSLLCRLVLS 111

QY 122 MDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLLMAISFISITPVWLY 181
   :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 112 VDAIMFTSIYCLTVLSIDRYISVHPPIKARTRPTAKMVNLGVMMFSILVILPIITIF 171

QY 182 ARLPEPGGAVGCGIRLPNDPTDLYW---FTLYQFLAFALPFVVTAAVYRILQRMSS 238
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 172 STTAPNSDGSVACNMQMEPERQ--WMAVEVYIAFLMGFLFPVIAICMCIYLLIVKMRV 229

QY 239 VAPASQSRIRLTKRVTRTAIAICLVFVGCMAPIYVQLTQLSISRPLTFVYLYNAIS 298
   | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 230 ALKAGWQQRKKSEKRTILVMVMVTVEVICMMPFHIMQLVSVFVQGHNAT---LSQLAVI 286

QY 299 LGYANSCLNPFVYIVLCETFRK 320
   ||||| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 287 LGYANSCANPILYGFSLDNFRR 308

RESULT 12
Q9PVF9 PRELIMINARY; PRT; 367 AA.
AC Q9PVF9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Somatostatin receptor type 1 subtype B.
GN SST1B.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20005543; PubMed=10537151;
RA Lin X., Janovick J.A., Brothers S., Conn P.M., Peter R.E.;
RT "Molecular cloning and expression of two type one somatostatin
  receptors in goldfish brain.";
RL Endocrinology 140:5211-5219(1999).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF097727; AAF08614.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
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DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 367 AA; 41614 MW; A5BA0AE68D47C455 CRC64;

Query Match      27.4%; Score 499.5; DB 13; Length 367;
Best Local Similarity 30.1%; Pred. No. 1.3e-38;
Matches 97; Conservative 80; Mismatches 120; Indels 25; Gaps 6;

QY 2 DLEASLPTGPNASNTSDGPDNLTSGSPRTGSSISYINIIMPSVFGTICLLGIIGNSTV 61
   :||| | :||| | :||| | :||| | :||| | :||| | :||| | :||| | :||| |
Db 9 NLEDGLYLINFSSNETHNGDSHGSSA-----IFISFYSVCLVGLCGNSMV 55

QY 62 IFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQMGNGVWHFGETMCTLITA 121
   | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 56 IYVIFRYAKMKKTATN---IYILNLAIADLMLSVPLVTSSLLHH-WPFGSLLCRLVLS 111

QY 122 MDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLLMAISFISITPVWLY 181
   :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 112 VDAIMFTSIYCLTVLSIDRYISVHPPIKARTRPTAKMVNLGVMMFSILVILPIITIF 171

QY 182 ARLPEPGGAVGCGIRLPNDPTDLYW---FTLYQFLAFALPFVVTAAVYRILQRMSS 238
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 172 STTAPNSDGSVACNMQMEPERQ--WMAVEVYIAFLMGFLFPVIAICMCIYLLIVKMRV 229

QY 239 VAPASQSRIRLTKRVTRTAIAICLVFVGCMAPIYVQLTQLSISRPLTFVYLYNAIS 298
   | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 230 ALKAGWQQRKKSEKRTILVMVMVTVEVICMMPFHIVQLVSVFVQGHNST---LSOLAVI 286

QY 299 LGYANSCLNPFVYIVLCETFRK 320
   ||||| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 287 LGYANSCANPILYGFSLDNFRR 308

RESULT 13
Q95KS6 PRELIMINARY; PRT; 346 AA.
AC Q95KS6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Somatostatin receptor subtype 1 (Fragment).
GN SST1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PIUTITARY;
RA Debuss N.; Dutour A.; Vuaroqueaux V.; Oliver C.; Ouafik L.;
RT "The ovine somatostatin receptor subtype 1 (osst1): Partial cloning
  and tissue distribution.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PIUTITARY;
RA Debuss N.;
RL Thesis (1999), 'Intercellular communications in Endocrinology,
  Department of Aix-Marseilles II, Marseilles, France.
RL University of Aix-Marseilles II, Marseilles, France.
DR EMBL; AJ314853; CAC69545.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 346 AA; 38479 MW; 65547713CF2CA5C6 CRC64;

Query Match      27.1%; Score 494.5; DB 6; Length 346;
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Thu Feb 20 11:33:09 2003

us-09-885-478-28.rspt

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Search completed: February 13, 2003, 14:00:17
Job time : 25.477 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:50:36 ; Search time 11.5013 Seconds
(without alignments)
1273.004 Million cell updates/sec

Title: US-09-885-478-28
Perfect score: 1824
Sequence: 1 MDLEASLPTGPNASNTSDG.....LRAVSNAQTADERTESKGT 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_A0:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1763	96.7	353	1 GP24_RAT	P97639 rattus norv
2	1692	92.8	402	1 GP24_HUMAN	Q99705 homo sapien
3	530.5	29.1	369	1 SSR2_HUMAN	P30874 homo sapien
4	529.5	29.0	369	1 SSR2_MOUSE	P30875 mus musculu
5	528	28.9	368	1 SSR2_BOVIN	P34993 bos taurus
6	524.5	28.8	369	1 SSR2_PIG	P34994 sus scrofa
7	524.5	28.8	369	1 SSR2_RAT	P30680 rattus norv
8	505.5	27.7	388	1 SSR4_HUMAN	P31391 homo sapien
9	504.5	27.7	418	1 SSR3_HUMAN	P32745 homo sapien
10	497.5	27.3	391	1 SSR1_RAT	P28646 rattus norv
11	496.5	27.2	391	1 SSR1_HUMAN	P30872 homo sapien
12	496.5	27.2	391	1 SSR1_MOUSE	P30873 mus musculu
13	494.5	27.1	384	1 SSR4_RAT	P30937 rattus norv
14	483	26.5	384	1 SSR4_MOUSE	P49660 mus musculu
15	480.5	26.3	364	1 SSR3_RAT	P30936 rattus norv
16	478.5	26.2	364	1 SSR5_HUMAN	P35346 homo sapien
17	472	25.9	428	1 SSR3_MOUSE	P30935 mus musculu
18	470.5	25.8	363	1 SSR5_RAT	P30938 rattus norv
19	456	25.0	362	1 SSR5_MOUSE	O08858 mus musculu
20	451	24.7	372	1 OPRD_HUMAN	P41143 homo sapien
21	450	24.7	400	1 OPRM_MACMU	Q9MYW9 macaca mula
22	446.5	24.5	372	1 OPRD_RAT	P33533 rattus norv
23	444	24.3	400	1 OPRM_HUMAN	P35372 homo sapien
24	442.5	24.3	398	1 OPRM_MOUSE	P42866 mus musculu
25	442.5	24.3	401	1 OPRM_BOVIN	P79350 bos taurus
26	442	24.2	398	1 OPRM_RAT	P33535 rattus norv
27	441	24.2	372	1 OPRD_MOUSE	P32300 mus musculu
28	436.5	23.9	401	1 OPRM_PIG	Q95247 sus scrofa
29	433.5	23.8	380	1 OPRK_HUMAN	P41145 homo sapien
30	426	23.4	380	1 OPRK_CAVPO	P41144 cavia porce
31	421	23.1	328	1 GPR7_HUMAN	P48145 homo sapien
32	419	23.0	380	1 OPRK_MOUSE	P33534 mus musculu
33	419	23.0	380	1 OPRK_RAT	P34975 rattus norv

34	418.5	22.9	370	1 OPRX_CAVPO	P47748 cavia porce
35	409.5	22.5	333	1 OPR8_HUMAN	P48146 homo sapien
36	408.5	22.4	370	1 OPRX_HUMAN	P41146 homo sapien
37	406.5	22.3	367	1 OPRX_MOUSE	P35377 mus musculu
38	406.5	22.3	367	1 OPRX_RAT	P35370 rattus norv
39	393.5	21.6	370	1 OPRX_PIG	P79292 sus scrofa
40	372.5	20.4	359	1 AG2R_CHICK	P79785 gallus gall
41	372.5	20.4	359	1 AG2R_MELGA	P73396 meleagris g
42	370	20.3	363	1 AG2S_XENLA	P35373 xenopus lae
43	368	20.2	362	1 AG2R_XENLA	P32303 xenopus lae
44	359.5	19.7	352	1 P2Y7_HUMAN	Q15722 homo sapien
45	350	19.2	353	1 CKR8_MOUSE	P56484 mus musculu

ALIGNMENTS

RESULT 1	ID	GP24_RAT	STANDARD;	PRT;	353 AA.
AC	P97639;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Probable G protein-coupled receptor GPR24 (SLC-1).				
GN	GPR24 OR SLC1.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=98193144; PubMed=9531978;				
RA	Lakaye B., Minet A., Zorzi W., Grisar T.;				
RT	"Cloning of the rat brain cDNA encoding for the SLC-1 G protein-				
RL	coupled receptor reveals the presence of an intron in the gene.";				
RN	Biochim. Biophys. Acta 1401:216-220(1998).				
RP	SEQUENCE OF 143-300 FROM N.A.				
RX	MEDLINE=97131607; PubMed=8977118;				
RA	Kolakowski L.F. Jr., Jung B.P., Nguyen T., Johnson M.P., Lynch K.R.,				
RT	Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;				
RL	"Characterization of a human gene related to genes encoding				
RT	somatostatin receptors.";				
FEBS	lett. 398:253-258(1996).				
CC	-1- FUNCTION: ORPHAN RECEPTOR. DOES NOT SEEM TO BIND TO SOMATOSTATIN.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	SIMILAR TO SOMATOSTATIN RECEPTORS.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AF008650; AAC27977.1; -.				
DR	EMBL; U77953; AAC14588.1; -.				
DR	InterPro; IPR000276; GPCR_Rhodpsn.				
DR	InterPro; IPR004047; MCH1receptor.				
DR	Pfam; PF00001; 7tm_1; 1.				
DR	PRINTS; PR00237; GPCRHRHODPSN.				
DR	PRINTS; PR01507; MCH1RECEPTOR.				
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.				
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.				
KW	G-protein coupled receptor; Transmembrane.				
FT	DOMAIN 1 45				
FT	TRANSMEM 46 66				
FT	DOMAIN 67 79				
FT	DOMAIN 80 100				
FT	TRANSMEM 80 100				
FT	2 (POTENTIAL).				

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FT DOMAIN 101 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 139 3 (POTENTIAL).
FT DOMAIN 140 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 182 4 (POTENTIAL).
FT DOMAIN 183 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 225 5 (POTENTIAL).
FT DOMAIN 226 256 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 277 6 (POTENTIAL).
FT DOMAIN 278 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 315 7 (POTENTIAL).
FT DOMAIN 316 353 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 353 AA; 39063 MW; F6EEB2DF381084A9 CRC64;

Query Match 96.7%; Score 1763; DB 1; Length 353;
Best Local Similarity 96.0%; Pred. No. 3.5e-95;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRRTGSISYINIMPSVFGTICLLGIGNST 60
   |||: ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MDLQTSLSLSTGPNASNISDQDNLTLPGSPRRTGSVSYINIMPSVFGTICLLGIGNST 60

QY 61 VIFAVVKKSKLHWCNNVPDIFIINLSYVDLFLGLGMPFMIHQMGNGVWHFGETMCTLIT 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 VIFAVVKKSKLHWCNSNPDIIFILNSYVDLFLGLGMPFMIHQMGNGVWHFGETMCTLIT 120

QY 121 AMDANSQFTSYILLTAMADRYLATVHPISSTKFRKPSVATLYICLLWALSFSISITPYWL 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 AMDANSQFTSYILLTAMTIDRYLATVHPISSTKFRKPSMATLYICLLWALSFSISITPYWL 180

QY 181 YARLIFPFGGAVCGCIRLPNPDITLYWFTLYQFPLAFALPFVYITAAVYRIQRMTSVA 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 YARLIFPFGGAVCGCIRLPNPDITLYWFTLYQFPLAFALPFVYITAAVYKIQRMTSSVA 240

QY 241 PASQSRIRLRKRVTRTAIAICLVFVCWAPYVYLQTLQSLISRPRTLTFVYLYNAAISLG 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 PASQSRIRLRKRVTRTAIAICLVFVCWAPYVYLQTLQSLISRPRTLTFVYLYNAAISLG 300

QY 301 YANSCLNPFVYIVLCETFRKRLVLSVKRPAQGLRAVSNAGTADERTESKGT 353
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 YANSCLNPFVYIVLCETFRKRLVLSVKRPAQGLRTVSNAGTADERTESKGT 353

RESULT 2
GP24_HUMAN STANDARD; PRT; 402 AA.
ID GP24_HUMAN 099705;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor GPR24 (SLC-1).
GN GPR24 OR SLC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiwich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burdill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

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RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurtry A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavlitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon I., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shaikh T., Kurahashi H., Saita S., Budarf M.L.,
RA Mcdermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyraud M., Kedra D.,
RA Seroussi E., Franszou I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tiliahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
CC -I- FUNCTION: ORPHAN RECEPTOR. DOES NOT SEEM TO BIND TO SOMATOSTATIN.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: GREATEST ABUNDANCE IN BRAIN, PARTICULARLY IN
CC THE FRONTAL CORTEX AND HYPOTHALAMUS. A LOWER LEVEL EXPRESSION IS
CC SEEN IN THE LIVER AND HEART.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC SIMILAR TO SOMATOSTATIN RECEPTORS.
CC -----
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CC -----
CC EMBL: U71092; AAC14587.1; -.
CC EMBL: Z86090; CAB62943.1; -.
CC Genew; HGNC:4479; GPR24.
CC MIM: 601751; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC InterPro; IPR004047; MCH1receptor.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRRHODPSN.
CC PRINTS; PR01507; MCH1RECEPTOR.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
CC PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane.
KW DOMAIN 1 94
FT TRANSMEM 95 115 1 (POTENTIAL).
FT DOMAIN 116 128 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 129 149 2 (POTENTIAL).
FT DOMAIN 150 167 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 168 188 3 (POTENTIAL).
FT DOMAIN 189 210 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 211 231 4 (POTENTIAL).
FT DOMAIN 232 253 EXTRACELLULAR (POTENTIAL).

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FT  TRANSMEM  254  274  5 (POTENTIAL).
FT  DOMAIN    275  305  CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM  306  326  6 (POTENTIAL).
FT  DOMAIN    327  343  EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM  344  364  7 (POTENTIAL).
FT  DOMAIN    365  402  CYTOPLASMIC (POTENTIAL).
SQ  SEQUENCE   402 AA; 44454 MW; 5D24B72E76CF4F82 CRC64;

Query Match          92.8%; Score 1692; DB 1; Length 402;
Best Local Similarity 99.4%; Pred. No. 4.7e-91;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  24  LTSAGSPRTGSISYINIIIMPSVFGTICLGIIGNSTVIFAVVKSKLHWCNNVPDIFI 83
DB  73  LLSPGSPRTGSISYINIIIMPSVFGTICLGIIGNSTVIFAVVKSKLHWCNNVPDIFI 132
QY  84  NLSVVDLFLGMPFMIHQLMNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIIDRYL 143
DB  133  NLSVVDLFLGMPFMIHQLMNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIIDRYL 192
QY  144  ATVHPISSTKFRKPSVATLVICLMLALSFISITPVWLYARLIPPEGAVGCGIRLPNPD 203
DB  193  ATVHPISSTKFRKPSVATLVICLMLALSFISITPVWLYARLIPPEGAVGCGIRLPNPD 252
QY  204  DLYWETLYQFFIAFALPFEVITAAYVRIQRMSTSSVAPASQSRIRLTKRVRTAIAICL 263
DB  253  DLYWETLYQFFIAFALPFEVITAAYVRIQRMSTSSVAPASQSRIRLTKRVRTAIAICL 312
QY  264  VEFVCMAPYVYQLTQLSISRPTLTFFVLYNNAISLGYSNCLENPFVYIVLCETFRKRLV 323
DB  313  VEFVCMAPYVYQLTQLSISRPTLTFFVLYNNAISLGYSNCLENPFVYIVLCETFRKRLV 372
QY  324  LSVKPAAGOLRAVSNAOQTADERETESKGT 353
DB  373  LSVKPAAGOLRAVSNAOQTADERETESKGT 402

RESULT 3
SSR2_HUMAN
ID  SSR2_HUMAN  STANDARD;  PRT;  369 AA.
AC  P30874;
DT  01-JUL-1993 (Rel. 26, Created)
DT  01-JUL-1993 (Rel. 26, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Somatostatin receptor type 2 (SS2R) (SRIF-1).
GN  SS2R2.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=92108031; PubMed=1346068;
RA  Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;
RT  "Cloning and functional characterization of a family of human and
RT  mouse somatostatin receptors expressed in brain, gastrointestinal
RT  tract, and kidney.";
RL  Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
RN  [2]
RP  ALTERNATIVE SPLICING.
RX  MEDLINE=93236586; PubMed=8386508;
RA  Patel Y.C., Greenwood M., Kent G., Panetta R., Srikant C.B.;
RT  "Multiple gene transcripts of the somatostatin receptor SS2R2: tissue
RT  selective distribution and cAMP regulation.";
RL  Biochem. Biophys. Res. Commun. 192:288-294(1993).
RN  [3]
RP  INTERACTION WITH SHANK1.
RX  MEDLINE=20020275; PubMed=10551867;
RA  Zitzer H., Hoencck H.-H., Baechner D., Richter D., Kreienkamp H.-J.;
RT  "Somatostatin receptor interacting protein defines a novel family of
RT  multidomain proteins present in human and rodent brain.";
RL  J. Biol. Chem. 274:32997-33001(1999).
CC  -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
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CC  COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC  ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
CC  PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC  SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CC  CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC  -1- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain.
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
CC  PRODUCED BY ALTERNATIVE SPLICING.
CC  -1- TISSUE SPECIFICITY: CEREBRUM AND KIDNEY. IN LESSER AMOUNTS IN
CC  JEJUNUM, COLON, AND LIVER.
CC  -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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CC  or send an email to license@isb-sib.ch).
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DB  EMBL; M81830; AAA58248.1; -.
DB  PIR; B41795; B41795.
DB  HSSP; P02699; IBOJ.
DB  Genew; HGNC:11331; SS2R2.
DB  MIM; 182452; -.
DB  InterPro; IPR000276; GPCR_Rhodpsn.
DB  Pfam; PF00001; 7tm_1; 1.
DB  PRINTS; PR00237; GPCR_RHODOPSIN.
DB  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DB  PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW  G-protein coupled receptor; Transmembrane; Glycoprotein;
KW  Multigene family; Lipoprotein; Palmitate; Alternative splicing.
FT  DOMAIN 1 44 43 43
FT  TRANSMEM 44 67 78
FT  DOMAIN 68 78 103
FT  TRANSMEM 79 103 103
FT  DOMAIN 104 118 118
FT  TRANSMEM 119 138 138
FT  DOMAIN 139 161 161
FT  TRANSMEM 162 181 181
FT  DOMAIN 182 207 207
FT  TRANSMEM 208 229 229
FT  DOMAIN 230 253 253
FT  TRANSMEM 254 278 278
FT  DOMAIN 279 288 288
FT  TRANSMEM 289 303 303
FT  DOMAIN 304 369 369
FT  CARBOHYD 9 9
FT  CARBOHYD 22 22
FT  CARBOHYD 29 29
FT  CARBOHYD 32 32
FT  DISULFID 115 193
FT  LIPID 328 328
FT  VARSPPLIC 332 369
SQ  SEQUENCE 369 AA; 41332 MW; 3B5D7D8A9AC246C6 CRC64;

Query Match          29.1%; Score 530.5; DB 1; Length 369;
Best Local Similarity 31.8%; Pred. No. 2.9e-24;
Matches 114; Conservative 75; Mismatches 128; Indels 41; Gaps 8;

QY  2  DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIIIMPSVFGTICLGIIGNSTY 61
DB  20  DLNGSVST--NTSNQTEPYDLTS-----NAVLTFYFVVCIIIGLCGNTLY 64
QY  62  IFAVVKSKLHWCNNVPDIFIINLSYVDLFLGMPF-----MIHQLMNGVWHFGETM 115
DB  65  IYVILRYAKM---KITINIIYILNLAIDELFMLGLPFLMAQVALVH-----WPEGKAI 114
QY  116  CTLITAMDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLMLALSFISI 175
DB  115  CRVVMYVDGINGQFTSIFCLTVMSIDRYLAVVHPIKSAKWRPRTAKMITMAVWGVSILVI 174
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[illegible]

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RESULT 4
SSR2_MOUSE
ID      SSR2_MOUSE      STANDARD;      PRT;      369 AA.
AC      P30875; P30934;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Somatostatin receptor type 2 (SS2R) (SRIF-1) (SS2RA and SS2RB).
GN      SS2R OR SMS2R2.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92108031; PubMed=1346068;
RA      Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Selino S.;
RT      "Cloning and functional characterization of a family of human and
RT      mouse somatostatin receptors expressed in brain, gastrointestinal
RT      tract, and kidney.";
RL      Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93012001; PubMed=1397330;
RA      Vanetti M., Kouba M., Wang X., Vogt G., Hoellt V.;
RT      "Cloning and expression of a novel mouse somatostatin receptor
RT      (SS2RB).";
RL      FEBS Lett. 311:290-294(1992).
RN      [3]
RP      SEQUENCE OF 99-309 FROM N.A.
RX      MEDLINE=94300079; PubMed=7913111;
RA      Elliott D.E., Metwalli A., Blum A.M., Sandor M., Lynch R.,
RA      Weinstein J.V.;
RT      "T lymphocytes isolated from the hepatic granulomas of schistosoma-
RT      infected mice express somatostatin receptor subtype II (SS2R2)
RT      messenger RNA.";
RL      J. Immunol. 153:1180-1186(1994).
RN      [4]
RP      CHARACTERIZATION.
RX      MEDLINE=93387480; PubMed=8104154;
RA      Vanetti M., Hoellt V.;
RT      "The two isoforms of the mouse somatostatin receptor (mSS2RA and
RT      mSS2RB) differ in coupling efficiency to adenylylate cyclase and in
RT      agonist-induced receptor desensitization.";
RL      FEBS Lett. 331:260-266(1993).
CC      -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC      COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC      ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
CC      PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC      SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CC      CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC      -1- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (By
CC      similarity).
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SS2RA (SHOWN HERE) AND SS2RB;
CC      ARE PRODUCED BY ALTERNATIVE SPLICING.
CC      -1- TISSUE SPECIFICITY: CEREBRUM AND KIDNEY.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----

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DR	EMBL; M81832; AAA58256.1; -. EMBL; X68951; CAA48766.1; -. EMBL; S71756; -; NOT_ANNOTATED_CDS. PIR; D41795; D41795. PIR; S29248; S29248. HSSP; P02699; 1BOJ. MGI; MGI:98328; Smstr2. InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1. PRINTS; PR00237; GPCR RHODOPSIN. PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1. PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1. KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate; Alternative splicing.	FT DOMAIN 1 43 FT TRANSMEM 44 67 FT DOMAIN 68 78 FT TRANSMEM 79 103 FT DOMAIN 104 118 FT TRANSMEM 119 138 FT DOMAIN 139 161 FT TRANSMEM 162 181 FT DOMAIN 182 207 FT TRANSMEM 208 229 FT DOMAIN 230 253 FT TRANSMEM 254 278 FT DOMAIN 279 288 FT TRANSMEM 289 303 FT DOMAIN 304 369 FT CARBOHYD 9 9 FT CARBOHYD 22 22 FT CARBOHYD 29 29 FT CARBOHYD 32 32 FT DISULFID 115 193 FT LIPID 328 328 FT VARSPLIC 332 369	FT CONFLICT 179 179 FT CONFLICT 305 305 SEQUENCE 369 AA; 41221 MW; A78845AF74823039 CRC64;
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Query Match	29.0%;	Score 529.5;	DB 1;	Length 369;	
Best Local Similarity	31.8%;	Pred. No. 3.3e-24;			
Matches 114;	Conservative 75;	Mismatches 128;	Indels 41;	Gaps	8;

QY	2	DLFASLPTGPNASNTSDGPNLTSAGSPPRGTSISYINIIIMPSVEGTCLIGIGNSTV	61
		: : : : : : :	
Db	20	DLNGSLGPS--NGSNQTEPYDMTS-----NAVLTFIYFVVCVGLCGNTLV	64
QY	62	IFAVVKKSKLHWCNNVDPDIFINLSVDLFLTGMF-----MIHQLMGNGVWHFETM	115
		: : : : : : : : : : : : : : :	
Db	65	IYVILRRAKM--KTITNIYILNLAIADLFMLGLPFLAMQVALVH-----WPF GKAI	114
QY	116	CTLITAMDANSQFTSTYIILFAMAIDRYLATVHPISSTFKRKPVSATVLICLIMALSFSI	175
		: : : : : : : : : : : : : : : : : :	
Db	115	CRVVMFTVDGINQFTSIFCLFTVMSIDRYLAVVHPIKSAKWRKRPRTAKMINVAWCVSLAVI	174
QY	176	TPVWLVAKLIPFGGAVGCGIRLENPDTDLV-WFTLQGFALFALPFVVTIAYVRIIQR	234
		: : : : : : : : : : :	
Db	175	LPIMITYAGLRSNQWGRSSCTINWGESGAWYGTGFTIYAFILGFLVPLTIICLCYLFITIK	234
QY	235	MTSSVAPASQORSIRLRTKRVTRTAIAICLVFVVCWAPYVVLQLTQLSIS-RPTLLTFVLY	293
		: : : : : : : : : : : : : : : :	
Db	235	VKSSGIRVSSKRRKKSEKKVTRNVAIVAVFIFCWLPEYIFENVSSVSAISIPALKGMF	294

QY 294 NAAISLGANSCNPEYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESK 351
Db 295 DEVLITLYANSCANPILYAFLSDNFKK-----SFQNVLCIVKVSGETEDGERSDSK 344

```
RESULT 5
SSR2_BOVIN          STANDARD:          PRT;          368 AA.
ID  SSR2_BOVIN
AC  P34993;
DT  01-FEB-1994 (Rel. 28, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Somatostatin receptor type 2 (SS2R) (SRIF-1).
GN  SS2R2.
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC  Bovidae; Bovinae; Bos.
OX  NCBI_TaxID=9913;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Brain;
RA  Xin W.W., Wong M.-L., Rimland J., Nestler E.J., Duman R.S.;
RL  Submitted (XXX-1992) to the EMBL/Genbank/DBJ databases.
CC  -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC  COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC  ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
CC  PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC  SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CC  CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC  -1- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (By
CC  similarity).
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC  -----
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CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; L06613; AAA30764.1; -.
DR  HSSP; P02699; 1BOJ.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCR_RHODOPSIN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW  G-protein coupled receptor; Transmembrane; Glycoprotein;
KW  Multigene family; Lipoprotein; Palmitate.
FT  DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 66 1 (POTENTIAL).
FT  DOMAIN 67 77 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 78 102 2 (POTENTIAL).
FT  DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 118 137 3 (POTENTIAL).
FT  DOMAIN 138 160 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 161 180 4 (POTENTIAL).
FT  DOMAIN 181 206 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 207 228 5 (POTENTIAL).
FT  DOMAIN 229 252 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 253 277 6 (POTENTIAL).
FT  DOMAIN 278 287 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 288 302 7 (POTENTIAL).
FT  DOMAIN 303 368 CYTOPLASMIC (POTENTIAL).
FT  CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  DISULFID 114 192 BY SIMILARITY.
FT  LIPID 327 327 PALMITATE (POTENTIAL).
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SEQ SEQUENCE 368 AA; 41133 MW; B5852262a6b808b CRC64;
Query Match 28.9%; Score 528; DB 1; Length 368;
Best Local Similarity 31.5%; Pred. No. 4e-24;
Matches 116; Conservative 76; Mismatches 134; Indels 42; Gaps 9;

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QY 1 MDLEASLPTGPNAS-----NTSDGPDNLTSGSPRRGISISYI---NIIMPSVEGTIC 51
Db 1 MDLVSELNETQPMWLTTPFDLNGSYGANISNQTEP-----YYDLASNVYLFIYFVVC 53
QY 52 LLGIIGNSTVIFAVVKSKSLHMCNNVPDIFIINLSYVDLLFLGMPF-----MIHQLMG 105
Db 54 IIGLCGNTLYIVYILRYAKM--KTITNITYILNLAIADLEFMLGLPFLAMQVALVH---- 106
QY 106 NGVWHFGEIMCTLITAMDANSQFTSYILLTAMADRYLATVHPISSTKFRKPSVATLIVIC 165
Db 107 ---WPFKALCRVMTVDGINQFTSFCLTVMSIDRYLAVVHPIKSAKWRDRRTAKMINV 163
QY 166 LLMALSFISTPVMLYARLIPFGAGVCGIRLPNPDILY-WFTLYQFFLAFLPENVI 224
Db 164 AVWGVSLLVILPIMITYAGLRSNQWGRSSCTINWPGESGAWTGFIIYAFILGLVPLTII 223
QY 225 TAAYVRILQRMNTSSVAPASQSRIRLRTKRVTRTAICLVFEVCMAPYVVLQTLQSLIS- 283
Db 224 CLCYLFIILIKYSSGIRVSSKRRKSEKVTBMVSIVAVFICWLPFIENVSYSVAI 283
QY 284 RPTLTFVLYNAISLGANSCNPEYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTA 343
Db 284 SPTPALKGMEFVVVLTLYANSCANPILYAFLSDNFKK-----SFQNVLCIVKVSGETD 335
QY 344 DEERTESK 351
Db 336 DGERSDSK 343
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RESULT 6
SSR2_PIG          STANDARD:          PRT;          369 AA.
ID  SSR2_PIG
AC  P34994;
DT  01-FEB-1994 (Rel. 28, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Somatostatin receptor type 2 (SS2R) (SRIF-1).
GN  SS2R2.
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX  NCBI_TaxID=9823;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=94168590; PubMed=8123027;
RA  Matsumoto K., Yokogoshi Y., Fujinaka Y., Zhang C., Saito S.;
RT  "Molecular cloning and sequencing of porcine somatostatin receptor
RT  2."
RL  Biochem. Biophys. Res. Commun. 199:298-305(1994).
CC  -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC  COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC  ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
CC  PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC  SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CC  CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC  -1- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (By
CC  similarity).
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
```

CC EMBL; D21338; BAA04810.1; -.
DR PIR; JC2083; JC2083.
DR HSSP; P02699; 1BOJ.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPS_N.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
Multi-gene family; Lipoprotein; Palmitate.
KW DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 67 1 (POTENTIAL).
FT DOMAIN 68 78 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 79 103 2 (POTENTIAL).
FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 138 3 (POTENTIAL).
FT DOMAIN 139 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 181 4 (POTENTIAL).
FT DOMAIN 182 207 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 208 229 5 (POTENTIAL).
FT DOMAIN 230 253 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 254 278 6 (POTENTIAL).
FT DOMAIN 279 288 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 289 303 7 (POTENTIAL).
FT DOMAIN 304 369 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 9 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 115 193 BY SIMILARITY.
FT LIPID 328 328 PALMITATE (POTENTIAL).
SQ SEQUENCE 369 AA; 41218 MW; C4C8347764EA2E70 CRC64;

Query Match 28.8%; Score 524.5; DB 1; Length 369;
Best Local Similarity 31.6%; Pred. No. 6.3e-24;
Matches 113; Conservative 75; Mismatches 129; Indels 41; Gaps 8;

QY 2 DLEASLLPTGPNASNTSDGPDNLTSAGSPRTGISISYINIIMPSVFGTICLLGIGNSTV 61
DB 20 DLNGSVATA--NSSNQTPEPYDLTS-----NAVLTFTYFVVCIIIGLCGNTLV 64
QY 62 IEAVVKKSKLHWCNNVDPDITINLSVVDLLFLGMPE-----MIHQLMGNGVWHFGETM 115
DB 65 IYVILRYAKM--KTITNIYILNLAIADLFMLGLPFLAMQVALVH-----WPF GKAI 114
QY 116 CTLITAMDANSQFTSYILITAMAIDRYLATVHPISSTKFKKPSVATLVICLLMALSFISI 175
DB 115 CRVYMTVDGINQFTSIFCLTWSIDRYLAVVHPKSAKWRPRPTAKMINAVAGVSLVI 174
QY 176 TPVWMLYARLIPFGGAVGCGIRLPNDTDLV-WFTLYQFELAFALPFVVITAAVYRILQR 234
DB 175 LPIIMTYAGLRSNQWGRSSCTINWPGESGAWYTGFIITAFILGLVPLTITICLCYLFIIIK 234
QY 235 MTSSVAPASQSRIRLRTKRYTRITAIACLVFVCAADPYVVLQTLQSLIS-RPTLTFVYLY 293
DB 235 VKSSGIRVGSSKRKKSEKVTTRVSVIVAVFIECWLPIYIFNVSSVSAISPTPALKGMF 294
QY 294 NAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAGQDLRAVSNAQTADEERTESK 351
DB 295 DFVVVLTLYANSCANPILYAFILSDNFK-----SFQNVLCLVKVSGETDGERSDSK 344

RESULT 7
SSR2_RAT
ID SSR2_RAT STANDARD; PRT; 369 AA.
AC P30680;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor type 2 (SS2R) (SRIF-1).
GN SSTR2.
OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92262491; PubMed=1374909;
RA Kluxen F.-W., Bruns C., Luebert H.;
RT "Expression cloning of a rat brain somatostatin receptor cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4618-4622(1992).
RN [2]
RP SEQUENCE OF 76-81; 179-189; 294-320 AND 350-358.
RC TISSUE=Pituitary;
RX MEDLINE=92231915; PubMed=1348934;
RA Hulmes J.D., Corbett M., Zysk J.R., Boehlen P., Epler C.M.;
RT "Partial amino acid sequence of a somatostatin receptor isolated from
GH4Cl pituitary cells.";
RL Biochem. Biophys. Res. Commun. 184:131-136(1992).
RN [3]
RP ALTERNATIVE SPLICING.
RX MEDLINE=93236586; PubMed=8386508;
RA Patel Y.C., Greenwood M., Kent G., Panetta R., Srikant C.B.;
RT "Multiple gene transcripts of the somatostatin receptor SSTR2: tissue
selective distribution and cAMP regulation.";
RL Biochem. Biophys. Res. Commun. 192:288-294(1993).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC -1- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (By
similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: CORTEX, HIPPOCAMPUS, PITUITARY GLAND, COLON
ADRENALS, PANCREAS-DERIVED CELL LINE, AND PANCREATIC TUMOR.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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or send an email to license@isb-sib.ch).

CC EMBL; M96817; AAA42166.1; -.
DR EMBL; M93273; AAA42165.1; -.
DR PIR; A45291; A45291.
DR HSSP; P02699; 1BOJ.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPS_N.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
Multi-gene family; Lipoprotein; Palmitate; Alternative splicing.
KW DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 67 1 (POTENTIAL).
FT DOMAIN 68 78 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 79 103 2 (POTENTIAL).
FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 138 3 (POTENTIAL).
FT DOMAIN 139 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 181 4 (POTENTIAL).
FT DOMAIN 182 207 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 208 229 5 (POTENTIAL).
FT DOMAIN 230 253 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 254 278 6 (POTENTIAL).
FT DOMAIN 279 288 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 289 303 7 (POTENTIAL).

FT DOMAIN 304 369 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 9 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 115 193 BY SIMILARITY.
FT LIPID 328 328 PALMITATE (POTENTIAL).
FT VARSPLIC 332 369 VSGAEDGERSDSKQDKSRINETTERORTLLNGDLQTSI ->
FT SEQUENCE 369 AA; 41199 MW; 4990E489E88D7D19 CRC64;

Query Match 28.8%; Score 524.5; DB 1; Length 369;
Best local Similarity 31.6%; Pred. No. 6.3e-24;
Matches 113; Conservative 75; Mismatches 129; Indels 41; Gaps 8;

QY 2 DLEASLPTGPNASNTSDGPNLTSAGSPRTGSISYINIIIMPSVFGTCLLGIIGNSTV 61
DB 20 DLNGSLGPS--NGSNQTEPYWMTS-----NAVLTFYFVVCVGLCGNTLY 64
QY 62 IFAVVKSKLHWCNNVPDIFITNLVVDLFLGMPF-----MIHQLMGNGVWHFGETM 115
DB 65 IYVILRYAKM--KITITNYILNLAIADLFLMLGLPEFLAMQVALVH-----WPEGKAI 114
QY 116 CTLITAMDANSQFTSTYILFAMAIDRYLATVHPISSTKFRKPSVATVLCILMALSFISI 175
DB 115 CRVVMYVDGINQFTSIFCLTVMSIDRYLAVVHPKSAKWRPRPTAKMINAVMGVSLVVI 174
QY 176 TPVWLVARLIPFPGGAVGCGIRLPNPDLDLY-WETLYQFLFALPFEVITAAYVRILQR 234
DB 175 LPMITVAGLRSNQWGRSSCTINMGESGAWYTGFIYAFILGFLVPLTICLCYLFITIK 234
QY 235 MTSSVAPASQSRIRLTKRVFTFAIAICLVFVCNAPYVVLQTLQLSIS-RPTLFEVLY 293
DB 235 VKSSGIRYSSSKRKSEKKVTIMVSIIVAVFICMLPEYIENVSSVSVALSPTPALKGMF 294
QY 294 NAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAQGLRAVSNAQTADERTESK 351
DB 295 DFVVLITYANSCANPILYAFLSDNFKK-----SFQNVLCLVKVSQAEDGERSDSK 344

RESULT 8
SSR4_HUMAN
ID SSR4_HUMAN STANDARD; PRT; 388 AA.
AC P31391; Q9UIY1;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor type 4 (SS4R).
GN SSTR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93290656; PubMed=8512564;
RA Xu Y., Song J., Bruno J.F., Berelowitz M.;
RT "Molecular cloning and sequencing of a human somatostatin receptor,
hsSTR4.";
RL Biochem. Biophys. Res. Commun. 193:648-652(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93248256; PubMed=8483934;
RA Rohrer L., Raulf F., Bruns C., Buettner R., Hofstaedter F.,
RA Schuele R.;
RT "Cloning and characterization of a fourth human somatostatin
receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:4196-4200(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93384611; PubMed=8373420;
RA Yamada Y., Kagimoto S., Kubota A., Yasuda K., Masuda K., Someya Y.,
RA Ihara Y., Li Q., Imura H., Seino S., Seino Y.;

RT "Cloning, functional expression and pharmacological characterization
of a fourth (hsSTR4) and a fifth (hsSTR5) human somatostatin receptor
subtype.";
RT Biochem. Biophys. Res. Commun. 195:844-852(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93302729; PubMed=8100352;
RA Demchyshyn L.L., Srikant C.B., Sunahara R.K., Kent G., Seeman P.,
RA van Tol H.H.M., Panetta R., Patel Y.C., Niznik H.B.;
RT "Cloning and expression of a human somatostatin-14-selective receptor
variant (somatostatin receptor 4) located on chromosome 20.";
RL Mol. Pharmacol. 43:894-901(1993).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagunley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McElay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Yau Din M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
CC CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF
CC ADENYLYLATE CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE
CC RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
CC MEDIATES ANTIPROLIFERATIVE ACTION OF SOMATOSTATIN IN TUMOR CELLS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN FETAL AND ADULT
CC BRAIN, LUNG TISSUE, STOMACH, AND IN LESSER QUANTITIES IN THE
CC KIDNEY, PITUITARY, AND ADRENALS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D16826; BAA04106.1; -.
CC EMBL: L14856; AAA36623.1; -.
CC EMBL: L07833; AAA60565.1; -.
CC EMBL: L07061; -, NOT_ANNOTATED_CDS.
CC EMBL: AL049651; CAB51953.1; -.
CC PIR: JN0605; JN0605.
CC PIR: JN0762; JN0762.
CC HSSP: P02699; IBOJ.
CC Genew: HGNC:11333; SSTR4.
CC MIM: 182454; -.
CC InterPro: IPR000276; GPCR_Rhodpsn.

DR pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_HODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECIP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate; Phosphorylation;
KW Polymorphism.
FT DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 47 73 1 (POTENTIAL).
FT DOMAIN 74 83 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 84 104 2 (POTENTIAL).
FT DOMAIN 105 120 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 121 142 3 (POTENTIAL).
FT DOMAIN 143 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 185 4 (POTENTIAL).
FT DOMAIN 186 208 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 232 5 (POTENTIAL).
FT DOMAIN 233 260 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 261 280 6 (POTENTIAL).
FT DOMAIN 281 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 314 7 (POTENTIAL).
FT DOMAIN 315 388 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 24 24 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 119 198 BY SIMILARITY.
FT LIPID 327 327 PALMITATE (POTENTIAL).
FT VARIANT 83 83 N -> T (IN DBSNP:1065191).
FT CONFLICT 284 284 /FTid=VAR_011703.
FT CONFLICT 321 321 V -> F (IN REF. 4 AND 5).
FT CONFLICT 365 365 S -> F (IN REF. 5).
FT CONFLICT 365 365 P -> K (IN REF. 2).
SQ SEQUENCE 388 AA; 41894 MW; 8BCCD69B5F3BC2F5 CRC64;

Query Match 27.7%; Score 505.5; DB 1; Length 388;
Best Local Similarity 32.0%; Pred. No. 8.2e-23;
Matches 107; Conservative 73; Mismatches 117; Indels 37; Gaps 9;

QY 6 SLPTG-----PNASNTSDGPDNLTASGSPRTGISYINIMPSVFGTICLGI 56
DB 5 STLPGEGLGTAMPSSANASSAPAEAEAVAGPGDARAAGM-VAICICIALVCLGLV 63
QY 57 GNSVIFAIVKSKLHWCNNVDFIINLSVVDLLFLGMPFI-----HQLMGNGVWH 110
DB 64 GNAIVFVILRYAKMKKTATN--TYLLNLAVALDELFLSVFVASSAALRH-----WP 113
QY 111 EGETMCTLTAMDANSQSTSTYILLTAMADRYLATVHPISSTKFRKPSVATLVICLWAL 170
DB 114 FGSVLCRAVLSDGLNMTSVFCLTVLSVDRYAVVHPLRAATYRPSVAKLINLGWLA 173
QY 171 SFISITPVWLARLIPPEGG-AVGGCIRLPNDTDLW--FTLYOFELAFALPEVITA 226
DB 174 SLVTLPIAIFADTRPARGGQAVACNLQWPHP---AWSAVFVVYTFLLGLPLVALIGL 229
QY 227 AAYVRLQMTSSVAPASQSRIRLTKRVTRIAICLVFVCWAPYVVLQTLQSLSRPT 286
DB 230 CYLLIVGKRAVALRAGWQRRRSEKKITRLVWVVFVLCWMPFYVQLNLVVTSLD 289
QY 287 LTFVYLYNAISLGYANCLNPFVYIVLCETFRK 320
DB 290 AT---VNHVSLILSYANSCANPILYGLSDNFR 320

RESULT 9
SSR3_HUMAN
ID SSR3_HUMAN STANDARD; PRT; 418 AA.
AC P32745;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor type 3 (SS3R) (SSR-28).
GN SSTR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93149123; PubMed=1337145;
RA Yamada Y., Reisine T., Law S.F., Ihara Y., Kubota A., Kagimoto S.,
RA Selnio M., Selnio Y., Bell G.I., Selnio S.;
RT "Somatostatin receptors, an expanding gene family: cloning and
RT functional characterization of human SSTR3, a protein coupled to
RT adenylyl cyclase.";
RT Mol. Endocrinol. 6:2136-2142(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93238970; PubMed=8097479;
RA Corness J.D., Demchyshyn L.L., Seeman P., van Tol H.H.M.,
RA Strikant C.B., Kent G., Patel Y.C., Niznik H.B.;
RT "A human somatostatin receptor (SSTR3), located on chromosome 22,
RT displays preferential affinity for somatostatin-14 like peptides.";
RT FEBS Lett. 321:279-284(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA Clump M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dochree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McClaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.T.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray E., Ren Q., Shauli S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelman L.,
RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RT Nature 402:489-495(1999).
RL -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLYL CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, PITUITARY AND PANCREAS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; M81829; AAA58247.1; -.
DR PIR; A41795; A41795.
DR Genew; HGNC:11330; SSTR1.
DR MIM; 182451; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate.
FT DOMAIN 1 56 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 57 84 1 (POTENTIAL).
FT DOMAIN 85 94 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 95 120 2 (POTENTIAL).
FT DOMAIN 121 131 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 132 153 3 (POTENTIAL).
FT DOMAIN 154 175 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 176 196 4 (POTENTIAL).
FT DOMAIN 197 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 244 5 (POTENTIAL).
FT DOMAIN 245 270 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 271 296 6 (POTENTIAL).
FT DOMAIN 297 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 327 7 (POTENTIAL).
FT DOMAIN 328 391 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 130 208 BY SIMILARITY.
FT LIPID 339 339 PALMITATE (POTENTIAL).
SQ SEQUENCE 391 AA; 42686 MW; 85C99AFFE339A43D CRC64;

Query Match 27.2%; Score 496.5; DB 1; Length 391;
Best Local Similarity 32.5%; Pred. No. 2.7e-22;
Matches 101; Conservative 68; Mismatches 121; Indels 21; Gaps 5;

QY 11 GPNASNTSDGPDNLTSAGSPRTGISITNIMPVSFGTICLGIGNSTVIEAVKSSK 70
   | ||| : || :::: ||||| :::: ||||| :::: ||
Db 42 GRNASQNGRLSEGQSA-----LLISFIYSVCLVGLCGNMVIYVILRYAK 88

QY 71 LHWCNVPDIFFIINLSVDLFLLGMPFMTHQLMGNGVMHFGETMCTLTAMDANSQETS 130
   | : ||||| : | : | :||| : : ||| : ||| : |||
Db 89 MKTATN--IYLNLAIADELMLSVPELVSTLLRH-WPFGALLCRVLVSDAVNMFTS 144

QY 131 TYLLTAMADRSLATVHPISSTKFKRPSVALTVICLLMALSFISTPYWLYARLPFPG 190
   | || :||| : |||| : ::||| : : ||| : ||| : |||
Db 145 IYCLTVLSVDRYAAVWHPIKARYRRPTAKVNVNLGVWLSLVILPIYVFSRTAANDSG 204

QY 191 AVGGGIRLPNP-DTDLYWFTLYQFFLAFALEFVVITAAYVRILQRMSSVAPASQRSIRL 249
   | : : || : ||| : |||| : ||| : ||| : ||| : |||
Db 205 TVACNMIMPDAQRWLVGFVLYTFIMGFLDPGAICLCYVLIATAKRMVAALKAGWQQRKR 264

QY 250 RTKRVRTTAIAICLVEFCWAPYYVLOLTQSISRPTLTFFVLYLNAAISIGYANSCLNPF 309
   ::| : : || : ||| : |||| : : | : ||||| ||
Db 265 SERKITLMVMVMVVFVICMPPFYVVOVLVNAFAEQDATVSQL--SVILGYANSCANPI 321

QY 310 VYIVLCETFRK 320
   : | : || :
Db 322 LYGFSLDNFKR 332

RESULT 12
SSRL_MOUSE STANDARD; PRT; 391 AA.
AC P30873;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)

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DE Somatostatin receptor type 1 (SSIR) (SRIF-2).
OS SSTR1 OR SMSSTR1.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92108031; PubMed=1346068;
RA Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;
RT "Cloning and functional characterization of a family of human and
RT mouse somatostatin receptors expressed in brain, gastrointestinal
RT tract, and kidney.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
CC -! FUNCTION: RECEPTOR FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR
CC SOMATOSTATIN-14 THAN -28. THIS RECEPTOR IS COUPLED VIA PERTUSSIS
CC TOXIN SENSITIVE G PROTEINS TO INHIBITION OF ADENYL CYCLASE. IN
CC ADDITION IT STIMULATES PHOSPHOTYROSINE PHOSPHATASE AND NA+/H+
CC EXCHANGER VIA PERTUSSIS TOXIN INSENSITIVE G PROTEINS.
CC -! SUBCELLULAR LOCATION: Integral membrane protein.
CC -! TISSUE SPECIFICITY: JEJUNUM AND STOMACH.
CC -! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M81831; AAA58255.1; -.
DR PIR; C41795; C41795.
DR MGD; MG1:98327; Smstr1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; glycoprotein;
KW Multigene family; Lipoprotein; Palmitate.
FT DOMAIN 1 56 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 57 84 1 (POTENTIAL).
FT DOMAIN 85 94 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 95 120 2 (POTENTIAL).
FT DOMAIN 121 131 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 132 153 3 (POTENTIAL).
FT DOMAIN 154 175 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 176 196 4 (POTENTIAL).
FT DOMAIN 197 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 244 5 (POTENTIAL).
FT DOMAIN 245 270 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 271 296 6 (POTENTIAL).
FT DOMAIN 297 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 327 7 (POTENTIAL).
FT DOMAIN 328 391 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 130 208 BY SIMILARITY.
FT LIPID 339 339 PALMITATE (POTENTIAL).
SQ SEQUENCE 391 AA; 42718 MW; 4461673956F2BD22 CRC64;

Query Match 27.2%; Score 496.5; DB 1; Length 391;
Best Local Similarity 32.5%; Pred. No. 2.7e-22;
Matches 101; Conservative 68; Mismatches 121; Indels 21; Gaps 5;

QY 11 GPNASNTSDGPDNLTSAGSPPTGTGISYSINIIMPVSFGTICLLGIIGNSTVFAVVKSK 70
   | ||| : || ::::: ||||| : ||| : |||
Db 42 GRNASONGTLSEGGSA-----ILISFIYSVCLVGLCGNSMVIYILLRYAK 88
   : |||:||||: ||:|:||||: : ||| : |||: |||: |||

71 LHWCMNVPDFIINLSVDLLFLGLMPFMHIOLMGNGVWHFGETMCTLTAMDANSQFTS 130
   : |||:||||: ||:|:||||: : ||| : |||: |||: |||

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Db      89 MKTATN--IYILNLAIADELMLMSVPELVSTILRH-WPGCALLCRLVLSVDAYNMFTS 144
OY      131 TYILTAMADRIATVHPISSTKERKPSVATLVICLLMALSFISITPWLYARLIPPGG 190
        | | : : | | | | : : : : | | : : | | : : | | : : |
Db      145 IYCLTVLSVDRYAVVHPKARYRPTAKVNMIGWVLSLVLPPIVVFSPRANSBG 204
OY      191 AVGGIRLPNP-DIDLWYFTLYQFLAFALPFVYITAAVVRILQRMSTSSVAPASQSRIRL 249
        | | : : | | | | | | | | | | | | | | | | : :
Db      205 TVACNMMLPEBAQRMVLGVFLYTFMGFLPLPGALICLCYVLLIAKMRMVALKAGWQQRK 264
OY      250 RTRKVRTTAIAICLVEFVCWAPYVVLQTLQLSISRPTLTFVYLYNMAISLGVANSCLNPF 309
        : : | : : : | | : : | | : : | : : : | | | | | |
Db      265 SERKITLMVMVMVMEVICMMPFYVVLVNVFAEQDDATVSQI--SVILGIANSKANPFI 321
OY      310 VYIVLCETFRK 320
Db      322 LYGFSLDNFKR 332

RESULT 13
SSR4_RAT
ID      SSR4_RAT          STANDARD;          PRT;          384 AA.
AC      P30937;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      01-FEB-1996 (Rel. 33, Last annotation update)
DE      Somatostatin receptor type 4 (SS4R).
GN      SSTR4.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxId=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=93087484; PubMed=1360663;
RA      Bruno J.F., Xu Y., Song J., Berelowitz M.;
RT      "Molecular cloning and functional expression of a brain-specific
RT      somatostatin receptor.";
RL      Proc. Natl. Acad. Sci. U.S.A. 89:11151-11155(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Sprague-Dawley; TISSUE=Hippocampus;
RX      MEDLINE=94230347; PubMed=8175684;
RA      Bito H., Mori M., Sakanaka C., Takano T., Honda Z., Gotoh Y.,
RA      Nishida E., Shimizu T.;
RT      "Functional coupling of SSTR4, a major hippocampal somatostatin
RT      receptor, to adenylate cyclase inhibition, arachidonate release and
RT      activation of the mitogen-activated protein kinase cascade.";
RL      J. Biol. Chem. 269:12722-12730(1994).
CC      -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS
CC      RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
CC      CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF
CC      ADENYLYL CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE
CC      RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- TISSUE SPECIFICITY: BRAIN, LUNGS, HEART AND ISLETS. MODERATE
CC      LEVELS IN THE HIPPOCAMPUS, CORTEX, AND OLFACTORY BULB.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M96544; AAA42180.1; -.
DR      EMBL; U04738; AAA17519.1; -.
DR      PIR; A47249; A47249.
DR      HSSP; P02699; 1BOJ.
DR      InterPro; IPR000276; GPCR_Rhodpsn.

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DR	Pfam; PF00001; 7tm_1; 1.	
DR	PRINTS; PR00237; GPCRHHODPSN.	
DR	PROSITE; PS00237; G_PROTEIN_RECPEP_F1_1; 1.	
DR	PROSITE; PS00262; G_PROTEIN_RECPEP_F1_2; 1.	
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;	
KW	MultiGene family; Lipoprotein; Palmitate.	
FT	DOMAIN	1 41
FT	TRANSMEM	42 69
FT	DOMAIN	70 79
FT	TRANSMEM	80 105
FT	DOMAIN	106 116
FT	TRANSMEM	117 138
FT	DOMAIN	139 160
FT	TRANSMEM	161 181
FT	DOMAIN	182 203
FT	TRANSMEM	204 228
FT	DOMAIN	229 254
FT	TRANSMEM	255 280
FT	DOMAIN	281 311
FT	TRANSMEM	288 312
FT	DOMAIN	312 384
FT	CARBOHYD	21 21
FT	DISULFD	115 194
FT	LIPID	323 323
SEQUENCE	384 AA; 42087 MW; 044542B4922411E5 CRC64;	

Query Match	27.1%;	Score 494.5;	DB 1;	Length 384;
Best Local Similarity	33.0%;	Pred. No. 3.5e-22;		
Matches 104;	Conservative 66;	Mismatches 116;	Indels 29;	Gaps 8;

QY	16	NTSDGPDNLTSAGSPBRTGISIYNIMPSVEFTICLLGIIGNSTVIFAUVKSKSLHMCN	75
		: : : : : : : : : : : :	
Db	21	NASWAPDEEEDAVNRSDGTGTAGMVTI--QCITYALVCVLGVGNALYIFVILRYAKMKTTAT	78
QY	76	NVPDIFIINLSVVDLLEFLGLMPFI-----HQLMGNGVWHHEGTEWTCLITAMDANSOFT	129
		: : : : : : : : :	
Db	79	N---IYLNLVAADELFMLSVPEVASAALRH-----WPFGAVLCRAVLSDGLNMFT	128
QY	130	STVILTAMAIIDRYLATVHPISSTKERKPSVATLVICLLMALSFISITPVMLYARLIPEEG	189
		: : : : : : : : : : : : :	
Db	129	SVECLTVLSVDRYVAVVHPLRATYRRPSAKLINLGWMLASLLVTLPIAFADTRPARG	188
QY	190	G-AVGCGIRLPNPFDULYM---FTLYQFLLAFALFEVVITAAYVRILQRTSSVAPASOR	245
		: : : : : : : : : :	
Db	189	GEAVACNLHWPHP-----AMSAAVEVIYTFELGLPLLVALAIGLCYLLIVGKMRAVALRAGWQ	244
QY	246	SIRLRTRKVRTATAICLVEFCWAPYYVLOLTQLSISRPTLFEVYLYNAAISLGYANSC	305
		: : : : : : : : : : : : : : :	
Db	245	QRRESEKKITRLVLMVYIVFVLCWMPEYVVOLNLLFVTSLDAT--VNHVSLILSYANSC	301
QY	306	LNPVYIIVLCETFRK 320	
		: : : : :	
Db	302	ANPILYGFLSDNFRR 316	

RESULT 14

SSR4_MOUSE	STANDARD;	PRT;	384 AA..
ID	SSR4_MOUSE		

DE	Somatostatin receptor type 4 (SS4R).
DT	30-MAY-2000 (Rel. 39, last annotation update)
DT	01-FEB-1996 (Rel. 33, last sequence update)
DT	01-FEB-1996 (Rel. 33, Created)
DE	

GN SSTR4 OR SMSTR4.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheri

OX NCE

	SEQUENCE FROM N.A.
RN	[1]
RP	

RC STRAIN=129/SvJ; TISSUE=Liver;
RX MEDLINE=96194903; PubMed=8654950;

RA Schwabe W., Brennan M.B., Hochgeschwender U.:

```

RT  "Isolation and characterization of the mouse (Mus musculus)
RT  somatostatin receptor type-4-encoding gene (msSTR4).";
RL  Gene 168:233-235(1996).
CC  -i- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS
CC  RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLATE
CC  CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF
CC  ADENYLATE CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE
CC  RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
CC  -i- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC  -----
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CC  or send an email to license@isb-sib.ch).

```

CC	EMBL; U26176; AAA67561.1; -.		
DR	HSSP; P02699; 1BOJ.		
DR	MGD; MGI:105372; Smstr4.		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCRHRHODPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.		
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.		
FT	DOMAIN	1	41
FT	TRANSMEM	42	69
FT	DOMAIN	70	79
FT	TRANSMEM	80	105
FT	DOMAIN	106	116
FT	TRANSMEM	117	138
FT	DOMAIN	139	160
FT	TRANSMEM	161	181
FT	DOMAIN	182	203
FT	TRANSMEM	204	228
FT	DOMAIN	229	254
FT	TRANSMEM	255	280
FT	DOMAIN	281	287
FT	TRANSMEM	288	311
FT	DOMAIN	312	384
FT	CARBOHYD	21	21
FT	DISULFID	115	194
FT	LIPID	323	323
SEQUENCE	384 AA; 42089 MW; 04DB0751481C6FB CRC64;		

Query Match	26.5%;	Score 483;	DB 1;	Length 384;
Best Local Similarity	31.9%;	Pred. No. 1.6e-21;		
Matches 105; Conservative	69;	Mismatches 133;	Indels 22;	Gaps 8;

```
QY      1 MDLEASLL-----PTGPNASNTSDGPDNLTSGAGSPRTGSISYINIMPSVEGTICLGI 55
```

Db 1 MNAPATLLRGVEDTTWTPGINASWAPEQEDDAMGSDGTGTAGMVTI--QCIALVCLVGL 58

100

56 IGSTVIFAVVKKSKLHMCNNVPDIFIINLSVDLLEFLGMPFMIHQLMGNGVWHFGETM 115

114

Db 59 VGNALVIEVILRYAKMKTATN--IYLLNLAVADELEMLSVPF-VRSAAALRHWPFCAVL 114

175

116 CTTLTAMDANSQFTSTYILTAMADRYLATVHPISSTKFKKPSVATLVICLLWALSF1SL 1/3

[illegible]

Db 115 CRAVLSVDGLNMFSTVFCLTVLSVDRYAAVHPLRLAIYKRPSVAKLLNLGVWLASLVI 1/4

176 EDITORIAL BOARD - AUGUST 1971 - EDITORIAL BOARD - AUGUST 1971 231

176 TPVWL YARLLIPFGG-AVGGGIRLBNPDIDLW---FLLIQEELAFALPVLIAKAVNI 231

```

      | : :: | | | | : | : | | | | : |
05   175 TPAVENDTPBACGCEAVACNT HWPDR---AWSAVEVTYTFELGETPRVIATIGLCYLLI 230

```

DB 1/5 LP1AVEADTRPARGGEAVALCNLHMFR--AMSHVEVLIIFDDEDFVHJOCLEEL 20

04 332 IORMTSSVAPASORSTRI.BTKRVTRTAIACLVFVVCWAPYVLOLTOLSISRPTLTfVY 291

QY Z3Z LQKMISSVAFASBQNSIKRILKNV I NIAINICUEFTVCMAE I V DGIJEDON...
 . : | : ||| : : ||| : : ||| : : |||

```
Db      231 VGKMBRAVALBGWOORRRSEKKITRLVLMVVTVFVLCMMPFYVOLNLFVTSIDAT--- 287
```

[illegible]


```

QY      292  LYNAAISLGYSNCINPVIYIVLCETPRK 320
          :  :  | | | | | | | | :  :  | | :
Db      288  VNHVSLILSYANSNCANPIIYGFLSDNFRR 316

RESULT 15
SSR3_RAT
ID  SSR3_RAT      STANDARD;      PRT;      428 AA.
AC  P30936;
DT  01-JUL-1993 (Rel. 26, Created)
DT  01-JUL-1993 (Rel. 26, Last sequence update)
DT  01-FEB-1996 (Rel. 33, Last annotation update)
DE  Somatostatin receptor type 3 (SS3R) (SSR-28).
GN  SSR3.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Wistar; TISSUE=Brain;
RX  MEDLINE=93066220; PubMed=1279674;
RA  Meyerhof W., Wulfsen I., Schoenrock C., Fehr S., Richter D.;
RT  "Molecular cloning of a somatostatin-28 receptor and comparison of
RT  its expression pattern with that of a somatostatin-14 receptor in rat
RT  brain.";
RL  Proc. Natl. Acad. Sci. U.S.A. 89:10267-10271(1992).
CC  -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC  COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC  ADENYLYL CYCLASE.
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -1- TISSUE SPECIFICITY: DENSELY EXPRESSED IN CEREBELLUM AND IN MODERATE
CC  LEVELS IN THE AMYGALA, CORTEX, STRIATUM, SPLEEN, LIVER,
CC  PITUITARY.
CC  -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC  EMBL; X63574; CAA45130.1; -.
DR  PIR; S30508; S30508.
DR  HSSP; P34996; 1DDD.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRHRHODPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW  G-protein coupled receptor; Transmembrane; Glycoprotein;
KW  Multigene family.
FT  DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 46 71 1 (POTENTIAL).
FT  DOMAIN 72 81 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 82 103 2 (POTENTIAL).
FT  DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 119 140 3 (POTENTIAL).
FT  DOMAIN 141 162 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 163 182 4 (POTENTIAL).
FT  DOMAIN 183 206 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 207 232 5 (POTENTIAL).
FT  DOMAIN 233 266 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 267 288 6 (POTENTIAL).
FT  DOMAIN 289 302 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 303 325 7 (POTENTIAL).
FT  DOMAIN 326 428 CYTOPLASMIC (POTENTIAL).
FT  CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  DISULFID 117 192 BY SIMILARITY.
FT  DOMAIN 358 373 POLY-GLU.

```

Seq	Sequence	428 AA;	47151 MW;	BE0AA948840A9E9D	CRC64;
QY	Query Match	26.3%;	Score 480.5;	DB 1;	Length 428;
DB	Best Local Similarity	31.3%;	Pred. No. 2.4e-21;		
QY	Matches 118; Conservative	73;	Mismatches 143;	Indels 43;	Gaps 11;
QY	6 SLPTGPNASNTSDG--PDNLTSAGSPPTGTSISYINIMPSVFETICLLGIGNSTVI	62			
DB	8 SSVPTTLDPGNASSAMPPLDTSLGNASAGTSLAGLAVSGILISLVYLVVCVVGILGNSLVI	67			
QY	63 FAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHOLMGNGV--WHFGETMCTLIT	120			
DB	68 YVVLRLHTS--SPSVTSVYILNLALDELFMGLPFLAAQ--NALSYWPFGLSMLCRLYM	121			
QY	121 AMDANSQFTSYIILTAMAIIDRYLAIVHPISSTKFKRPSVATLVICLLMALSFISITPVL	180			
DB	122 AYDGINQFTSIFCILTVMQSVDRYLAIVVHPTRSARWRITAPVARMYSAAVWVASAVVLLPVVY	181			
QY	181 YARLIPFGGAVGCGIRLPNPDITLYW--FTLYQFELAPALPFVITAAVYRIIORMTS	237			
DB	182 FSGV--PRGMSTCHMQWPEPAA--AMRTAFIITYAALGFFGPPLLVICLCYLLIYVKVRS	236			
QY	238 SY-----APASQRSIRLRKRYTRTAIAICLVFVCWAPYVYLQIDISIRP	285			
DB	237 TTRRVRAPSCQWQAPACQRR-RRSERRVTRMVAVVALFVLCWMPFYLLNINVVYCPLP	295			
QY	286 -TLTFVYLYNMAISLGYANSCLNPFVYIVLCETFRK-----RLVLSVKPAAQGQL	334			
DB	296 EEPAFFGLYLVVALPYANSKANPILYGLSYRFKQGGFRILLRPSRRVRSQEPGSGPPE	355			
QY	335 RAVSNAQTADERTESK	351			
DB	356 KTEEEDEEEERREEE	372			

Search completed: February 13, 2003, 13:58:48
Job time : 12.5013 secs

```

SQ      SEQUENCE    428 AA;  47151 MW;   BE0AA948840A9E9D CRC64;
Query Match          26.3%; Score 480.5; DB 1; Length 428;
Best Local Similarity 31.3%; Pred. No. 2.4e-21;
Matches 118; Conservative 73; Mismatches 143; Indels 43; Gaps 11;

QY      6 SLPTGPNASNTSDG--PDNLTSAGSPPRTGSIYSINIMPSVFETICLLIGNSTVI 62
        |::| : | | : | : | : | : | : | : | : | : | : | : | : |
DB       8 SSVPTTLDPGNASSAMPPLDTSLGNASAGTSLAGLAVSGILISLVYLVCVWGGLGNSLVI 67
QY      63 FAVVKKSKLHMCNVPDIFIINLSVDLLFLGMPEMHHOLMGNGV--WHFGETMCTLIT 120
        | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB       68 YVLRHTS---SPSVTSVYILNLALADELFMLGLPFLAQ---NALSYWPFGSIMCRLVM 121
QY      121 AMDANSOFTSTYIILTAMAIIDRYLATVHPDISSTKFRRKPSVAATLVICLLMALSFISTIPVWL 180
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      122 AVDGINQFTSIFCLTVMSVDRLAVVHPTRSARWRTPAPVARMYSAAVWVASAVVLPVVV 181
QY      181 YARLIFFPGAVGCGIRLPNPDTLYW---FTLYQFLAFALPEVVITAAYVRILQRMTS 237
        :: : | | : : | | : | : | : | : | : | : | : | : | : | : |
DB      182 FSGV--PRGMSICHMQWPEPA--AMRTAFIIYYTAALGFEGPLLIVICLCYLLIYKVRS 236
QY      238 SY-----APASQRSIRLRFRKVRTATAIAICLVFFYCWAAPPYVLQLTQLSISR 285
        : | | | | | : | : | : | : | : | : | : | : | : | : | : |
DB      237 TTRRVRAPSCQWYQAACQRR-RRSEKRVTRMVAVVALFVLCWMFPYLLNIYNVVCPLP 295
QY      286 -TLTFVYLYNAISLGYSANSCLNPFVYIVLCETERK-----RLVLSVKPAQGQL 334
        | | | : : | | | | | : | : | : | : | : | : | : | : | : |
DB      296 EEPAFFGLYFLVVALPYANSCANPILYGFLSYRFKGGRILLRPSSRRVRSQEPGSGPPE 355
QY      335 RAVSNAQTADDEERTESK 351
        : : | | | : | : | : | : | : | : | : | : | : | : | : |
DB      356 KTEEEDEEEEEERREEE 372

Search completed: February 13, 2003, 13:58:48
Job time : 12.5013 secs
```

4
3
2
1



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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:56:01 ; Search time 12.6809 Seconds

(without alignments)
2676.114 Million cell updates/sec

Title: US-09-885-478-28

Perfect score: 1824

Sequence: 1 MDLEASLPTGPNASNTSDG.....LRAVSNAGTADERTESKGT 353

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1824	100.0	422	2	JC7080 melanin-concentrat
2	565.5	31.0	340	2	JC7695 G protein-coupled
3	530.5	29.1	369	2	B41795 somatostatin recep
4	529.5	29.0	369	2	D41795 somatostatin recep
5	524.5	28.8	369	2	JC2083 somatostatin recep
6	524.5	28.8	369	2	A45291 somatostatin recep
7	511.5	28.0	346	2	S29248 somatostatin recep
8	505.5	27.7	388	2	JN0605 somatostatin recep
9	504.5	27.7	418	2	A46226 somatostatin recep
10	497.5	27.3	391	2	A39297 somatostatin recep
11	496.5	27.2	391	2	A41795 somatostatin recep
12	496.5	27.2	391	2	C41795 somatostatin recep
13	494.5	27.1	384	2	A47249 brain-specific som
14	483	26.5	384	2	JC4629 somatostatin recep
15	480.5	26.3	428	2	S30508 somatostatin recep
16	478.5	26.2	363	2	I57955 probable G protein
17	478.5	26.2	364	2	JN0763 somatostatin recep
18	472	25.9	428	2	A44021 somatostatin recep
19	470.5	25.8	363	2	I57940 somatostatin recep
20	452.5	24.8	372	2	I38532 delta opioid recep
21	446.5	24.5	372	2	S34592 delta opioid recep
22	444	24.3	392	2	S65693 opioid receptor mu
23	444	24.3	400	2	I56553 mu opiate receptor
24	443	24.3	398	2	I56517 mu opioid receptor
25	442.5	24.3	398	2	A57510 mu opioid receptor
26	441	24.2	372	2	B48227 delta opioid recep
27	436	23.9	398	2	I56504 mu opioid receptor
28	433.5	23.8	380	2	JC2338 kappa opioid recep
29	426	23.4	380	2	A55259 kappa opioid recep

30	421	23.1	328	2	I38973 G protein-coupled
31	419	23.0	380	2	A48227 kappa opioid recep
32	419	23.0	380	2	S36143 kappa opioid recep
33	409.5	22.5	333	2	I38974 G protein-coupled
34	408.5	22.4	370	2	S43087 orphan opioid rece
35	408	22.4	380	2	JC2434 kappa opioid recep
36	407	22.3	373	2	JE0087 kappa opioid recep
37	406.5	22.3	367	2	I49022 delta opioid recep
38	406.5	22.3	367	2	JC2421 kappa opioid recep
39	406.5	22.3	367	2	I56520 opioid receptor ho
40	372.5	20.4	359	2	I51372 G protein-coupled
41	368	20.2	362	2	JN0694 angiotensin II rec
42	361	19.8	423	2	JC7677 angiotensin II rec
43	347	19.0	371	2	JC5796 allatostatin recep
44	341	18.7	350	2	A42009 probable chemotatr
45	341	18.7	359	2	A42656 N-formyl peptide r
					angiotensin II rec

ALIGNMENTS

RESULT 1
JC7080
melanin-concentrating hormone receptor [validated] - human
N;Alternate names: MCHR; orphan somatostatin-like receptor 1 (SLC-1)
C;Species: Homo sapiens (man)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: JC7080
R;Shimomura, Y.; Mori, M.; Sugo, T.; Ishibashi, Y.; Abe, M.; Kurokawa, T.; Onda, H.;
Biochem. Biophys. Res. Commun. 261, 622-626, 1999
A;Title: Isolation and identification of melanin-concentrating hormone as the endogen
A;Reference number: JC7080; MUID:99373129; PMID:10441476
A;Accession: JC7080
A;Molecule type: mRNA
A;Residues: 1-422 <SH1>
A;Note: It is uncertain wheather Met-1, Met-6 or Met-70 is the Initiation codon
C;Superfamily: neurokinin 1 receptor
C;Keywords: hormone receptor; transmembrane protein

Query Match	100.0%;	Score 1824;	DB 2;	Length 422;
Best Local Similarity	100.0%;	Pred. No. 3.5e-152;		
Matches 353;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIIMPVFGTICLLGIGNST 60			
Db 70	MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIIMPVFGTICLLGIGNST 129			
QY 61	VIFAVKKSKLHWCNNVPDIFIINLSYVDLFLGLGMPFIHQLMGNGVWHFGETMCTLIT 120			
Db 130	VIFAVKKSKLHWCNNVPDIFIINLSYVDLFLGLGMPFIHQLMGNGVWHFGETMCTLIT 189			
QY 121	AMDANSQFTSTYIILTAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALSFSISTPVMWL 180			
Db 190	AMDANSQFTSTYIILTAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALSFSISTPVMWL 249			
QY 181	YARLIPFGGAVCGGIRLPNPDITLYWFTLYQFFLAFLPFVVITTAAYVRILQRMTSVA 240			
Db 250	YARLIPFGGAVCGGIRLPNPDITLYWFTLYQFFLAFLPFVVITTAAYVRILQRMTSVA 309			
QY 241	PASQSRIRLRKRVTRTAIAICLVFVCWAPYVYLQLTQLSISRPTLTFVLYNAAISLG 300			
Db 310	PASQSRIRLRKRVTRTAIAICLVFVCWAPYVYLQLTQLSISRPTLTFVLYNAAISLG 369			
QY 301	YANSCLNPFYIVLCETFRKRLVLSVKPAAQGLRAVSNAGTADERTESKGT 353			
Db 370	YANSCLNPFYIVLCETFRKRLVLSVKPAAQGLRAVSNAGTADERTESKGT 422			

RESULT 2
JC7695
G protein-coupled receptor, SLR receptor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001

```
C;Accession: JC7695
R;Mori, M.; Harada, M.; Terao, Y.; Sugo, T.; Watanabe, T.; Shimomura, Y.; Abe, M.; Shint
Biochem. Biophys. Res. Commun. 283, 1013-1018, 2001
A;Title: Cloning of a novel G protein-coupled receptor, SLT, a subtype of the melanin-co
A;Reference number: JC7695; MUID:21255282; PMID:11355873
A;Contents: Hippocampus
A;Accession: JC7695
A;Molecule type: mRNA
A;Residues: 1-340 <MOR>
A;Cross-references: DDBJ:AB060151
C;Comment: This receptor, a second subtype of the melanin-concentrating hormone (MCH) re
memory.
C;Genetics:
A;Gene: slt
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match          31.0%; Score 565.5; DB 2; Length 340;
Best Local Similarity 37.0%; Pred. NO. 5.5e-42;
Matches 113; Conservative 62; Mismatches 119; Indels 11; Gaps 4;

QY 41 IIMPSVFGTICLLGIGNSTVFIAVVKSKSLHMCNNVPDIFINLSVVDLFLGLMPFI 100
    :|::||:| | | | ::||:| ::|:| | | | | | | | | | | | | | | | |
Db 35 VILPMSGITICSTGLGVNILLIVFTIIRSRK---KTVPDIIYICNLAVADLVHTVGMPFLL 90

QY 101 HOLMGNGVWHFGETMCTLLTAMDANSQFTSTYILTAMAIDRYLATVHPISSEFKRKPSVA 160
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 91 HQWARGGEWVEGGPLCTTTITSLDTCNQFACSAITMTVMSVDYRFALVQPFRLTRWRTKYKT 150

QY 161 TLVICLLMALSFISTIPWLYARLIPEPGAGVGCGIRLPNDTDLYWFITYOFFLAFLAP 220
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 151 IRINGLMAASFILALPAAVWYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFEFP 209

QY 221 FVVITAAVVRIL----QEMTSVAPASQRSI-RLRTKRVTRTAIAICLVFEVCWAPYYV 274
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 210 LPLILVCYLILICYTWEMYQQNKDARCNPSPVKQRYMKLTKMLVLVLVVFILSAPYHV 269

QY 275 IQLTLQLSISRPTLTFEVLYNAAISLGANSCLNPFEVYIVLCETFRKRLVLSVKPAQGQL 334
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 270 IQLVNLQMEQPTLAFYVGYIISICLSYASSINSINFLYITLLSGNFQKRLPQIQRRATEKEI 329

QY 335 RAVSN 339
    : |
Db 330 NNMGN 334

RESULT 3
B41795
somatostatin receptor 2 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
C;Accession: B41795
R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of human and mouse somatost
A;Reference number: A41795; MUID:92108031; PMID:1346068
A;Accession: B41795
A;Molecule type: DNA
A;Residues: 1-369 <YAM>
A;Cross-references: GB:M81830; NID:g307435; PIDN:AAA58248.1; PID:g307436
A;Note: sequence extracted from NCBI backbone (NCBIN:74769, NCBIPI:74770)
C;Genetics:
A;Gene: GDB:SSMR2
A;Cross-references: GDB:134186; OMIM:182452
A;Map position: 17q24-17q24
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phos
```

```

F;254-281/Domain: transmembrane #status predicted <TM6>
F;288-315/Domain: transmembrane #status predicted <TM7>
F;9,22,29,32,351/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;115-193/Disulfide bonds: #status predicted
F;250/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pre
F;328/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match          29.1%; Score 530.5; DB 2; Length 369;
Best Local Similarity 31.8%; Pred. No. 7e-39;
Matches 114; Conservative 75; Mismatches 128; Indels 41; Gaps 8;

QY 2 DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVEGTICLLIGNSTV 61
   |||::| | | |::| | | | | | | | | | | | | | | | | | | | | | |
Db 20 DLNGSVST--NTSNQTEPYDLIS-----NAVLTIFYFVVCILGCGNTLV 64

QY 62 IFAVYKSKLHWCNNVPDIFITINLSVDDLFLGMPF-----MIHQLMGNGVWHFGETM 115
   |:::|::| | | |::| | | | | | | | | | | | | | | | | | | | | | |
Db 65 IYVILRYAKM---KTITNIIYILMLAIADLEMLGLPFLAMQVALVH-----WPF GKAI 114

QY 116 CTLITAMDANGQETSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFSI 175
   |:::|::| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 115 CRVMTVDGINQFTSIFCLTWSIDRYLAVVHPIKSAKMRPRPTAKMITMAWGVSLVI 174

QY 176 TPVWLARLIRPEPGAVGCGIRLPNDTDLY-WFTLYQFFLAFLPEFVITAAVRIQR 234
   |:::|::| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 175 LPIMIVAGLRISNQWRSSCTINWPGHSGAWYTGFIYTFILGFLVPLTICLCYFIIRK 234

QY 235 MTSSVAPASQSRIRLRTKRVTRTAIAICLVEFVCWAPYYVLQTLQSLIS-RPTLTFFVLY 293
   |::| | | |::| | | | | | | | | | | | | | | | | | | | | | |
Db 235 VKSSGIRVGSKRKKEKKVTRMVSIVAVFICWLPFYIFNVSSVMAISPFAKGMF 294

QY 294 NAAISLGYANCLNPFYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESK 351
   |::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 295 DFVVVLTYSANSCANPILYAFLSDNEK-----SFQNVLCIVKVSGETDGERDSK 344

RESULT 4
D41795
somatostatin receptor 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999
C;Accession: D41795; I56236
R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Selino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of human and mouse somat
A;Reference number: A41795; MUID:92108031; PMID:1346068
A;Accession: D41795
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-369 <YAM>
A;Cross-references: GB:M81832; NID:g201060; PIDN:AAA58256.1; PID:g201061
J;Elliot, D.E.; Metwali, A.; Blum, A.M.; Sandor, M.; Lynch, R.; Weinstock, J.V.
J. Immunol. 153, 1180-1186, 1994
A;Title: T lymphocytes isolated from the hepatic granulomas of schistosoma-infected m
A;Reference number: I56236; MUID:94300079; PMID:7913111
A;Accession: I56236
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 99-309 <RES>
A;Cross-references: GB:S71756; NID:g560631
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match          29.0%; Score 529.5; DB 2; Length 369;
Best Local Similarity 31.8%; Pred. NO. 8.6e-39;
Matches 114; Conservative 75; Mismatches 128; Indels 41; Gaps 8;

QY 2 DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVEGTICLLIGNSTV 61
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 20 DLNGSLGPS--NGSNQTEPYDMTS-----NAVLTIFYFVVCVGLCGNTLV 64

QY 62 IFAVYKSKLHWCNNVPDIFITINLSVDDLFLGMPF-----MIHQLMGNGVWHFGETM 115
   |:::|::| | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db      65  IYVILRYAKM--KTTFNIIYLMLAIADELFMGLPFLMAQVALVH-----WPF GKAI 114
QY      116  CTLITAMDANSOFTSTYILTAIAIDRYLATVHPISSTKERKESVATLVICLMAISFISI 175
      115  CRVVMTVDGINOFTSIFCLTFWASIDRYLAVHPIKSAKWRRPTAKMINVAVMCVSLVI 174
QY      176  TPVWLYARLIPFPGAVCGGIRLPNPDTDLY-WFTLYQFPLAFALPFVVTAAVYRILOR 234
Db      175  LPIMITYAGLRSNOMWGRSSCTINWPGESGAWYTGFIYAFLIGFLVPLTIIICLYFLIIIK 234
QY      235  MTSSVAPASQRSIRLRKRYTRTAIAICLVFEVCWAPYVYLQTLQLSIS-RPTLTFFVLYL 293
Db      235  VKSSGIRVGSKRKKSEKRVTRMVSIVAVAFIECWLPLFYIFNVSSVSVAISPTPALKGMF 294
QY      294  NAAISLGYANSCLNPFYIVILCETFRKRRLVLSVKKPAAGOLRAVSNQAOTADEERTESK 351
Db      295  DFVVILTYANSCANPILYAFLSDNEKK-----SFQNVLCIVKVSGETEDGERSDSK 344

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RESULT 5
JC2083

somatostatin receptor 2 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jul-2000
C:Accession: J02083
R:Matsumoto, K.; Yokogoshi, Y.; Fujinaka, Y.; Zhang, C.; Saito, S.
Biochem. Biophys. Res. Commun. 199, 298-305, 1994
A:Title: Molecular cloning and sequencing of porcine somatostatin receptor 2+.
A:Reference number: J02083, MUID:94168590, PMID:8123027
A:Accession: J02083
A:Molecule type: DNA
A:Residues: 1-369 <MAT>
A:Cross-references: GB:D21338; NID:g415606; PIDN:BA04810.1; PID:g472306
C:Comment: This protein inhibits growth hormone release.
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; phosphoprotein; receptor
F:44-69/Domain: transmembrane #status predicted <TM1>
F:77-105/Domain: transmembrane #status predicted <TM2>
F:117-138/Domain: transmembrane #status predicted <TM3>
F:158-182/Domain: transmembrane #status predicted <TM4>
F:205-235/Domain: transmembrane #status predicted <TM5>
F:254-286/Domain: transmembrane #status predicted <TM6>
F:292-316/Domain: transmembrane #status predicted <TM7>
F:9,22,29,32/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:115-193/Disulfide bonds: #status predicted
F:244,343/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #
F:250/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
F:328/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match	28.8%;	Score 524.5;	DB 2;	Length 369;
Best Local Similarity	31.6%;	Pred. NO. 2.4e-38;		
Matches 113;	Conservative 75;	Mismatches 129;	Indels 41;	Gaps 8;

[illegible]

```
QY 294 NAAISLGVANSCLNPFVYIVLCETFERKRLVSVKPAQOGLRAVSNAGTADAEERTESK 351
: : | | | | | : : : | : : | : | | | : | |
Db 295 DFVVVLITVANSKANPILYAFLSDNKK-----SFQNVLCVKKVSGTDDGERDSK 344
```

RESULT 6
A45291

somatostatin receptor, somatotropin release-inhibiting factor receptor, SRIF receptor,
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
 C:Accession: A45291
 R:Kluxen, F.W.; Bruns, C.; Lubbert, H.
 Proc. Natl. Acad. Sci. U.S.A. 89, 4618-4622, 1992
 A:Title: Expression cloning of a rat brain somatostatin receptor cDNA.
 A:Reference number: A45291; MUID:92262491; PMID:1374909
 A:Accession: A45291
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-369 <KLU>
 A:Cross-references: GB:M93273; NID:g207026; PIDN:AAA42165.1; PID:g207027
 A:Note: sequence extracted from NCBI backbone (NCBIN:102315, NCBIP:102316)
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	28.8%;	Score 524.5;	DB 2;	Length 369;
Best Local Similarity	31.6%;	Pred. No. 2.4e-38;		
Matches 113; Conservative	75;	Mismatches 129;	Indels 41;	Gaps 8;

```
QY      2 DLEASLEPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVEGTICLLGILGNSTY 61
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db     20 DLNGSLGPS--NGSNQTEPYDMTS-----NAVLTIFYFVVCVVGIGCNTY 64
```

Qy		62 IFAAVVKSKLHCNNVPDIFIIINSVDLLFLGMPT-----MIHQLMGNVGWHFEGTM	115
	: :: :	: :: :: : :: :	:
Db		65 IYILIRAKM---KTITNIVYLNTAIDELFMLGLPELMOVALVH-----WPFGRAT	114

QY 116 CTLIFANDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFTSI 175
| :: | : ||| : || : ||||| ||| | : : | : : : :
Db 115 CRVAVMYDGINQFTSIECLTVMSDRYLATVHPIKSAKWRBPTAKMINVAVWGVSLLVI 174

QY 176 TPVWLYARLIPFGAVGCGIRLBNPDTDLY-WFTLYQFFLAFALPEFVITAAVYRIQR 234
| : : | | | | | : | | | | : : | : : | : :
Db 175 LPIMTYAGLRSNQWGRSSCTIIMPGESEGAWYTGFIYAFILGFLVPLTIICLCYFLTIIK 234

QY	235	MTSSVAPASQSRIRLRTKRVTPFAIAICLVFFVCWAPYVYLQTLQLSIS-RPTLFEVYLY	293
	:	:	:
	:	:	:
Db	235	VKSSGIRVGGSSKRKKSEKKVTRMVSIVAVFIFCWLPTLFNVSSVSVAISPTPAIKGMF	294

QY 294 NAAISLGVANSCLNPFVVIVICETFERKRLVLVKPAAOGLRAVSNAQTADDEERTESK 351
:
: : | | | | | | : : : : : :
Db 295 DEVIILTYANSCANPILYAFSTDNFK-----SFONYICIWKVSGAEFGERSRSRK 344

RESULT 7
S29248

somatostatin receptor 2B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Nov-1999
C:Accession: S29248
R:Vanetti, M.; Kouba, M.; Wang, X.; Vogt, G.; Hoelltt, V.
FEBS Lett. 311, 290-294, 1992
A:Title: Cloning and expression of a novel mouse somatostatin receptor (SSTR2B).
A:Reference number: S29248; MUID:93012001; PMID:1397330
A:Accession: S29248
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-346 <VAN>
A:Cross-references: EMBL:X68951; NID:g54197; PIDN:CAA48766.1; PID:g54198
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	28.0%;	Score 511.5;	DB 2;	Length 346;
Best Local Similarity	31.38;	Pred. No. 3e-37;		

	Matches	111, Conservative	75; Mismatches	126; Indels	43; Gaps	9;
QY	2	DLEASLLPTGENASNTSDGPDNLTSACSPPRGTGISYINIMPSVEGTICLLIGTIGNSTV	61			
		: : : :		: : : : : :		
Db	20	DLNGLSGPS--NGSNQTEPYDMTS-----	NAVLTFIYFVVCVGLCGNTLV	64		
QY	62	IFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPF-----	MIHQLMGNGVWHGETM	115		
		: : : : : : : : : :		: :		
Db	65	IYVILRYAKM---KTITNIYIILNLAIDELFMLGLPFLAMQVALVH-----	WPGKAI	114		
QY	116	CTLITAMDANSOFTSTYILTMADIRLATVHPISSTKFRKPSVATLVICLLMALSFISI	175			
		: : : : : : : : : : : : : :		: : :		
Db	115	CRVVMTVDDGINOFTSIFCLFTVMSIDRYLAVVHPIKSAKWRPRPTAKMINVAWCVSLLVI	174			
QY	176	TPVWLRYARLIDPPGGAVGCGIRLPNDTDLY-WFTLYQFLAFALPFVVITAAYRILQR	234			
		:		: : : : : : : : : : :		
Db	175	LPIMLYAGLRSNOMGRSSCTINWPGESGAWYTGFIITAFILGFLVPLTIICLCYLFIIIK	234			
QY	235	MTSSVAPASQSRIRLRTKRYTRITATACLVFVCWAPFYVLOLTQLSIS-RPTLTFVYLY	293			
		: : : : : : : : : : : : :		: : : : : : : : : : :		
Db	235	VKSSGIRVGSRRKKSEKKVTRMVSIVYAVFICWLPFIYFNVS SVSAISP TPA LKGMF	294			
QY	294	NAAISLGYANCLNPFVYIVLCETPRKRLL-VLSVKPAAGOLRAVSNMQTADDEE	346			
		: : : : : : : : : : : : :		: : : : : : : : : : :		
Db	295	DFVILTYANTCANPILYAFILSDNRKKSFO NVLC LVKA-----	DNSOGAED	341		

RESULT 8
JN06005
somatostatin receptor 4 - human
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C/Accession: JN06005; JN0762; A47457
R/Xu, Y.; Song, J.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 193, 648-652, 1993
A/Title: Molecular cloning and sequencing of a human somatostatin receptor, hSSTR4.
A/Reference number: JN06005; MUID:93290656; PMID:8512564
A/Accession: JN06005
A/Molecule type: DNA
A/Residues: 1-388 <XUY>
A/Cross-references: GB:L14856; NID:g292499; PIDN:AAA36623.1; PID:g292500
R/Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; I
Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A/Title: Cloning, functional expression and pharmacological characterization of a fourth
A/Reference number: JN0762; MUID:93384611; PMID:8373420
A/Accession: JN0762
A/Molecule type: DNA
A/Residues: 1-388 <YAM>
A/Cross-references: GB:D16826; NID:g693907; PIDN:BAA04106.1; PID:g693908
R/Rohrer, L.; Raulf, F.; Bruns, C.; Buettner, R.; Hofstaedter, F.; Schule, R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
A/Title: Cloning and characterization of a fourth human somatostatin receptor.
A/Reference number: A47457; MUID:93248256; PMID:8483934
A/Accession: A47457
A/Molecule type: DNA
A/Residues: 1-82, 'T', 84-364, 'K', 366-388 <ROH>
A/Cross-references: GB:L07833; NID:g307429; PIDN:AAA60565.1; PID:g307430
A/Note: sequence extracted from NCBI backbone (NCBIN:130856, NCBIPI:130858)
C/Comment: This protein mediates the diverse actions of the tetradecapptide somatostatin.
C/Genetics:
A/Gene: GDB:SSTR4
A/Cross-references: GDB:202662; OMIM:182454
A/Map position: 20p11.2-20p11.2
A/Introns: #status absent
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phoc
F/47-73/Domain: transmembrane #status predicted <TM1>
F/84-109/Domain: transmembrane #status predicted <TM2>
F/121-142/Domain: transmembrane #status predicted <TM3>
F/162-184/Domain: transmembrane #status predicted <TM4>
F/208-238/Domain: transmembrane #status predicted <TM5>
F/257-284/Domain: transmembrane #status predicted <TM6>
F/291-314/Domain: transmembrane #status predicted <TM7>

F;24/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;119-198/Disulfide bonds: #status predicted
F;161,253/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status: predicted
F;327/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match	27.7%	Score 505.5;	DB 2;	Length 388;
Best Local Similarity	32.0%;	Pred. No. 1.2e-36;		
Matches 107;	Conservative 73;	Mismatches 117;	Indels 37;	Gaps 9;

QY	6	SLLPTG-----PNA	SDGPDNDLTSAGSP	PRGTGS	ISYINIMPSV	EGTICLLGI	56
			:	:	:	: :	
Db	5	STLP	PGGEEGLGTAMP	SAANAASSAPAEAE	AVAGPGDARAAGM-VA	IQCITYALVCLGLV	63
QY	57	GNSTVIFAVVKKSKLHWCNNV	PDIFILNSVDLLFTLGM	EFMI-----HQLMG	GVWH		110
		: : : : :	: : :	:			
Db	64	GNALVIFVILRYAKMK	TATN---IYLLN	LAVADELFM	LSPEVFASSALRH-----WP		113
QY	111	EGETMCTLLITAMDANSQ	ETSTYLLTAMADRYLATV	HPISSTKERKPSVAT	LVICLLMAL		170
		: : : :	: : :	: :	:		
Db	114	FGSVLCRAVL	SDGLNMFTSFECLTVLS	VDRYVAVHPLE	RATYRRPSVAKLLIN	GVWLA	173
QY	171	SFISITPVWL	YARLIPFGG-AVGC	GIRLPNDT	LYW---FTLYQ	EF	226
		: : : :	:	:	:		
Db	174	SLLVTLPIAIFADTR	PARGGAVACNLQW	PHP---AMS	AVFVYTFLLG	FLPVALIGL	229
QY	227	AYVRILQ	RTSSVAPASQ	RSTRLTRKVRT	TAITAI	CLVF	286
		: : :	: :	: : :	:	: :	
Db	230	CYLLIVG	KRAVALRACG	WQRRRSEK	KITRLVLMVVV	VFVLCMMP	289
QY	287	LTFVYLYN	MAISLGYAN	SCLNPFVYIVL	CETFRK		320
		: : :	: :	: :			
Db	290	AT--VN	HVSLILSYAN	SCANPILLYG	FLSDNFR		320

RESULT 9
A46226
somatostatin receptor 3 - human
C/Species: Homo sapiens (man)
C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C/Accession: A46226; S32501
R/Yamada, Y.; Reisine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Selino, M.,
Mol. Endocrinol. 6, 2136-2142, 1992
A/Title: Somatostatin receptors, an expanding gene family: cloning and functional cha
A/Reference number: A46226; MUID:93149123; PMID:1337145
A/Accession: A46226
A/Molecule type: DNA
A/Residues: 1-418 <YAM>
A/Cross-references: GB:M96738; NID:q338498; PIDN:AAA60592.1; PID:q338499
A/Note: sequence extracted from NCBI backbone (NCBIN:123685, NCBI:P:123690)
R/Corness, J.D.; Demchyshyn, L.L.; Seeman, P.; van Tol, H.H.M.; Srikant, C.B.; Kent,
FEBS Lett. 321, 279-284, 1993
A/Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays pr
A/Reference number: S32501; MUID:93238970; PMID:8097479
A/Accession: S32501
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-418 <COR>
C/Genetics:
A/Gene: GDB:SSTR3
A/Cross-references: GDB:134187; OMIM:182453
A/Map position: 22q13.1-22q13.1
A/Introns: #status absent
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F:44-70/Domain: transmembrane #status predicted <TM1>
F:81-106/Domain: transmembrane #status predicted <TM2>
F:118-139/Domain: transmembrane #status predicted <TM3>
F:159-181/Domain: transmembrane #status predicted <TM4>
F:203-233/Domain: transmembrane #status predicted <TM5>
F:255-282/Domain: transmembrane #status predicted <TM6>
F:289-316/Domain: transmembrane #status predicted <TM7>
F:17_30/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:116-191/Disulfide bonds: #status predicted

Db 145 IYCLFVLSVDRYVAVVHPRIKARYRRTVAKVNLGVWVLSLLVILPIVVEFKTAANS DG 204
QY 191 AVGCGIRLNP-DTDLWYFTLYQFLAFALPFVYITAAVRILOQMTSSVAPASQSRIRL 249
Db 205 TVACNMMLPEPAQRWLGVFVLYTFLMGFLLPVGAICLCYVLIIAKRMVVALKAGWQQRKR 264
QY 250 RTKRVRTAIAICLVFVCAAPYVYLQTLQSLISRPITLTFVYLYNNAISLGYANSCLNPF 309
Db 265 SERKITLMMVMVMVVFVVCWMPFVYVQLVNVFAEQDDATVSOL---SVILIGYANSCANPI 321
QY 310 VYIVLCETFRK 320
Db 322 LYGFLLSDNFKR 332

RESULT 12
C41795
somatostatin receptor 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
C:Accession: C41795
Riyamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A:Title: Cloning and functional characterization of a family of human and mouse somatost
A:Reference number: A41795; MUID:92108031; PMID:1346068
A:Accession: C41795
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-391 <YAM>
A:Cross-references: GB:M81831; NID:g201058; PIDN:AAA58255.1; PID:g201059
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match 27.2%; Score 496.5; DB 2; Length 391;
Best Local Similarity 32.5%; Pred. No. 7.1e-36;
Matches 101; Conservative 68; Mismatches 121; Indels 21; Gaps 5;

QY 11 GPNASNTSDGPDNLTSGSPPRGTSISYINIMPSVEGTICLLGIGNSTVIFAVVKSK 70
Db 42 GRNASQNGTLEGGSA-----ILISFTYSVCLVGLCGNSMVIYVILRYAK 88
QY 71 LHMGNVVDIFIINLSVVDLFLGLMPFMIHQLMNGVWHFGETMCTLTAMDANSQFTS 130
Db 89 MKTATN--IYILNLAIDELMLSVPLVSTLLRH-WPFGALLCRVLSVDAVNMFTS 144
QY 131 TYILTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSITPVWLYARLIPFG 190
Db 145 IYCLFVLSVDRYVAVVHPRIKARYRRTVAKVNLGVWVLSLLVILPIVVEFKTAANS DG 204
QY 191 AVGCGIRLNP-DTDLWYFTLYQFLAFALPFVYITAAVRILOQMTSSVAPASQSRIRL 249
Db 205 TVACNMMLPEPAQRWLGVFVLYTFLMGFLLPVGAICLCYVLIIAKRMVVALKAGWQQRKR 264
QY 250 RTKRVRTAIAICLVFVCAAPYVYLQTLQSLISRPITLTFVYLYNNAISLGYANSCLNPF 309
Db 265 SERKITLMMVMVMVVFVVCWMPFVYVQLVNVFAEQDDATVSOL---SVILIGYANSCANPI 321
QY 310 VYIVLCETFRK 320
Db 322 LYGFLLSDNFKR 332

RESULT 13
A47249
brain-specific somatostatin receptor SSTR-4 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A47249
R;Bruno, J.F.; Xu, Y.; Song, J.; Berelowitz, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 1151-1155, 1992
A:Title: Molecular cloning and functional expression of a brain-specific somatostatin re
A:Reference number: A47249; MUID:93087484; PMID:1360663
A:Accession: A47249

A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-384 <BRU>
A:Cross-references: GB:M96544; NID:g207072; PIDN:AAA42180.1; PID:g207073
A:Note: sequence extracted from NCBI backbone (NCBIN:119731, NCBI:P:119732)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.1%; Score 494.5; DB 2; Length 384;
Best Local Similarity 33.0%; Pred. No. 1e-35;
Matches 104; Conservative 66; Mismatches 116; Indels 29; Gaps 8;

QY 16 NTSDDPDNLTSGSPPRGTSISYINIMPSVEGTICLLGIGNSTVIFAVVKSKLHWCN 75
Db 21 NASWAPDEEDAVRSDGTGTAGMVTI--QCIYALVCLVGLVGNALVIFVILRYAKMKTAT 78
QY 76 NVPDIFIINLSVVDLFLGLMPFMI-----HQLMNGVWHFGETMCTLTITAMDANSQFT 129
Db 79 N---IYLLNLAVADELFLSVFPFVASAALRH-----WFGAVLCRAVLSVDGLNMT 128
QY 130 STYILTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSITPVWLYARLIPFG 189
Db 129 SVFCLTVLSVDRYVAVVHPRLAATYRPSVAKLINLGVWLASLLVTLPIAVEADTRPARG 188
QY 190 G-AVGCGIRLNPDDTLW--FTLYQFLAFALPFVYITAAVRILOQMTSSVAPASQR 245
Db 189 GEAVACNLHWPHP---AWSAVEFVITFLLGLFLLPVLAIGLCYLLIVGKMRAYALRAGWQ 244
QY 246 SIRLRTKRVRTAIAICLVFVCAAPYVYLQTLQSLISRPITLTFVYLYNNAISLGYANSC 305
Db 245 QRRSEKKITRLVLMVTVTFVLCWMPFVYVQLNLFVTSIDAT--VNHVSLISYANSC 301
QY 306 LNPVYIVLCETFRK 320
Db 302 ANPILYGFLLSDNFKR 316

RESULT 14
JC4629
somatostatin receptor type-4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 24-Nov-1999
C:Accession: JC4629
R;Schwabe, W.; Brennan, M.B.; Hochgeschwender, U.
Gene 168, 233-235, 1996
A:Title: Isolation and characterization of the mouse (Mus musculus) somatostatin rece
A:Reference number: JC4629; MUID:96194903; PMID:8654950
A:Accession: JC4629
A:Molecule type: DNA
A:Residues: 1-384 <SCH>
A:Cross-references: GB:U26176; NID:g833840; PIDN:AAA67561.1; PID:g833841
C:Comment: This protein works through the G-proteins and plays a role in mediating in
C:Genetics:
A:Gene:sstr4
C:Superfamily: vertebrate rhodopsin
C:Keywords: receptor; transmembrane protein
F;46-349/Domain: transmembrane #status predicted <TMM>

Query Match 26.5%; Score 483; DB 2; Length 384;
Best Local Similarity 31.9%; Pred. No. 1.1e-34;
Matches 105; Conservative 69; Mismatches 133; Indels 22; Gaps 8;

QY 1 MDLEASL-----PTGPNASNTSDGPDNLTSGSPPRGTSISYINIMPSVEGTICLLGI 55
Db 1 MNAPATLRLRGVEDTWTTPGINASNAPEQEDAMGSDGTGTAGMVTI--QCIYALVCLVGL 58
QY 56 IGNSTVIFAVVKSKLHWCNNVDPDIFIINLSVVDLFLGLMPFMIHQLMNGVWHFGETM 115
Db 59 VGNALVIFVILRYAKMKTATN--IYLLNLAVADELFLSVFP-VRSAAALRHMPFGAVL 114
QY 116 CTLTAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLWALSFSISI 175
Db 115 CRAVLSVDGLNMTSVFCLTVLSVDRYVAVVHPRLAATYRPSVAKLINLGVWLASLLVT 174


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QY 176 TPVMTYARLIPFPGC-AVGGCIGRLPNDDTDLYW---FTLYQFFLAFLAPFVVTAAIVRI 231
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Db 175 LPIAVFADTRPARGGEAACNLHWPHP---AWSAVFIYTFLLGLFDPVLAIGLCYLLI 230
      | : : : | | | | | : | : | : | | | : | : | : |
QY 232 LQRMSSVAPASQRSIRLRTKRVTRTAIAICLVFVGCWAPYVVLQTLQSLISRPTLFVY 291
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Db 231 VGMRAVALRGWQQRRRSEKKITRLVLMVTVFVLCMPEYVVLNLFVTSIDAT--- 287
      | : : : | : | : | : | : | : | : | : | : | : |
QY 292 LYNAALSLGYANSCLNPFVYIVLCETFRK 320
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Db 288 VNHSVLSILSYANSCANPILYGLFSLDNERR 316
      | : : : | | | | | | : | : | : | : | : | : |
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RESULT 15

S30508
probable G protein-coupled receptor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
C/Accession: S30508
R/Meyerhof, W.; Wulfsen, I.; Schoenrock, C.; Fehr, S.; Richter, D.
Proc. Natl. Acad. Sci. U.S.A. 89, 10267-10271, 1992
A/Title: Molecular cloning of a somatostatin-28 receptor and comparison of its expression
A/Reference number: S30508; MUID:93066220; PMID:1279674
A/Accession: S30508
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-428 <MEY>
A/Cross-references: EMBL:X63574; NID:956315; PIDN:CAA45130.1; PID:956316
C/Superfamily: vertebrate rhodopsin
C/keywords: G protein-coupled receptor; transmembrane protein

Query Match	26.3%;	Score 480.5;	DB 2;	Length 428;
Best Local Similarity	31.3%;	Pred. No. 2e-34;		
Matches 118;	Conservative 73;	Mismatches 143;	Indels 43;	Gaps 11;

[illegible]

Search completed: February 13, 2003, 14:01:07
Job time : 13.6809 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 14:00:22 ; Search time 11.7962 Seconds
(without alignments)
764.550 Million cell updates/sec

Title: US-09-885-478-28

Perfect score: 1824

Sequence: 1 MDLEASLLPTGPNASNTSDG.....LRAVSNAGTADERTESKGT 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*

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7: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*

10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*

12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*

14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1824	100.0	353	10	US-09-925-776-2	Sequence 2, Appli
2	1824	100.0	353	10	US-09-885-478-28	Sequence 28, Appl
3	1824	100.0	422	10	US-09-885-478-2	Sequence 2, Appli
4	1819	99.7	422	10	US-09-885-478-26	Sequence 26, Appl
5	1819	99.7	422	10	US-09-885-478-27	Sequence 27, Appl
6	1808	99.1	353	10	US-09-895-686-2	Sequence 2, Appli
7	1763	96.7	353	10	US-09-885-478-4	Sequence 4, Appli
8	1692	92.8	439	9	US-09-990-940-19	Sequence 19, Appli
9	1224	67.1	239	10	US-09-864-761-38414	Sequence 38414, A
10	565.5	31.0	340	9	US-09-791-932-117	Sequence 117, App
11	565.5	31.0	340	9	US-09-990-940-2	Sequence 2, Appli
12	524.5	28.8	369	10	US-09-823-114-9	Sequence 9, Appli
13	504.5	27.7	418	9	US-09-992-331-17	Sequence 17, Appl
14	496.5	27.2	391	9	US-09-990-940-20	Sequence 20, Appl
15	480.5	26.3	428	9	US-09-992-331-16	Sequence 16, Appl
16	472	25.9	428	9	US-09-992-331-15	Sequence 15, Appl
17	470.5	25.8	363	9	US-09-992-331-14	Sequence 14, Appl
18	456	25.0	362	9	US-09-992-331-13	Sequence 13, Appl
19	456	25.0	370	10	US-09-823-114-21	Sequence 21, Appl

20	452.5	24.8	372	9	US-10-112-599A-4	Sequence 4, Appli
21	449	24.6	372	10	US-09-966-871-80	Sequence 80, Appl
22	449	24.6	372	12	US-10-039-645-80	Sequence 80, Appl
23	449	24.6	415	10	US-09-823-114-20	Sequence 20, Appl
24	445.5	24.4	382	10	US-09-993-844-4	Sequence 4, Appli
25	444	24.3	400	10	US-09-966-871-85	Sequence 85, Appl
26	444	24.3	400	12	US-10-039-645-85	Sequence 85, Appl
27	443.5	24.3	405	10	US-09-966-871-84	Sequence 84, Appl
28	443.5	24.3	405	12	US-10-039-645-84	Sequence 84, Appl
29	443	24.3	398	10	US-09-823-114-16	Sequence 16, Appl
30	443	24.3	398	10	US-09-966-871-1	Sequence 1, Appli
31	443	24.3	398	12	US-10-039-645-1	Sequence 1, Appli
32	442.5	24.3	390	10	US-09-761-962-25	Sequence 25, Appl
33	442.5	24.3	391	10	US-09-761-962-26	Sequence 26, Appl
34	442.5	24.3	392	10	US-09-761-962-19	Sequence 19, Appl
35	442.5	24.3	398	10	US-09-214-904-2	Sequence 2, Appli
36	442.5	24.3	398	10	US-09-761-962-29	Sequence 29, Appl
37	442.5	24.3	398	10	US-09-966-871-83	Sequence 83, Appl
38	442.5	24.3	398	12	US-10-039-645-83	Sequence 83, Appl
39	442.5	24.3	401	10	US-09-761-962-20	Sequence 20, Appl
40	442.5	24.3	409	10	US-09-761-962-27	Sequence 27, Appl
41	442.5	24.3	438	10	US-09-761-962-17	Sequence 17, Appl
42	442.5	24.3	444	10	US-09-761-962-28	Sequence 28, Appl
43	442	24.2	372	10	US-09-823-114-8	Sequence 8, Appli
44	442	24.2	398	10	US-09-966-871-79	Sequence 79, Appl
45	442	24.2	398	12	US-10-039-645-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1

US-09-925-776-2

; Sequence 2, Application US/09925776

; Patent No. US20020038007A1

; GENERAL INFORMATION:

; APPLICANT: AMES, ROBERT S. , JR.

; APPLICANT: SARAU, HENRY M.

; APPLICANT: FOLEY, JAMES J.

; APPLICANT: BERGSMAN, DEK J.

; APPLICANT: ELLIS, CATHERINE E.

; APPLICANT: CHAMBERS, JON K.

; TITLE OF INVENTION: A METHOD OF FINDING AGONIST AND

; TITLE OF INVENTION: ANTAGONIST TO HUMAN 11CB SPLICE VARIANT

; FILE REFERENCE: GP-50003-D2

; CURRENT APPLICATION NUMBER: US/09/925,776

; CURRENT FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: 60/032,763

; PRIOR FILING DATE: 1996-12-11

; PRIOR APPLICATION NUMBER: 08/984,288

; PRIOR FILING DATE: 1997-12-03

; PRIOR APPLICATION NUMBER: 60/073,747

; PRIOR FILING DATE: 1998-02-05

; PRIOR APPLICATION NUMBER: 09/060,504

; PRIOR FILING DATE: 1998-04-15

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 353

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-925-776-2

Query Match 100.0%; Score 1824; DB 10; Length 353;

Best Local Similarity 100.0%; Pred. No. 9.8e-162;

Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYNIIMPSVFGTICLLIGNST 60

|||||

Db 1 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYNIIMPSVFGTICLLIGNST 60

OY 61 VIFAVKKSKLHWCNNVPDIFINISVVDLFLGLGMPMIHQMGNGVWHFGETMCTLT 120

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Db 61 VIFAVVKKSKLHMCNNVPDIFIINLSVVDLFLFLGMPEMIHQLMGNGVWHFGETMCTLIIT 120
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Db 121 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWL 180
QY 181 YARLIPFPGGAVGCGIRLPNPDLDLWFTLYQFFLAFALPFEVVITAAYVRILQRMSSVA 240
Db 181 YARLIPFPGGAVGCGIRLPNPDLDLWFTLYQFFLAFALPFEVVITAAYVRILQRMSSVA 240
QY 241 PASQRSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVYLYNNAISLG 300
Db 241 PASQRSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVYLYNNAISLG 300
QY 301 YANSCLNPFVYIVLCETFRKRLVLSVKPAAQQLRAVSNQOTADEERTESKGT 353
Db 301 YANSCLNPFVYIVLCETFRKRLVLSVKPAAQQLRAVSNQOTADEERTESKGT 353

RESULT 2

US-09-885-478-28
; Sequence 28, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH1
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 353
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-28

Query Match 100.0%; Score 1824; DB 10; Length 353;
Best Local Similarity 100.0%; Pred. No. 9.8e-162;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWL 180
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Db 181 YARLIPFPGGAVGCGIRLPNPDLDLWFTLYQFFLAFALPFEVVITAAYVRILQRMSSVA 240
QY 241 PASQRSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVYLYNNAISLG 300
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QY 301 YANSCLNPFVYIVLCETFRKRLVLSVKPAAQQLRAVSNQOTADEERTESKGT 353
Db 301 YANSCLNPFVYIVLCETFRKRLVLSVKPAAQQLRAVSNQOTADEERTESKGT 353

RESULT 3
US-09-885-478-2
; Sequence 2, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-885-478-2

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Best Local Similarity 100.0%; Pred. No. 1.2e-161;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 VIFAVVKKSKLHMCNNVPDIFIINLSVVDLFLFLGMPEMIHQLMGNGVWHFGETMCTLIIT 120
Db 130 VIFAVVKKSKLHMCNNVPDIFIINLSVVDLFLFLGMPEMIHQLMGNGVWHFGETMCTLIIT 189
QY 121 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWL 180
Db 190 AMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWL 249
QY 181 YARLIPFPGGAVGCGIRLPNPDLDLWFTLYQFFLAFALPFEVVITAAYVRILQRMSSVA 240
Db 250 YARLIPFPGGAVGCGIRLPNPDLDLWFTLYQFFLAFALPFEVVITAAYVRILQRMSSVA 309
QY 241 PASQRSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVYLYNNAISLG 300
Db 310 PASQRSIRLRTKRVTRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVYLYNNAISLG 369
QY 301 YANSCLNPFVYIVLCETFRKRLVLSVKPAAQQLRAVSNQOTADEERTESKGT 353
Db 370 YANSCLNPFVYIVLCETFRKRLVLSVKPAAQQLRAVSNQOTADEERTESKGT 422

RESULT 4
US-09-885-478-26
; Sequence 26, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26

; LENGTH: 422
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-26

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Best Local Similarity 100.0%; Pred. No. 3.5e-161;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 62 IFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLITA 121
Db 131 IFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLITA 190
QY 122 MDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLLWALSFSISTPVMWLY 181
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Db 251 ARLIPEPGGAVGCGIRLPNPDLDLWFTLYQFFLAFALPEVVITAAYVRILQRMSTSSVAP 310
QY 242 ASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPPTLTFVYLYNNAISLGY 301
Db 311 ASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPPTLTFVYLYNNAISLGY 370
QY 302 ANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 353
Db 371 ANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 422

RESULT 5
US-09-885-478-27
; Sequence 27, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH1
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 422
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-27

Query Match 99.7%; Score 1819; DB 10; Length 422;
Best Local Similarity 100.0%; Pred. No. 3.5e-161;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLGIIGNSTV 61
Db 71 DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLGIIGNSTV 130
QY 62 IFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLITA 121
Db 131 IFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLITA 190

QY 122 MDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLLWALSFSISTPVMWLY 181
Db 191 MDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLLWALSFSISTPVMWLY 250
QY 182 ARLIPEPGGAVGCGIRLPNPDLDLWFTLYQFFLAFALPEVVITAAYVRILQRMSTSSVAP 241
Db 251 ARLIPEPGGAVGCGIRLPNPDLDLWFTLYQFFLAFALPEVVITAAYVRILQRMSTSSVAP 310
QY 242 ASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPPTLTFVYLYNNAISLGY 301
Db 311 ASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPPTLTFVYLYNNAISLGY 370
QY 302 ANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 353
Db 371 ANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 422

RESULT 6
US-09-895-686-2
; Sequence 2, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020106655A1 1459432CD1
US-09-895-686-2

Query Match 99.1%; Score 1808; DB 10; Length 353;
Best Local Similarity 99.2%; Pred. No. 3e-160;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLGIIGNST 60
Db 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLGIIGNST 60
QY 61 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
Db 61 VIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLIT 120
QY 121 AMDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLLWALSFSISTPVMWLY 180
Db 121 AMDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLLWALSFSISTPVMWLY 180
QY 181 YARLIPEPGGAVGCGIRLPNPDLDLWFTLYQFFLAFALPEVVITAAYVRILQRMSTSSVA 240
Db 181 YARLIPEPGGAVGCGIRLPNPDLDLWFTLYQFFLAFALPEVVITAAYVRILQRMSTSSVA 240
QY 241 PASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPPTLTFVYLYNNAISLGY 300
Db 241 PASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPPTLTFVYLYNNAISLGY 300
QY 301 YANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 353
Db 301 YANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESKGT 353

RESULT 7
US-09-885-478-4

```

; Sequence 4, application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH1
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: RATTUS NORVEGICUS
US-09-885-478-4

```

Query Match	96.7%;	Score 1763;	DB 10;	Length 353;	
Best Local Similarity	96.0%;	Pred. No. 4.4e-156;			
Matches 339;	Conservative 6;	Mismatches 8;	Indels 0;	Gaps 0;	
QY	1	MDLEASLLETPGNASNTSDGPDNLTSAGSPPRGTSGISYINIIIMPSVEFGTICLLGIIGNST	60		
Db	1	MDLQTSLSLTGPNASNISDGDNLTLPGSPPRGTGSYSYINIIIMPSVEFGTICLLGIIGNST	60		
QY	61	VIFAFAVKKSKLHWCNNVPDIFINLVSVDLLFLMGPEMIHQLMGNGVWHEGEMCTLIT	120		
Db	61	VIFAFAVKKSKLHWCNNVPDIFINLVSVDLLFLMGPEMIHQLMGNGVWHEGEMCTLIT	120		
QY	121	AMDANSQETSTYILTAMADIRYLATVHPISSTKFKRPSAVTLVICLMALESFISITPVMWL	180		
Db	121	AMDANSQETSTYILTAMTIDRYLATVHPISSTKFKRPSMATLVICLMALESFISITPVMWL	180		
QY	181	YARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAALPFVVITAAVYRILQMTSSVA	240		
Db	181	YARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAALPFVVITAAVYKILQMTSSVA	240		
QY	241	PASQRSIRLTKRVTRTAIAICLVEFVCWAPYYVLQTLQSLISRPITLTFVYLYNAAISLG	300		
Db	241	PASQRSIRLTKRVTRTAIAICLVEFVCWAPYYVLQTLQSLISRPITLTFVYLYNAAISLG	300		
QY	301	YANSCLNPFVYIVLCETFRRKRLVLSVKKPAAQGLRAVSNQAOTADEERTESKGT	353		
Db	301	YANSCLNPFVYIVLCETFRRKRLVLSVKKPAAQGLRIYVSNQAOTADEERTESKGT	353		

```

RESULT 8
US-09-990-940-19
; Sequence 19, Application US/09990940
; Publication No. US20030027252A1
GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiayang
; APPLICANT: Chen, Jin-long
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupte, Jamila S.
; APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. US20030027252A1el Receptors
FILE REFERENCE: 018781-007410US
CURRENT APPLICATION NUMBER: US/09/990,940
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/252,841
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/257,636
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 60/261,377

```

```

; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human melanin-concentrating hormone receptor
; OTHER INFORMATION: (MCHr1)
US-09-990-940-19

```

	Query Match	92.8%;	Score 1692;	DB 9;	Length 402;	
	Best Local Similarity	99.4%;	Pred. No. 2e-149;			
	Matches 328;	Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	24	LTSAGSPPRKTSISYINIMPSVEFGTICLLGIGNSTVIFAVVKSKLHWCNNYPDIFI	83			
Db	73	LLSPGPSPPRCSISYINIIMPVSEGTICLLGIGNSTVIFAVVKSKLHWCNNYPDIFI	132			
QY	84	NLSVDLLFLGLMPFMIHQLMGNVWHFGETMCTLTITAMANSQTSTYILTFMAIDRYL	143			
Db	133	NLSVDLLFLGLMPFMIHQLMGNVWHFGETMCTLTITAMANSQTSTYILTFMAIDRYL	192			
QY	144	ATVHPISSTFKRRKPSVATLVICLLNALSFISTPWLKYARLIPEPGAVGGIRLPNPD	203			
Db	193	ATVHPISSTFKRRKPSVATLVICLLNALSFISTPWLKYARLIPEPGAVGGIRLPNPD	252			
QY	204	DLWFTLYQFEFLAFALPFVVITAAYVRILQRM TSSVAPASQRSIRLTRKRVTPRAIACL	263			
Db	253	DLWFTLYQFEFLAFALPFVVITAAYVRILQRM TSSVAPASQRSIRLTRKRVTPRAIACL	312			
QY	264	VFFVCWAPYYVLQTLQLSISRPTLFVYLYNNAISLGANSCLNPFVYIVLCETFRKRLV	323			
Db	313	VFFVCWAPYYVLQTLQLSISRPTLFVYLYNNAISLGANSCLNPFVYIVLCETFRKRLV	372			
QY	324	LSVKPAAQGLRAVSNAQTADERTESKGT	353			
Db	373	LSVKPAAQGLRAVSNAQTADERTESKGT	402			

RESULT 9
US-09-864-761-38414
; Sequence 38414, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

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PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 38414
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO 286090.10
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.74
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
OTHER INFORMATION: EST_HUMAN HIT: BE701073.1, EVALUATE 6.00e-44
OTHER INFORMATION: SWISSPROT HIT: Q99705, EVALUATE 0.00e+00
US-09-864-761-38414

```

Query Match	67.1%;	Score 1224;	DB 10;	Length 239;
Best Local Similarity	100.0%;	Pred. No. 2.8e-106;		
Matches 239; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

QY	115	MCTLITAMDANSQFTSTYILTAMADRYLATVHPISSTKERKPSVATLVICLLMALSTIS	174
Dd	1	MCTLITAMDANSQFTSTYILTAMADRYLATVHPISSTKERKPSVATLVICLLMALSTIS	60
QY	175	ITPVMVLARLIPEPGGAVGCCIRLENDPTDLYMFTLYQFELAFALPFVVITAAVRRIOR	234
Dd	61	ITPVMVLARLIPEPGGAVGCCIRLENDPTDLYMFTLYQFELAFALPFVVITAAVRRIOR	120
QY	235	MTSSVAPASORSIRLRTRKRVTRTAIAICLVEFVCWAPYYVLOLTQLSISRPTLTFEYLYN	294
Dd	121	MTSSVAPASQRSIRLRTRKRVTRTAIAICLVEFVCWAPYYVLOLTQLSISRPTLTFEYLYN	180
QY	295	AAISLGYNASCINPFVYIVLCETFRKRRLVSVKPAAQGLRAVSNQAOTADEERTESKGT	353
Dd	181	AAISLGYNASCINPFVYIVLCETFRKRRLVSVKPAAQGLRAVSNQAOTADEERTESKGT	239

RESULT 10
US-09-791-932-117

```

; Sequence 117, Application US/097919132
; Publication No. US20030003451A1
;
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
;

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```

; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huf, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030003451a1e1 G Protein-Coupled Receptors Cross-Refer
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/09/791,932
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/194,344
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/218,337
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 117
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-932-117

```

Query Match	31.0%;	Score 565.5;	DB 9;	Length 340;
Best Local Similarity	37.0%;	Pred. No. 5.1e-45;		
Matches 113; Conservative	62;	Mismatches 119;	Indels 11;	Gaps 4;

OY	41	IIMPSVEGTICLLGIIGNSTVIEPAVVKKSKLHWCCNNVPDIFITINLSVDLLFLGMPFMI	100
	:	: : : : : : : : : : : :	
Db	35	VILPMSIGIISTGLVGNILIVETIRSRK---KTVPDIYCINLAVALDVHIHVGMPFLI	90
OY	101	HOLMGNGVWHEGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKERKPSVA	160
	:	: : : : : : : : : :	
Db	91	HOWARGEWFGGPLCTIIITSLDTCNQACSAIMTWSVDYRFALVOFRLTRWRTRYKT	150
OY	161	TLVICLTWALSFISITPVMWLARLPBPGGAVGCGRLPNPBDLYWFTLYQFFLAFAFP	220
	:	: : : : :	
Db	151	IRINGLWMAFSILALPWVWYSKVIKRKGVESCAFDLTSPD-DVLWYTLYLTITTFEFP	209
OY	221	FVVITAAYRIL-----QRMTSSVAPASQRSI-RLRTKRVRTPATAICLVFEVCWAPYYV	274
	:	: : : : : : : : : : :	
Db	210	LPLILVCYLILICYTWEMYQQNKDARCNCPSVPKQRVMKLTKNVLLVVFILSAPHYH	269
OY	275	LQTLQLSIBRPULTFVYLYNNAISLGYANSCNPFVIYVLCETFERKRLVSVKPPAQQL	334
	:	: : :	
Db	270	IQLVNLQMEOPTLAFYVGYLLSIGLSYASSSINPFYILLSGNFQKRLPQIQRRATEKEI	329
OY	335	RAVSN 339	
	:		
Db	330	NNMGN 334	

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RESULT 11
US-09-990-940-2
; Sequence 2, Application US/09990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiayang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupte, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030027252A1el Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR342,
; OTHER INFORMATION: melanin-concentrating hormone receptor 2 (MCHR2)
US-09-990-940-2

```

Query Match	31.0%;	Score 565.5;	DB 9;	Length 340;	
Best Local Similarity	37.0%;	Pred. No. 5.1e-45;			
Matches 113;	Conservative 62;	Mismatches 119;	Indels 11;	Gaps 4;	
QY	41	IIMPSVEGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFITINLSVVDLFLFLGMPFMI	100		
		: : : : : : : : :			
Db	35	VILPSMIGIICSTGLVGNILIVFTIIRSRK---KTPVDIYICNLAVADLVHIVGMPFLI	90		
QY	101	HQLMGNGVHFGETMCTLTAMDANSQFTSTYILTPAMAIDRYLATVHPISSTKFRKPSVA	160		
		: : : : : : : : : : : : : :			
Db	91	HQWARGGEWVEGGPLCTIITSIDTCNQFACSAIMTWSVDRYFALVQPFRLTRWTRYKT	150		
QY	161	TLVICLLWALSFISITPVLWTLARLIPFGAVGCGIRPNPDTDLWTFLLQFFLAFALP	220		
		: : : : : : :			
Db	151	IRINIGMAASFILALPVMVYSKVIKFKDGVESCAFIDLSPD-DVLWYTLTLTITTEFFP	209		
QY	221	FFVITAAVYRIL-----GRMTSSVAPASQRSI-RLPRKRVTRTAIACLVFEVCWAPYYV	274		
		: : : : : : : : : : : :			
Db	210	LPFLIVLCYILILCYTWEMYQQNDARCCNPSPVKQRYMKLTKMVLVLVVVFILSAARYHV	269		
QY	275	LQLTQESTSRPTLTFFVLYLNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAQGOGL	334		
		: : : : :			
Db	270	IQLVNLQMEQPTLAFYVGVYLSICLSYASSINPFYIILLSGNFQKRRLPOLQRATEKEI	329		
QY	335	RAVSN 339			
		:			
Db	330	NNMGN 334			

RESULT 12
US-09-823-114-9
; Sequence 9, Application US/09823114
; Patent No. US20020061554A1

```

: GENERAL INFORMATION:
: APPLICANT: EVANS, CHRISTOPHER J.
: KEITH, DUANE E.
: TITLE OF INVENTION: OPIOID RECEPTOR GENES
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1888
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/823,114
: FILING DATE: 29-Mar-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/148,351
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20526.22
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: TELEX: 90-4030 MRSNFOERSWSH
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 369 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 9:
:
: US-09-823-114-9

```

Query Match	28.88;	Score 524.5;	DB 10;	Length 369;
Best Local Similarity	31.68;	Pred. No. 3,6e-41;		
Matches 113;	Conservative 75;	Mismatches 129;	Indels 41;	Gaps 8;
QY 2	DLEASLLPTGPNASNTSDGPDNLTSGSPPRGTGISISYINIMPSVEGTICLLGIIGNSTV	61		
	: : : : : : : : : : : : :			
Db 20	DLNGSLGPS--NGSNQTEPYDDMTS-----NAVLTFYFVVCVGVGLCGNTLV	64		
QY 62	IFAVVKKSKLHWCNPNVPDIFITINISVDDLFLGMPF-----MIHQLMGNGVHFGETM	115		
	: : : : : : : : : : : : : : : :			
Db 65	IYVILRYAKM---KITINIXILNTAIADELFMLGLPFLMAQVALVH-----MPFGKAI	114		
QY 116	CTLITAMDANSQFTSYILITAMADRYLATVHPISSTKRRKPSVATLVICLMALESFISI	175		
	: : : : : : : : : : : : : :			
Db 115	CRVVMTVQDINGQFTSIFCLTVMSIDRYLAVVHPIKSAKMRPRRTAKMINVAWGVSLVI	174		
QY 176	TPVWLRYARLIPFGGAVGCGIRLPNDTDLY-WFTLYQEFALFALPFVVITAAVYRILQR	234		
	: : : : : : : : : : : : :			
Db 175	LPIMITYAGLRSNQWGRSSCTINWPBEGAWYTGFIITAFILGFLVPLTIIICLCYFIIRK	234		
QY 235	MTSSVAPASQSRIRLRTKRVTRTALAICLVFFVCWAPYVYLQTLQSLIS-RPTLLTFVYLY	293		
	: : : : : : : : : : : : : :			
Db 235	VKSSGIRVGSKKRKKSEKKVTRMVSIVAVFIFCWLPTFIIFNVSSVSVAISPTALKGMF	294		
QY 294	NAAISLGYANSCNLPFYVYIVLCETFERKRLVSVKPPAAGOLRAVSNQOTADERTESEK	351		
	: : : : : : : : : : :			
Db 295	DFVVLITVANSKANPILYAFLSDNEKK-----SFQNVLCIVKVGAEDEGRSDSK	344		

RESULT 13
US-09-992-331-17
; Sequence 17, Application US/09992331


```

; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 20
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human somatostatin receptor 1 (SSTR1)
US-09-990-940-20

Query Match      27.2%; Score 496.5; DB 9; Length 391;
Best Local Similarity 32.5%; Pred. No. 1.5e-38;
Matches 101; Conservative 68; Mismatches 121; Indels 21; Gaps 5;

QY      11 GPNASNTSDGPNLTSGSPPRTCISYINIIIMPVSFGTICLLGIIGNSTYFAVVKSSK 70
      1111 : 11 1: : : : : : : : : : : : : : : : : : : : : : : :
Db      42 GRNASQNGTISEGQSA-----ILISFIYSVCLVGLCGNSMVIYILRYAK 88

QY      71 LHWCNVNPDIPIINLSVVDLFLGLGPMFIHQLMGNGVWHFGETMCTLTITAMDANSQFTS 130
      : 1 1:1:1: : 1 : 1:1: : : 1 1 : 1 1 : : 1 1 : : 1 1
Db      89 MKTATN---ITLNLAIADDELLMLSPFLVTSTLLRH-WPFGALLCRLTLSVDAYNMFTS 144

QY      131 TYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLLMAISFISTPVMILYARLIPFGG 190
      1 1 : : : : : : : : : : : : : : : : : : : : : : : :
Db      145 IYCLTVLSVDRYAAVHPKAKARYRRPTVAKVNNLGNWVLSLVILPIVVESRTAANS DG 204

QY      191 AVGCGIRLPNP-DTDLYWFTLYQFELAFALPFWITAYVRILQRTSSVAPASQSRIRL 249
      1 : : : 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 : :
Db      205 TVACNMMLPEPAQRWLVGFVLYTFLMGFLLPVGAICLCYLIIAKRMVALKAGWQQRK 264

QY      250 RTKRVTRTAICLVFVFCWAPYVYLQTLQLSISRPTLTFVYLYNNAISLGANSCLNPF 309
      : : : : : : : : : : : : : : : : : : : : : : : :
Db      265 SERKITLMVAVVAVFVICMFPYVQLVNVFAEQDDATVSQ---SVILGANS CANPI 321

QY      310 VYIVLCETFRK 320
      : 1 1 : : : :
Db      322 LYGLFLSDNFKR 332

RESULT 15
US-09-992-331-16
; Sequence 16, Application US/09992331
; Publication No. US20030022186A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, JOHN N.
; APPLICANT: MINTIER, GABE
; APPLICANT: RAMANATHAN, CHANDRA S.
; APPLICANT: HAWKEN, DONALD R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY18,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN PITUITARY GLAND AND COLON CARCINOMA
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: D0048NP
; CURRENT APPLICATION NUMBER: US/09/992,331
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/308,540
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/261,782
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/248,483
; PRIOR FILING DATE: 2000-11-14

```


XX	30-DEC-1999;	99WO-US31169.
PF		
XX	31-DEC-1998;	98US-0224426.
PR		
XX	(SYNA-) SYNAPTIC PHARM CORP.	
PA		
XX	Salon JA, Laz TM, Nagorny R, Wilson AE;	
PI		
XX	WPI; 2000-548644/50.	
DR		
XX		
PT	Novel nucleic acid encoding human melanin concentrating hormone	
PT	receptor useful for treating cardiovascular disorders, hypertension and	
PT	diabetes, whose mutant form is activated by melanin concentrating	
PT	hormone	
XX		
PS	Claim 9; Fig 14; 173pp; English.	
XX		
CC	Neuroregulators modulate communication in the nervous system. Melanin	
CC	concentrating hormone 1 (MCH) is one such neuroregulator. MCH may serve	
CC	as an integrative neuropeptide, involved in stress response, feeding	
CC	regulation and sexual activity. Also, MCH is thought to participate in	
CC	water balance regulation, energy metabolism, general arousal/attention	
CC	state, memory and cognitive functions and psychiatric disorders. The	
CC	present sequence is the mutant human MCH1 receptor encoded by plasmid	
CC	R114. The present sequence is a G-protein coupled receptor. MCH1 receptor	
CC	may be used in the therapy for a variety of disorders: steroid or	
CC	pituitary hormone disorder, epinephrine release disorder,	
CC	gastrointestinal disorder, cardiovascular disorder, electrolyte balance	
CC	disorder, hypertension, diabetes, respiratory disorder, asthma,	
CC	reproductive function disorder, immune disorder, endocrine disorder,	
CC	musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,	
CC	memory disorder e.g. Alzheimer's disease, sensory modulation and	
CC	transmission disorder, motor coordination disorder, sensory integration	
CC	disorder, dopaminergic function disorder e.g. Parkinson's disease,	
CC	olfaction disorder, sympathetic innervation disorder, depression, stress,	
CC	fluid-imbalance disorder, urinary disorder e.g. urinary incontinence,	
CC	seizure, pain, psychotic behaviour e.g. schizophrenia, morphine	
CC	tolerance, opiate addiction or migraine.	
XX		
SQ	Sequence	422 AA;
	Query Match	100.0%; Score 2210; DB 21; Length 422;
	Best Local Similarity	100.0%; Pred. No. 1.4e-221;
	Matches 422; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MSVGAAKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGGGRRRLPQPAWEGSSARL	60
DB	1 MSVGAAKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGGGRRRLPQPAWEGSSARL	60
QY	61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTASGSPRTGSISTYINIIMPSVFGTIC	120
DB	61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTASGSPRTGSISTYINIIMPSVFGTIC	120
QY	121 LGGIGNSTVIFAVVKKSKLHWCNNVPDIFITINLSVDLFLLGMPMIHQLMGNGVWHF	180
DB	121 LGGIGNSTVIFAVVKKSKLHWCNNVPDIFITINLSVDLFLLGMPMIHQLMGNGVWHF	180
QY	181 GETMCTLITAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLMALS	240
DB	181 GETMCTLITAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLMALS	240
QY	241 FISITPVMLYARLPPPGAVGCGIRLPNPBDLWFTLYQFLAFALPFWVITAAYVRI	300
DB	241 FISITPVMLYARLPPPGAVGCGIRLPNPBDLWFTLYQFLAFALPFWVITAAYVRI	300
QY	301 LQRMSSVAPASQSRIRLTKRVRTAIAICLVFVCWAPYYVLQTLQSLISRPTLTFVY	360
DB	301 LQRMSSVAPASQSRIRLTKRVRTAIAICLVFVCWAPYYVLQTLQSLISRPTLTFVY	360
QY	361 LYNAAISLGYANSCLNPFYIIVLCETFRRKRLVLSVKPAAGQLRAVSNQTADEERTESK	420
DB	361 LYNAAISLGYANSCLNPFYIIVLCETFRRKRLVLSVKPAAGQLRAVSNQTADEERTESK	420

QY	421 GT 422
DB	421 GT 422
RESULT 2	
ID	AAU75858 standard; Protein; 422 AA.
XX	AAU75858;
AC	
XX	08-MAY-2002 (first entry)
DT	
XX	Human melanin concentrating hormone receptor, MCH1, R114 mutant.
DE	
XX	Human; melanin concentrating hormone receptor; MCH1; R114;
KW	steroid hormone disorder; pituitary hormone disorder;
KW	epinephrine release disorder; gastrointestinal disorder; mutein;
KW	cardiovascular disorder; hypertension; diabetes; respiratory disorder;
KW	asthma; reproductive function disorder; immune disorder; mutant;
KW	musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
KW	memory disorder; motor coordination disorder; obesity; eating disorder;
KW	dopaminergic function disorder; pain; psychosis; opiate addiction;
XX	affective disorder; migraine; transgenic.
OS	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Location/Qualifiers
FT	Key
FT	Misc-difference 6 /note= "Wild-type Met substituted by Ala"
FT	Misc-difference 70 /note= "Wild-type Met substituted by Ala"
FT	
XX	WO200202744-A2.
PN	
XX	10-JAN-2002.
PD	
XX	05-JUL-2001; 2001WO-US21350.
PF	
XX	05-JUL-2000; 2000US-0610635.
PR	
XX	(SYNA-) SYNAPTIC PHARM CORP.
PA	
XX	Salon JA, Laz TM, Nagorny R, Wilson AE;
PI	
XX	WPI; 2002-164532/21.
DR	
XX	Purified human melanin concentrating hormone receptor protein and
PT	polynucleotides for screening modulator useful for treating memory
PT	disorder, sensory modulation and transmission disorder, motor
PT	coordination disorder
XX	
PS	Claim 9; Fig 14; 524pp; English.
XX	
CC	The invention relates to a purified human melanin concentrating hormone
CC	(MCH1) receptor protein and its encoding nucleic acid (or mutant
CC	activated by MCH or its analogue or homologue). Also included are
CC	expression vectors, probes, transformed insect cells, antisense
CC	oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting the
CC	the binding of the antibody to MCH1, a transgenic animal expressing the
CC	protein, or a homologous knockout or antisense complementary to the MCH1
CC	nucleic acid, ant/agonists of MCH1, and methods of isolating chemical
CC	compounds which activate MCH1. The protein, nucleic acid, antibody,
CC	ant/agonists and compound are useful for diagnosing and treating a
CC	steroid or pituitary hormone disorder, an epinephrine release disorder, a
CC	gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC	disorder, hypertension, diabetes, respiratory disorder, asthma,
CC	reproductive function disorder, immune disorder, endocrine disorder,
CC	musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC	memory disorder, sensory modulation and transmission disorder, motor
CC	coordination disorder, sensory integration disorder, motor integration

CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder,
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC represents human MCH1 mutant encoded by plasmid R114, which has a
CC methionine residue mutated to alanine in order to investigate the true
CC start codon of MCH1.

XX
SQ Sequence 422 AA;

Query Match 100.0%; Score 2210; DB 23; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.4e-221;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGAAKKGVGRAVGLGGSGQATEEDPLPDCGACAPGGGRRMRLPQPAWEGSSARL 60
Db 1 MSVGAAKKGVGRAVGLGGSGQATEEDPLPDCGACAPGGGRRMRLPQPAWEGSSARL 60
QY 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSAGSPPTGTSISTINIIMPSVFGTIC 120
Db 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSAGSPPTGTSISTINIIMPSVFGTIC 120
QY 121 LGGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHF 180
Db 121 LGGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHF 180
QY 181 GETMCTLTITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLLWALS 240
Db 181 GETMCTLTITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLLWALS 240
QY 241 FISITPVMLYARLIPEPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFLPFVVITAAYVRI 300
Db 241 FISITPVMLYARLIPEPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFLPFVVITAAYVRI 300
QY 301 LQRTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
Db 301 LQRTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
QY 361 LYNAAISLGYANSCINPFVYIVLCETFRKRLVSVKPPAOGQLRAVSNAGTADERTESK 420
Db 361 LYNAAISLGYANSCINPFVYIVLCETFRKRLVSVKPPAOGQLRAVSNAGTADERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 3
AAB13440
ID AAB13440 standard; Protein; 422 AA.
XX
AC AAB13440;
XX
DT 17-NOV-2000 (first entry)
XX
DE Mutant human MCH1 receptor encoded by plasmid R106.
XX
KW Human; MCH1 receptor; melanin concentrating hormone; neuroregulator;
KW G-protein coupled; feeding; water balance; energy metabolism; arousal;
KW attention; memory; cognitive function; psychiatric disorder; stress;
KW sexual activity; hormone disorder; hypertension; diabetes;
KW cardiovascular; gastrointestinal; electrolyte balance; respiratory;
KW asthma; reproductive function; immune; endocrine; musculoskeletal;
KW Alzheimer's disease; sensory modulation; transmission;
KW motor coordination; Parkinson's disease; olfaction; urinary; depression;
KW seizure; pain; schizophrenia; morphine tolerance; opiate addiction;
KW migraine; mutant; mutein.

XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers

FT Misc-difference 70
/note= "Wild-type Met substituted by Ala"

XX
XX WO200039279-A2.
XX
XX 06-JUL-2000.
XX
XX
XX 30-DEC-1999; 99WO-US31169.
XX
XX
XX 31-DEC-1998; 98US-0224426.
XX
XX
XX (SYNA-) SYNAPTIC PHARM CORP.
XX
XX
XX Salon JA, Laz TM, Nagorny R, Wilson AE;
XX
XX WPI; 2000-548644/50.

PT Novel nucleic acid encoding human melanin concentrating hormone
PT receptor useful for treating cardiovascular disorders, hypertension and
PT diabetes, whose mutant form is activated by melanin concentrating
PT hormone
PS
PS Claim 8; Fig 13; 173pp; English.

CC Neuroregulators modulate communication in the nervous system. Melanin
CC concentrating hormone 1 (MCH1) is one such neuroregulator. MCH may serve
CC as an integrative neuropeptide, involved in stress response, feeding
CC regulation and sexual activity. Also, MCH is thought to participate in
CC water balance regulation, energy metabolism, general arousal/attention
CC state, memory and cognitive functions and psychiatric disorders. The
CC present sequence is the mutant human MCH1 receptor encoded by plasmid
CC R106. The present sequence is a G-protein coupled receptor. MCH1 receptor
CC may be used in the therapy for a variety of disorders: steroid or
CC pituitary hormone disorder, epinephrine release disorder,
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder e.g. Alzheimer's disease, sensory modulation and
CC transmission disorder, motor coordination disorder, sensory integration
CC disorder, dopaminergic function disorder e.g. Parkinson's disease,
CC olfaction disorder, sympathetic innervation disorder, depression, stress,
CC fluid-imbalance disorder, urinary disorder e.g. urinary incontinence,
CC seizure, pain, psychotic behaviour e.g. schizophrenia, morphine
CC tolerance, opiate addiction or migraine.

SQ Sequence 422 AA;

Query Match 99.8%; Score 2205; DB 21; Length 422;
Best Local Similarity 99.8%; Pred. No. 4.6e-221;
Matches 421; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSVGAAKKGVGRAVGLGGSGQATEEDPLPDCGACAPGGGRRMRLPQPAWEGSSARL 60
Db 1 MSVGAAMKKGVGRAVGLGGSGQATEEDPLPDCGACAPGGGRRMRLPQPAWEGSSARL 60
QY 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSAGSPPTGTSISTINIIMPSVFGTIC 120
Db 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSAGSPPTGTSISTINIIMPSVFGTIC 120
QY 121 LGGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHF 180
Db 121 LGGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHF 180
QY 181 GETMCTLTITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLLWALS 240
Db 181 GETMCTLTITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLLWALS 240
QY 241 FISITPVMLYARLIPEPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFLPFVVITAAYVRI 300
Db 241 FISITPVMLYARLIPEPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFLPFVVITAAYVRI 300
QY 301 LQRTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360

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|||||
Db 301 LQRM TSSVAPASQRSIRLRTKRYRTAIAICLVFVCWAPYYVLQTLQLSISRP LTFEY 360
Oy 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVSVKPPAAQGQLRAVSNAGTADERTESK 420
Db 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVSVKPPAAQGQLRAVSNAGTADERTESK 420
Oy 421 GT 422
Db 421 GT 422

RESULT 4
AAU75857
ID AAU75857 standard; Protein; 422 AA.
AC AAU75857;
XX
XX 08-MAY-2002 (first entry)
DE Human melanin concentrating hormone receptor, MCH1, R106 mutant.
XX
KW Human; melanin concentrating hormone receptor; MCH1; R106;
KW steroid hormone disorder; pituitary hormone disorder;
KW epinephrine release disorder; gastrointestinal disorder; mutein;
KW cardiovascular disorder; hypertension; diabetes; respiratory disorder;
KW asthma; reproductive function disorder; immune disorder; mutant;
KW musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
KW memory disorder; motor coordination disorder; obesity; eating disorder;
KW dopaminergic function disorder; pain; psychosis; opiate addiction;
KW affective disorder; migraine; transgenic.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 70
FT /note= "Wild-type Met substituted by Ala"
XX
PN WO200202744-A2.
XX
PD 10-JAN-2002.
XX
PF 05-JUL-2001; 2001WO-US21350.
XX
PR 05-JUL-2000; 2000US-0610635.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Salon JA, Laz TM, Nagorny R, Wilson AE;
XX
DR WPI; 2002-164532/21.
XX
PT Purified human melanin concentrating hormone receptor protein and
PT polynucleotides for screening modulator useful for treating memory
PT disorder, sensory modulation and transmission disorder, motor
PT coordination disorder
XX
PS Claim 8; Fig 13; 524pp; English.
XX
XX The invention relates to a purified human melanin concentrating hormone
CC (MCH1) receptor protein and its encoding nucleic acid (or mutant
CC activated by MCH or its analogue or homologue). Also included are
CC expression vectors, probes, transformed insect cells, antisense
CC oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting
CC the binding of the antibody to MCH1, a transgenic animal expressing the
CC protein, or a homologous knockout or antisense complementary to the MCH1
CC nucleic acid, ant/agonists of MCH1, and methods of isolating chemical
CC compounds which activate MCH1. The protein, nucleic acid, antibody,
CC ant/agonists and compound are useful for diagnosing and treating a
CC steroid or pituitary hormone disorder, an epinephrine release disorder, a
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma,
```

```
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder, sensory modulation and transmission disorder, motor
CC coordination disorder, sensory integration disorder, motor integration
CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder,
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC represents human MCH1 mutant encoded by plasmid R106, which has a
CC methionine residue mutated to alanine in order to investigate the true
CC start codon of MCH1.
XX
SQ Sequence 422 AA;
XX
Query Match 99.8%; Score 2205; DB 23; Length 422;
Best Local Similarity 99.8%; Pred. No. 4.6e-221;
Matches 421; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 MSVGAARKGVGRAVGLGGSGGQATEEDPLPDGCACAPGGGRRWRLPQPAWYEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSGGQATEEDPLPDGCACAPGGGRRWRLPQPAWYEGSSARL 60
Oy 61 WEQATGTGWADLEASLLPTGNASNTSDGPDNLTSGSPRTGSIYINIMPSVFGTIC 120
Db 61 WEQATGTGWADLEASLLPTGNASNTSDGPDNLTSGSPRTGSIYINIMPSVFGTIC 120
Oy 121 LLGIGNSTVIFAVVKKSKLHCNNVPDIFINLSVVDLFLGLMPFMHQMGNGVWHF 180
Db 121 LLGIGNSTVIFAVVKKSKLHCNNVPDIFINLSVVDLFLGLMPFMHQMGNGVWHF 180
Oy 181 GETMCTLTAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLWALS 240
Db 181 GETMCTLTAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLWALS 240
Oy 241 FISITPVWLVARLIPEPGAVGGGIRLPNPDLDLYWFTLYQEFALPFEVVTAAVRI 300
Db 241 FISITPVWLVARLIPEPGAVGGGIRLPNPDLDLYWFTLYQEFALPFEVVTAAVRI 300
Oy 301 LQRM TSSVAPASQRSIRLRTKRYRTAIAICLVFVCWAPYYVLQTLQLSISRP LTFEY 360
Db 301 LQRM TSSVAPASQRSIRLRTKRYRTAIAICLVFVCWAPYYVLQTLQLSISRP LTFEY 360
Oy 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVSVKPPAAQGQLRAVSNAGTADERTESK 420
Db 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVSVKPPAAQGQLRAVSNAGTADERTESK 420
Oy 421 GT 422
Db 421 GT 422

RESULT 5
AAB13436
ID AAB13436 standard; Protein; 422 AA.
XX
AC AAB13436;
XX
DT 17-NOV-2000 (first entry)
XX
DE Human MCH1 receptor.
XX
KW Human; MCH1 receptor; melanin concentrating hormone; neuroregulator;
KW G-protein coupled; PEXJ.HR-TL231; feeding; water balance;
KW energy metabolism; arousal; attention; memory; cognitive function;
KW psychiatric disorder; stress; sexual activity; hormone disorder;
KW hypertension; diabetes; cardiovascular; gastrointestinal;
KW electrolyte balance; respiratory; asthma; reproductive function;
KW immune; endocrine; musculoskeletal; Alzheimer's disease;
KW sensory modulation; transmission; motor coordination;
KW Parkinson's disease; olfaction; urinary; depression; seizure; pain;
KW schizophrenia; morphine tolerance; opiate addiction; migraine.
XX
```

OS	Homo sapiens.	
XX	Key	Location/Qualifiers
FT	Region	110..135
FT	Region	/label= Transmembrane_region_1
FT	Region	149..169
FT	Region	/label= Transmembrane_region_2
FT	Region	193..208
FT	Region	/label= Transmembrane_region_3
FT	Region	228..262
FT	Region	/label= Transmembrane_region_4
FT	Region	274..301
FT	Region	/label= Transmembrane_region_5
FT	Region	323..349
FT	Region	/label= Transmembrane_region_6
FT	Region	358..383
FT	Region	/label= Transmembrane_region_7
XX		
PN		WO200039279-A2.
XX		
PD		06-JUL-2000.
XX		
PF		30-DEC-1999; 99WO-US31169.
XX		
PR		31-DEC-1998; 98US-0224426.
XX		
PA		(SYNA-) SYNAPTIC PHARM CORP.
XX		
PI		Salon JA, Laz TM, Nagorny R, Wilson AE;
XX		
DR		WPI: 2000-548644/50.
DR		N-PSDB; AAA63240.
XX		
PT		Novel nucleic acid encoding human melanin concentrating hormone
PT		receptor useful for treating cardiovascular disorders, hypertension and
PT		diabetes, whose mutant form is activated by melanin concentrating
PT		hormone
XX		
PS		Claim 7; Fig 2; 173pp; English.
XX		
CC		Neuroregulators modulate communication in the nervous system. Melanin
CC		concentrating hormone 1 (MCH1) is one such neuroregulator. MCH may serve
CC		as an integrative neuropeptide, involved in stress response, feeding
CC		regulation and sexual activity. Also, MCH is thought to participate in
CC		water balance regulation, energy metabolism, general arousal/ attention
CC		state, memory and cognitive functions and psychiatric disorders. The
CC		present sequence is the human MCH1 receptor. The present sequence is a
CC		G-protein coupled receptor and has 7 transmembrane regions. MCH1 receptor
CC		may be used in the therapy for a variety of disorders: steroid or
CC		pituitary hormone disorder, epinephrine release disorder,
CC		gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC		disorder, hypertension, diabetes, respiratory disorder, asthma,
CC		reproductive function disorder, immune disorder, endocrine disorder,
CC		musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC		memory disorder e.g. Alzheimer's disease, sensory modulation and
CC		transmission disorder, motor coordination disorder, sensory intergration
CC		disorder, dopaminergic function disorder e.g. Parkinson's disease,
CC		olfaction disorder, sympathetic innervation disorder, depression, stress,
CC		fluid-imbalance disorder, urinary disorder e.g. urinary incontinence,
CC		seizure, pain, psychotic behaviour e.g. schizophrenia, morphine
CC		tolerance, opiate addiction or migraine. The coding sequence for the
CC		present protein is also contained in plasmid pEXJ.HR-TL231 (ATCC 203197).
XX		
SQ	Sequence	422 AA;
	Query Match	99.5%; Score 2200; DB 21; Length 422;
	Best Local Similarity	99.5%; Pred. No. 1.5e-220;
	Matches 420; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 MSVGA	KKGVRAVLGGSGCQATEEDPLPDGCACAPGQGGRRWRLPQPAWVEGSSARL 60
Db	1 MSVG	AMKKGVRAVLGGSGCQATEEDPLPDGCACAPGQGGRRWRLPQPAWVEGSSARL 60

QY	61	WEQATGTGWADLEASLLPTGPNASNTSDGPDNLT	SAGSP	PTG	SIS	YIN	IMP	SV	GTIC 120
Db	61	WEQATGTGWM	DL	EAS	LL	PTG	P	NAS	NTSDGPDNLT
QY	121	LLGI	GN	ST	V	IF	AA	V	KKSKL
Db	121	LLGI	GN	ST	V	IF	AA	V	KKSKL
QY	181	GETM	CT	LT	I	T	A	M	D
Db	181	GETM	CT	LT	I	T	A	M	D
QY	241	FIS	I	T	P	V	M	L	Y
Db	241	FIS	I	T	P	V	M	L	Y
QY	301	LQ	R	M	T	S	S	V	A
Db	301	LQ	R	M	T	S	S	V	A
QY	361	LY	N	A	I	S	L	G	Y
Db	361	LY	N	A	I	S	L	G	Y
QY	421	GT	422						
Db	421	GT	422						

RESULT 6	
AAU75853	
ID	AAU75853 standard; Protein; 422 AA.
XX	
AC	AAU75853;
XX	
DT	08-MAY-2002 (first entry)
XX	
DE	Human melanin concentrating hormone receptor, MCH1.
XX	
KW	Human; melanin concentrating hormone receptor; MCH1;
KW	steroid hormone disorder; pituitary hormone disorder;
KW	epinephrine release disorder; gastrointestinal disorder;
KW	cardiovascular disorder; hypertension; diabetes; respiratory disorder;
KW	asthma; reproductive function disorder; immune disorder;
KW	musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
KW	memory disorder; motor coordination disorder; obesity; eating disorder;
KW	dopaminergic function disorder; pain; psychosis; opiate addiction;
XX	
OS	Homo sapiens.
XX	
PN	WO200202744-A2.
XX	
PD	10-JAN-2002.
XX	
PF	05-JUL-2001; 2001WO-US21350.
XX	
PR	05-JUL-2000; 2000US-0610635.
XX	
PA	(SYNA-) SYNAPTIC PHARM CORP.
XX	
PI	Salon JA, Laz TM, Nagorny R, Wilson AE;
XX	
DR	WPI: 2002-164532/21.
DR	N-PSDB; ABK14548.
XX	
PT	Purified human melanin concentrating hormone receptor protein and
PT	polynucleotides for screening modulator useful for treating memory
PT	disorder, sensory modulation and transmission disorder, motor
PT	coordination disorder
XX	
PS	Example; Fig 2; 524pp; English.

CC The invention relates to a purified human melanin concentrating hormone
CC (MCH) receptor protein and its encoding nucleic acid (or mutant
CC activated by MCH or its analogue or homologue). Also included are
CC expression vectors, probes, transformed insect cells, antisense
CC oligonucleotides, anti-MCH antibodies, an agent capable of inhibiting
CC the binding of the antibody to MCH, a transgenic animal expressing the
CC protein, or a homologous knockout or antisense complementary to the MCH1
CC nucleic acid, ant/agonists of MCH1, and methods of isolating chemical
CC compounds which activate MCH1. The protein, nucleic acid, antibody,
CC ant/agonists and compound are useful for diagnosing and treating a
CC steroid or pituitary hormone disorder, an epinephrine release disorder, a
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder, sensory modulation and transmission disorder, motor
CC coordination disorder, sensory integration disorder, motor integration
CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder,
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC represents human MCH1.
XX
SQ Sequence 422 AA;

Query Match 99.5%; Score 2200; DB 23; Length 422;
Best Local Similarity 99.5%; Pred. No. 1.5e-220;
Matches 420; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAKKGVGRAVGLGGSSCOATEEDPLPDCGACAPGGGRRWRLPQPAWEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSSCOATEEDPLPDCGACAPGGGRRWRLPQPAWEGSSARL 60
QY 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSA GSPRTGSISYINIIIMPSVFGTIC 120
Db 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSA GSPRTGSISYINIIIMPSVFGTIC 120
QY 121 LIGIIGNSTVIFA VVKSKSLHWCNNVPDIFIINLSVVDLLFLLGMPFMIHQLMGNGVWHF 180
Db 121 LIGIIGNSTVIFA VVKSKSLHWCNNVPDIFIINLSVVDLLFLLGMPFMIHQLMGNGVWHF 180
QY 181 GETMCTLITAMDANSOFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLWALS 240
Db 181 GETMCTLITAMDANSOFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLWALS 240
QY 241 FISITPVMLYARLIPFPGAVGCGIRLPNPDLDLWFTLYQFFLA FALPFVVITAAYVRI 300
Db 241 FISITPVMLYARLIPFPGAVGCGIRLPNPDLDLWFTLYQFFLA FALPFVVITAAYVRI 300
QY 301 LQRM TSSVAPASQSRIRLRTKRVTRTAIAICLVFVWCWAPYYVLQLTQLSISRPTLTFVY 360
Db 301 LQRM TSSVAPASQSRIRLRTKRVTRTAIAICLVFVWCWAPYYVLQLTQLSISRPTLTFVY 360
QY 361 LYNAATISLG YANSCINPFVYIVLCETFRRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
Db 361 LYNAATISLG YANSCINPFVYIVLCETFRRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 7
AAB12779
ID AAB12779 standard; Protein; 422 AA.
XX
AC AAB12779;
XX
DT 22-NOV-2000 (first entry)
XX
DE Human SLC-1 protein sequence SEQ ID NO:11.
XX

KW SLC-1; MHC; melanin concentrating hormone; screening; eating;
KW appetite stimulator; appetite regulator; period pain; atonic bleeding;
KW caesarean section; milk congestion; antioesthetic agent; drug;
KW foetal asphyxia; cervical rupture; premature birth; uterine rupture;
KW Prader-Willi syndrome; anorectic; gynaecological; abortifaciant;
KW antoanaemia; anabolic; orphan G protein-couple receptor protein.
XX
OS Homo sapiens.
XX
PN WO200040725-A1.
XX
PD 13-JUL-2000.
XX
XX 27-DEC-1999; 99WO-JP07336.
XX
PF 28-DEC-1998; 98JP-0374454.
PR 28-APR-1999; 99JP-0122688.
PR 02-SEP-1999; 99JP-0249300.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Mori M, Shimomura Y, Takekawa S, Sugo T, Ishibashi Y, Kitada C;
PI Suzuki N;
XX
DR WPI; 2000-475832/41.
DR N-PSDB; AAA72918.

PT Screening methods for compounds as SLC-1 (ant)agonists useful in the
PT treatment of eating disorders and as preventives and remedies for e.g.
PT atonic bleeding and Prader-Willi syndrome -
PS Claim 6; Page 111-113; 123pp; Japanese.

CC The present invention describes a method for screening components (I) or
CC their salts that can alter the binding properties of melanin-
CC concentrating hormone (MCH) or its derivative or salt to SLC-1 or its
CC salt. Compounds identified by (I) are useful as SLC-1 (ant)agonists in
CC eating disorders and as preventives and remedies for e.g. period pains,
CC uterine recovery failure, caesarean section, artificial interruption of
CC pregnancy, galactostosis, tonic uterine contraction, foetal asphyxia,
CC rupture of uterus, cervical rupture, premature birth and Prader-Willi
CC syndrome. The present sequence represents the human SLC-1 protein
CC sequence, which is used in an example from the present invention.
XX
SQ Sequence 422 AA;

Query Match 99.3%; Score 2195; DB 21; Length 422;
Best Local Similarity 99.3%; Pred. No. 5.1e-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAKKGVGRAVGLGGSSCOATEEDPLPDCGACAPGGGRRWRLPQPAWEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSSCOATEEDPLPDCGACAPGGGRRWRLPQPAWEGSSARL 60
QY 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSA GSPRTGSISYINIIIMPSVFGTIC 120
Db 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSA GSPRTGSISYINIIIMPSVFGTIC 120
QY 121 LIGIIGNSTVIFA VVKSKSLHWCNNVPDIFIINLSVVDLLFLLGMPFMIHQLMGNGVWHF 180
Db 121 LIGIIGNSTVIFA VVKSKSLHWCNNVPDIFIINLSVVDLLFLLGMPFMIHQLMGNGVWHF 180
QY 181 GETMCTLITAMDANSOFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLWALS 240
Db 181 GETMCTLITAMDANSOFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLWALS 240
QY 241 FISITPVMLYARLIPFPGAVGCGIRLPNPDLDLWFTLYQFFLA FALPFVVITAAYVRI 300
Db 241 FISITPVMLYARLIPFPGAVGCGIRLPNPDLDLWFTLYQFFLA FALPFVVITAAYVRI 300
QY 301 LQRM TSSVAPASQSRIRLRTKRVTRTAIAICLVFVWCWAPYYVLQLTQLSISRPTLTFVY 360
Db 301 LQRM TSSVAPASQSRIRLRTKRVTRTAIAICLVFVWCWAPYYVLQLTQLSISRPTLTFVY 360

OY 361 LYNAISLGYANCLNPFYIIVLCETFRKRLVLSVKPPAOGQLRAVSNQOTADERTESK 420
|||
Db 361 LYNAISLGYANCLNPFYIIVLCETFRKRLVLSVKPPAOGQLRAVSNQOTADERTESK 420
OY 421 GT 422
||
Db 421 GT 422

RESULT 8
AAE07330
ID AAE07330 standard; Protein; 422 AA.
XX

AC AAE07330;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human melanin-concentrating hormone receptor variant #3.

KW Human; melanin-concentrating hormone; MCH analogue; signal transduction;
KW appetite; therapy; anorexia; acquired immune deficiency syndrome; AIDS;
KW wasting; cachexia; frail elderly; weight maintenance; cancer; anorectic;
KW pain reduction; stress reduction; sexual dysfunction; variant.

XX
OS Homo sapiens.
OS Synthetic.

PN WO200157070-A1.

PD 09-AUG-2001.

PF 01-FEB-2001; 2001WO-US03293.

PR 03-FEB-2000; 2000US-0179967.

XX (MERI) MERCK & CO INC.

XX Bednarek M;

XX WPI; 2001-483416/52.

DR N-PSDB; AAD13654.

PT Novel peptide encoding a melanin-concentrating hormone analog useful
PT for increasing weight or appetite -

XX
PS Disclosure; Page 35-36; 66pp; English.

CC The present invention relates to truncated melanin-concentrating hormone
CC (MCH) analogues active at the MCH receptor. The truncated MCH analogues
CC are optionally modified peptide derivatives of mammalian MCH. The MCH
CC analogues can bind to the MCH receptor and bring about signal
CC transduction. The MCH agonists can be used to facilitate a weight gain,
CC maintenance of weight and/or an appetite increase. The MCH agonists can
CC also be used to treat disorders such as anorexia, acquired immune
CC deficiency syndrome (AIDS), wasting, cachexia and frail elderly. The MCH
CC antagonists can be used to facilitate weight loss, appetite decrease,
CC weight maintenance, cancer treatment, pain reduction, stress reduction
CC and/or treatment of sexual dysfunction. The present sequence is a human
CC MCH receptor variant.

XX
SQ Sequence 422 AA;

Query Match 99.3%; Score 2195; DB 22; Length 422;
Best Local Similarity 99.3%; Pred. No. 5.1e-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSVGAARKGVRAVGLGGSGQATEEDPLPDGACAPGQGGRWRLLPPAWVEGSSARL 60
|||||
Db 1 MSVGAMRKGVRAVGLGGSGQATEEDPLPNCGACAPGQGGRRWRLLPPAWVEGSSARL 60
OY 61 WEQATGTGWMADLEASLLPTGPNASNTSDGPDNLTSGSPRTGSISYINIMPSVFGTIC 120
|||||

Db 61 WEQATGTGWMADLEASLLPTGPNASNTSDGPDNLTSGSPRTGSISYINIMPSVFGTIC 120
OY 121 LIGIIGNSTVIFAVVKKSKLHWCNVVDIFILNSVVDLFLLGMPFMHQLMGNGWHF 180
|||||
Db 121 LIGIIGNSTVIFAVVKKSKLHWCNVVDIFILNSVVDLFLLGMPFMHQLMGNGWHF 180
OY 181 GETMCTLTITAMANSQFTSTYIITAMAIDRYLATVHPISSTKPKPSVATLVICLLMALS 240
|||||
Db 181 GETMCTLTITAMANSQFTSTYIITAMAIDRYLATVHPISSTKPKPSVATLVICLLMALS 240
OY 241 FISITPWLVARLIPPGGAVGCGIRLPNPDLDYWFLLYQFLAFALPFVVTAAVRI 300
|||||
Db 241 FISITPWLVARLIPPGGAVGCGIRLPNPDLDYWFLLYQFLAFALPFVVTAAVRI 300
OY 301 LQMTSSVAPASQSRIRLTKRVTRTAIAICLVFVCMAPYVVLQTLQSLISRPTLTFVY 360
|||||
Db 301 LQMTSSVAPASQSRIRLTKRVTRTAIAICLVFVCMAPYVVLQTLQSLISRPTLTFVY 360
OY 361 LYNAISLGYANCLNPFYIIVLCETFRKRLVLSVKPPAOGQLRAVSNQOTADERTESK 420
|||||
Db 361 LYNAISLGYANCLNPFYIIVLCETFRKRLVLSVKPPAOGQLRAVSNQOTADERTESK 420
OY 421 GT 422
||
Db 421 GT 422

RESULT 9
AAB81123
ID AAB81123 standard; Protein; 422 AA.
XX
AC AAB81123;
XX
DT 05-JUL-2001 (first entry)
XX
DE Human melanin concentrating hormone receptor (SLC-1).

XX
KW Melanin concentrating hormone; MCH; antagonist; diamine compound;
KW anorectic; antidiabetic; ophthalmological; neuroprotective; nephrotropic;
KW antiarteriosclerotic; antiarthritic; obesity; diabetes; arteriosclerosis;
KW arthritis; melanin concentrating hormone receptor; SLC-1; human.

XX Homo sapiens.

PN WO200121169-A1.

PD 29-MAR-2001.

PF 19-SEP-2000; 2000WO-JP06376.

PR 20-SEP-1999; 99JP-0266278.

PR 17-JUL-2000; 2000JP-0221055.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Kato K, Mori M, Suzuki N, Shimomura Y, Takekawa S, Choh N;

XX WPI; 2001-328055/34.

DR N-PSDB; AAF86229.

PT Melanin concentrating hormone antagonists comprise new and known
PT diamine compounds for treating obesity -

XX
PS Examples; Page 271-273; 284pp; Japanese.

CC This invention relates to melanin concentrating hormone (MCH)
CC antagonists, comprising a diamine compound or its prodrug and/or salt.
CC Use of the MCH antagonists can result in anorectic, antidiabetic,
CC ophthalmological, neuroprotective, nephrotropic, antiarteriosclerotic,
CC and antiarthritic activity. Melanin concentrating hormone (MCH)
CC antagonists can be used for treating obesity (e.g. exogenous obesity,
CC hypophyseal adiposity, hypothalamic obesity and hyperphagia) and
CC associated disorders such as diabetes, diabetic complications (such as

CC diabetic retinopathy, diabetic neuropathy and diabetic nephropathy),
CC arteriosclerosis and arthritis in the knees. The present sequence
CC represents the human melanin concentrating hormone receptor (SLC-1). The
CC SLC-1 cDNA is used in examples to demonstrate the use of the antagonists
CC of the invention.

XX Sequence 422 AA;

Query Match 99.3%; Score 2195; DB 22; Length 422;
Best Local Similarity 99.3%; Pred. No. 5.1e-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAARKGVGRAVGLGGSGCQATEEDPLPDGACAPGQGRRRLPQPAWEGSSARL 60
DB 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPNCGACAPGQGRRRLPQPAWEGSSARL 60
QY 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSA GSPPRTGSIYINIMPSVFGTIC 120
DB 61 WEQATGTGWMDLEASLLPTGPNASNTSDGPDNLTSA GSPPRTGSIYINIMPSVFGTIC 120
QY 121 LLGIGNSTVIFAVVKKSKLHWCNNVPDIFINLSVVDLFLGMPFMHQLMGNGVWHF 180
DB 121 LLGIGNSTVIFAVVKKSKLHWCNNVPDIFINLSVVDLFLGMPFMHQLMGNGVWHF 180
QY 181 GETMCTLTAMDANSQFTSTYILLTAMADRYLATVHPISSTKFRKPSVATLVICLWALS 240
DB 181 GETMCTLTAMDANSQFTSTYILLTAMADRYLATVHPISSTKFRKPSVATLVICLWALS 240
QY 241 FISTPFWLYARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFALEPVVITAAYVRI 300
DB 241 FISTPFWLYARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFALEPVVITAAYVRI 300
QY 301 LQRMSSVAPASQSRIRLTKRVRTAIAICLVFVWCWAPYVVLQTLQLSISRPTLTFVY 360
DB 301 LQRMSSVAPASQSRIRLTKRVRTAIAICLVFVWCWAPYVVLQTLQLSISRPTLTFVY 360
QY 361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
DB 361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
QY 421 GT 422
DB 421 GT 422

RESULT 10
AAB96871
ID AAB96871 standard; Protein; 422 AA.
XX AAB96871;
AC AAB96871;
XX 06-JUL-2001 (first entry)
DT 06-JUL-2001 (first entry)
XX Human SLC-1.
DE Human SLC-1.
XX Rat; human; SLC-1; MCH receptor; melanin-concentrating hormone;
KW obesity; diabetes; hypertension; arteriosclerosis; hyperphagia;
KW emotional disorder; reproductive disorder; memory disorder;
KW dementia; hormonal disorder; gonitis.
XX Homo sapiens.
OS Homo sapiens.
XX WO200121577-A2.
PN WO200121577-A2.
XX 29-MAR-2001.
PD 29-MAR-2001.
XX 19-SEP-2000; 2000WO-JP06375.
PF 19-SEP-2000; 2000WO-JP06375.
XX 20-SEP-1999; 99JP-0266298.
PR 20-SEP-1999; 99JP-0266298.
AC 16-DEC-1999; 99JP-0357889.
XX 20-APR-2000; 2000JP-0126272.
PR 20-APR-2000; 2000JP-0126272.
XX (TAKE) TAKEDA CHEM IND LTD.
PA (TAKE) TAKEDA CHEM IND LTD.

XX kato K, Terauchi J, Mori M, Suzuki N, Shimomura Y, Takekawa S;
PI Ishihara Y;
XX WPI; 2001-354775/37.
DR N-PSDB; AAF86975.
XX

PT New aromatic compounds are melanin concentrating hormone antagonists,
PT useful as anorectic agents, for treating or preventing obesity, also
PT memory or hormonal disorders or diabetes -

PS Examples; Page 358-360; 363pp; English.

XX The present invention describes aromatic compounds capable of acting as
CC melanin-concentrating hormone (MCH) antagonists. Melanin-concentrating
CC hormone is an appetite control factor and antagonists were expected to be
CC useful as anti-obesity agents. They can be used in the treatment of
CC obesity, including malignant mastocytosis, exogenous, hyperinsular,
CC hypoplasmic, hypothyroid, hypothalamic, symptomatic, infantile, upper
CC body, alimentary, hypogonadal, simple and central obesity, systemic
CC mastocytosis and hypophyseal adiposity, hypertension, arteriosclerosis,
CC hyperphagia, emotional disorders, reproductive function disorders, memory
CC disorders, dementia, hormonal disorders, diabetes and gonitis. MCH binds
CC to the SLC-1 receptor. The present sequence is the human SLC-1 protein
CC sequence.

SQ Sequence 422 AA;

Query Match 99.3%; Score 2195; DB 22; Length 422;
Best Local Similarity 99.3%; Pred. No. 5.1e-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAARKGVGRAVGLGGSGCQATEEDPLPDGACAPGQGRRRLPQPAWEGSSARL 60
DB 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPNCGACAPGQGRRRLPQPAWEGSSARL 60
QY 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSA GSPPRTGSIYINIMPSVFGTIC 120
DB 61 WEQATGTGWMDLEASLLPTGPNASNTSDGPDNLTSA GSPPRTGSIYINIMPSVFGTIC 120
QY 121 LLGIGNSTVIFAVVKKSKLHWCNNVPDIFINLSVVDLFLGMPFMHQLMGNGVWHF 180
DB 121 LLGIGNSTVIFAVVKKSKLHWCNNVPDIFINLSVVDLFLGMPFMHQLMGNGVWHF 180
QY 181 GETMCTLTAMDANSQFTSTYILLTAMADRYLATVHPISSTKFRKPSVATLVICLWALS 240
DB 181 GETMCTLTAMDANSQFTSTYILLTAMADRYLATVHPISSTKFRKPSVATLVICLWALS 240
QY 241 FISTPFWLYARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFALEPVVITAAYVRI 300
DB 241 FISTPFWLYARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFALEPVVITAAYVRI 300
QY 301 LQRMSSVAPASQSRIRLTKRVRTAIAICLVFVWCWAPYVVLQTLQLSISRPTLTFVY 360
DB 301 LQRMSSVAPASQSRIRLTKRVRTAIAICLVFVWCWAPYVVLQTLQLSISRPTLTFVY 360
QY 361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
DB 361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
QY 421 GT 422
DB 421 GT 422

RESULT 11
AA97670
ID AA97670 standard; Protein; 422 AA.
XX AA97670;
AC AA97670;
XX 08-MAY-2001 (first entry)
DT 08-MAY-2001 (first entry)
XX

DE Human MCH-R3 protein sequence.
XX
KW Human; melanin-concentrating hormone receptor; MCH-R1; MCH-R2; MCH-R3;
KW weight loss; weight gain; cancer; pain; diabetes; stress; therapy;
KW sexual dysfunction.
XX
OS Homo sapiens.
XX
PN WO200105947-A1.
XX
PD 25-JAN-2001.
XX
PF 10-JUL-2000; 2000WO-US18733.
XX
PR 14-JUL-1999; 99US-0143706.
XX
PA (MERI) MERCK & CO INC.
XX
PI Howard AD;
XX
DR WPI; 2001-159528/16.
DR N-PSDB; AAA91189, AAA91192.
XX
XX
PT Melanin-concentrating hormone receptor polypeptides for increasing or
PT decreasing appetite, reducing stress and to screen for compounds that
PT bind to the receptor -
XX
XX
PS Claim 21; Page 23; 43pp; English.
XX
XX This sequence is a melanin-concentrating hormone (MCH) receptor
CC protein of the invention, designated MCH-R3. MCH receptor fragments and
CC polypeptides are useful in assays to screen for compounds that bind to
CC the MCH receptor and modulate the activity of the receptor. MCH Receptor
CC activity is modulated to achieve weight loss, weight gain, to treat
CC cancer (e.g. colon or breast), reduce pain, treat diabetes, reduce stress
CC or treat sexual dysfunction. Nucleic acid coding for the MCH receptor can
CC be used to cause an increase in appetite and to create a test system
CC (e.g. a transgenic animal) for screening for compounds affecting MCH
CC receptor expression. Inhibition of MCH receptor nucleic acid activity is
CC useful to inhibit appetite or stress.
XX
SQ Sequence 422 AA;

Query Match 99.3%; Score 2195; DB 22; Length 422;
Best Local Similarity 99.3%; Pred. No. 5.1e-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAARKGVRAVGLGGSGCOATEEDPLPDGACAPGGGRRWRLPQPAWVEGSSARL 60
Db 1 MSVGAMKKGVRAVGLGGSGCOATEEDPLPNCGACAPGGGRRWRLPQPAWVEGSSARL 60

QY 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFGTIC 120
Db 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFGTIC 120

QY 121 LIGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLLGMPFMIHQMGNGVWHF 180
Db 121 LIGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLLGMPFMIHQMGNGVWHF 180

QY 181 GETMCTLITAMDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLLWALS 240
Db 181 GETMCTLITAMDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLLWALS 240

QY 241 FISITPVWLARLIPFPGGAVGCGIRLPNDTDLWFTLYQFFLAFALEPVVITAAYVRI 300
Db 241 FISITPVWLARLIPFPGGAVGCGIRLPNDTDLWFTLYQFFLAFALEPVVITAAYVRI 300

QY 301 LQRMSSVAPASQSRIRLRTKRVTRTAIAICLVEFVCWAPYYVLQLTQLSISRPTLTFVY 360
Db 301 LQRMSSVAPASQSRIRLRTKRVTRTAIAICLVEFVCWAPYYVLQLTQLSISRPTLTFVY 360

QY 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAQGQLRAVSNQTADEERTESK 420
|||||

Db 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAQGQLRAVSNQTADEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 12
AAB85894
ID AAB85894 standard; Protein; 422 AA.
XX
AC AAB85894;
XX
DT 30-NOV-2001 (first entry)
XX
DE Human long form MCH1R sequence.
XX
KW Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion;
KW fluorescent polypeptide; orexigenic; anabolic; food intake; MCH1R.
XX
OS Homo sapiens.
XX
PN WO200168706-A1.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-US08071.
XX
PR 15-MAR-2000; 2000US-0189698.
XX
PA (MERI) MERCK & CO INC.
XX
PI Marsh DJ;
XX
DR WPI; 2001-565791/63.
DR N-PSDB; AAH47297.
XX
PT Fusion proteins comprising melanin concentrating hormone receptor
PT peptides and fluorescent proteins, useful for identifying appetite
PT stimulants -
XX
XX
PS Claim 1; Page 12-13; 71pp; English.
XX
XX The invention provides melanin concentrating hormone (MCH) receptor
CC (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise
CC MCHR polypeptide regions from different species. The MCHR fusion protein
CC comprise MCHR polypeptide region and a fluorescent polypeptide region
CC joined directly, or via a linker, to the carboxy side of the MCHR
CC polypeptide region. The MCHR fusion proteins can be expressed by standard
CC recombinant methodology. MCH action promotes feeding (orexigenic) and up
CC regulation of MCH activity stimulates food intake. The present sequence
CC represents a human long form MCH1R protein sequence.
XX
SQ Sequence 422 AA;

Query Match 99.3%; Score 2195; DB 22; Length 422;
Best Local Similarity 99.3%; Pred. No. 5.1e-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAARKGVRAVGLGGSGCOATEEDPLPDGACAPGGGRRWRLPQPAWVEGSSARL 60
Db 1 MSVGAMKKGVRAVGLGGSGCOATEEDPLPNCGACAPGGGRRWRLPQPAWVEGSSARL 60

QY 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFGTIC 120
Db 61 WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFGTIC 120

QY 121 LIGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLLGMPFMIHQMGNGVWHF 180
Db 121 LIGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLLGMPFMIHQMGNGVWHF 180

QY 181 GETMCTLITAMDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLLWALS 240
Db 181 GETMCTLITAMDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLLWALS 240
|||||

Db 181 GETMCTLTITAMDANSQFTSTYILTFAMAIDRYLATVHPISSTKFRKPSVATLVICLWALS 240
QY 241 FISITPWLTYARLIPEPGAVGCGIRLPNDPTDLYWFTLYQFFLAFALPEFVITAAYVRI 300
Db 241 FISITPWLTYARLIPEPGAVGCGIRLPNDPTDLYWFTLYQFFLAFALPEFVITAAYVRI 300
QY 301 LQRTSSVAPASQSRIRLRTKRVTRTAIAICLVFVWCWAPYVYLQTLQLSISRPTLTFVY 360
Db 301 LQRTSSVAPASQSRIRLRTKRVTRTAIAICLVFVWCWAPYVYLQTLQLSISRPTLTFVY 360
QY 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAQGQLRAVSNAQTADDEERTESK 420
Db 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAQGQLRAVSNAQTADDEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 13
AAU77541
ID AAU77541 standard; Protein; 422 AA.
XX
AC AAU77541;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human melanin concentrating hormone receptor, SLC-1.
XX
KW G protein-coupled orphan; receptor; SLC; melanin-concentrating hormone;
KW MCH; appetite-stimulating agent; obesity; malignant mastocytosis;
KW exogenous obesity; hyperinsulinar obesity; sexual function disorder;
KW overpowering intermittent pain; still born; uterus rupture;
KW premature birth; Prader-Willi syndrome; SLC-1; human.
XX
OS Homo sapiens.
XX
PN WO200203070-A1.
XX
PD 10-JAN-2002.
XX
PF 04-JUL-2001; 2001WO-JP05809.
XX
PR 05-JUL-2000; 2000JP-0208254.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Mori M, Shimomura Y, Harada M, Sugo T, Shintani Y;
XX
DR WPI; 2002-164552/21.
DR N-PSDB; ABK10854.
XX
XX

PT Screening for compounds or salts which alter affinity of
PT melanin-concentrating hormone with its receptor to provide agonists as
PT appetite-stimulating agents and its antagonist for preventing or
PT treating obesity, uses a protein or hormone -
XX
PS Disclosure; Page 103-105; 112pp; Japanese.
XX

CC The invention describes a method of screening for compounds or their
CC salts that can change affinity of melanin-concentrating hormone (MCH)
CC with its G protein-coupled orphan receptor protein, SLC. The screened
CC MCH receptor agonists are useful as appetite-stimulating agents and its
CC antagonist for preventing or treating obesity e.g. malignant
CC mastocytosis, exogenous obesity and hyperinsulinar obesity, and also
CC for treating sexual function disorders, overpowering intermittent pains,
CC still borns, uterus rupture, premature birth and Prader-Willi syndrome.
CC This is the amino acid sequence of the human melanin concentrating
CC hormone SLC-1, described in the invention.
XX
XX

SQ Sequence 422 AA;

Query Match 99.3%; Score 2195; DB 23; Length 422;

Best Local Similarity 99.3%; Pred. No. 5.1e-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAARKGVGRAVGLGGSGCQATEEDLPDCGACAPGQGGRRRLPQPAWEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDLPNCGACAPGQGGRRRLPQPAWEGSSARL 60
QY 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSAGSPPRTGSIYINIIMPSVFETIC 120
Db 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSAGSPPRTGSIYINIIMPSVFETIC 120
QY 121 LIGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFIHQLMNGVWHF 180
Db 121 LIGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFIHQLMNGVWHF 180
QY 181 GETMCTLTITAMDANSQFTSTYILTFAMAIDRYLATVHPISSTKFRKPSVATLVICLWALS 240
Db 181 GETMCTLTITAMDANSQFTSTYILTFAMAIDRYLATVHPISSTKFRKPSVATLVICLWALS 240
QY 241 FISITPWLTYARLIPEPGAVGCGIRLPNDPTDLYWFTLYQFFLAFALPEFVITAAYVRI 300
Db 241 FISITPWLTYARLIPEPGAVGCGIRLPNDPTDLYWFTLYQFFLAFALPEFVITAAYVRI 300
QY 301 LQRTSSVAPASQSRIRLRTKRVTRTAIAICLVFVWCWAPYVYLQTLQLSISRPTLTFVY 360
Db 301 LQRTSSVAPASQSRIRLRTKRVTRTAIAICLVFVWCWAPYVYLQTLQLSISRPTLTFVY 360
QY 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAQGQLRAVSNAQTADDEERTESK 420
Db 361 LYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAQGQLRAVSNAQTADDEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 14
ABB04941
ID ABB04941 standard; Protein; 422 AA.
XX
AC ABB04941;
XX
DT 14-MAR-2002 (first entry)
XX
DE Human SLC-1 protein SEQ ID NO:9.
XX
KW Human; SLC-1; melanin concentrating hormone antagonist; obesity;
KW anorectic; antidiabetic; hypotensive; antiarteriosclerotic;
KW diabetes; hypertension; arteriosclerosis.
XX
OS Homo sapiens.
XX
PN WO200182925-A1.
XX
PD 08-NOV-2001.
XX
PF 26-APR-2001; 2001WO-JP03614.
XX
PR 28-APR-2000; 2000JP-0134295.
PR 13-DEC-2000; 2000JP-0384897.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Ishihara Y, Suzuki N, Takekawa S;
XX
DR WPI; 2002-075131/10.
DR N-PSDB; ABA92411.
XX
PT Melanin aggregating hormone antagonist for treating obesity -
PT
XX
PS Example; Page 210-212; 223pp; Japanese.
CC

The present invention describes a melanin aggregating hormone antagonist

CC (I). (I) has anorectic, antidiabetic, antiarteriosclerotic and
CC hypotensive. (I) can be used in the treatment and prevention of obesity.
CC It may be combined with treatments for diabetes, hypertension or
CC arteriosclerosis. The present sequence represents human SLC-1, which is
CC used the exemplification of the present invention.

XX Sequence 422 AA;

Query Match 99.3%; Score 2195; DB 23; Length 422;
Best Local Similarity 99.3%; Pred. No. 5.1e-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAARKGVGRAVGLGGSGCQATEEDPLPDGACAPGGGRRRLPQPAWEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPNCACAPGGGRRRLPQPAWEGSSARL 60
QY 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSGSPRTGSISYINIMPSVFGTIC 120
Db 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSGSPRTGSISYINIMPSVFGTIC 120
QY 121 LGGIGNSTVIFAVVKKSKLHWCNNVPDIFINLSVVDLLFLGMPMIHQLMNGVWHF 180
Db 121 LGGIGNSTVIFAVVKKSKLHWCNNVPDIFINLSVVDLLFLGMPMIHQLMNGVWHF 180
QY 181 GETMCTLITAMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLMAALS 240
Db 181 GETMCTLITAMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLMAALS 240
QY 241 FISITPWLRYARLIPFGGAVGCGIRLPNPDIDLWFTLYQFFLAFLPFWVITAAYVRI 300
Db 241 FISITPWLRYARLIPFGGAVGCGIRLPNPDIDLWFTLYQFFLAFLPFWVITAAYVRI 300
QY 301 LQRMSSVAPASQSRIRLTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
Db 301 LQRMSSVAPASQSRIRLTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
QY 361 LYNAISLGYANSCNPFVYIVLCETFRKRLVSVKPPAOGQLRAVSNAQTADERTESEK 420
Db 361 LYNAISLGYANSCNPFVYIVLCETFRKRLVSVKPPAOGQLRAVSNAQTADERTESEK 420
QY 421 GT 422
Db 421 GT 422

RESULT 15
AAG80611

ID AAG80611 standard; Protein: 422 AA.

XX AAG80611;
XX
DT 28-FEB-2002 (first entry)
XX
DE Human SLC-1 protein.

XX SLC-1; melanin-concentrating hormone antagonist; anorectic; depression;
KW antidiabetic; hypotensive; antiarteriosclerotic; antilipaeamic; obesity;
KW antiarthritic; antidepressant; tranquiliser; malignant mastocytosis;
KW hypophyseal adiposity; hypothyroid obesity; hyperphagia; diabetes;
KW hypertension; arteriosclerosis; hyperlipidaemia; arthritis; anxiety;
KW human.

XX Homo sapiens.

XX WO200187834-A1.

XX 22-NOV-2001.

XX 15-MAY-2001; 2001WO-JP04015.

XX 16-MAY-2000; 2000JP-0148674.
PR 13-APR-2001; 2001JP-0116219.
XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX Ishihara Y, Terauchi J, Suzuki N, Takekawa S, Aso K;

XX WPI; 2002-055668/07.

DR N-PSDB; AAI69442.

XX Use of new and known amine derivatives as melanin concentrating hormone
PT antagonists for treating e.g. obesity, diabetes, hypertension and
PT arteriosclerosis -
PS
XX Disclosure; Page 252-254; 283pp; Japanese.

CC This invention describes a novel use of an amine derivative (I) as a
CC melanin concentrating hormone antagonist which has anorectic,
CC antidiabetic, hypotensive, antiarteriosclerotic, antilipaeamic,
CC antiarthritic, antidepressant and tranquiliser activity. The products of
CC the invention can be used as melanin concentrating hormone antagonists
CC for treating and preventing obesity (including malignant mastocytosis,
CC hypophyseal adiposity, hypothyroid obesity, infantile obesity and
CC hyperphagia), diabetes, hypertension and arteriosclerosis as well as
CC diabetic complications, hyperlipidaemia, arthritis, depression and
CC anxiety. This sequence represents the human melanin-concentrating hormone
CC SLC-1 gene described in the method of the invention.

XX Sequence 422 AA;

Query Match 99.3%; Score 2195; DB 23; Length 422;
Best Local Similarity 99.3%; Pred. No. 5.1e-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAARKGVGRAVGLGGSGCQATEEDPLPDGACAPGGGRRRLPQPAWEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPNCACAPGGGRRRLPQPAWEGSSARL 60
QY 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSGSPRTGSISYINIMPSVFGTIC 120
Db 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSGSPRTGSISYINIMPSVFGTIC 120
QY 121 LGGIGNSTVIFAVVKKSKLHWCNNVPDIFINLSVVDLLFLGMPMIHQLMNGVWHF 180
Db 121 LGGIGNSTVIFAVVKKSKLHWCNNVPDIFINLSVVDLLFLGMPMIHQLMNGVWHF 180
QY 181 GETMCTLITAMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLMAALS 240
Db 181 GETMCTLITAMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLMAALS 240
QY 241 FISITPWLRYARLIPFGGAVGCGIRLPNPDIDLWFTLYQFFLAFLPFWVITAAYVRI 300
Db 241 FISITPWLRYARLIPFGGAVGCGIRLPNPDIDLWFTLYQFFLAFLPFWVITAAYVRI 300
QY 301 LQRMSSVAPASQSRIRLTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
Db 301 LQRMSSVAPASQSRIRLTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
QY 361 LYNAISLGYANSCNPFVYIVLCETFRKRLVSVKPPAOGQLRAVSNAQTADERTESEK 420
Db 361 LYNAISLGYANSCNPFVYIVLCETFRKRLVSVKPPAOGQLRAVSNAQTADERTESEK 420
QY 421 GT 422
Db 421 GT 422

Search completed: February 13, 2003, 13:58:01
Job time : 34.4921 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 14:00:22 ; Search time 14.1019 Seconds
(without alignments)
764.550 Million cell updates/sec

Title: US-09-885-478-27

Perfect score: 2210
Sequence: 1 MSVGAAKKGVGRAVGLGGG.....LRVSNAGTADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2210	100.0	422	10 US-09-885-478-27	Sequence 27, Appl
2	2205	99.8	422	10 US-09-885-478-26	Sequence 26, Appl
3	2200	99.5	422	10 US-09-885-478-2	Sequence 2, Appl
4	1819	82.3	353	10 US-09-925-776-2	Sequence 2, Appl
5	1819	82.3	353	10 US-09-885-478-28	Sequence 28, Appl
6	1803	81.6	353	10 US-09-895-686-2	Sequence 2, Appl
7	1758	79.5	353	10 US-09-885-478-4	Sequence 4, Appl
8	1696	76.7	402	9 US-09-990-940-19	Sequence 19, Appl
9	1224	55.4	239	10 US-09-864-761-38414	Sequence 38414, A
10	565.5	25.6	340	9 US-09-791-932-117	Sequence 117, App
11	565.5	25.6	340	9 US-09-990-940-2	Sequence 2, Appl
12	548	24.8	100	10 US-09-885-478-17	Sequence 17, Appl
13	537	24.3	100	10 US-09-885-478-16	Sequence 16, Appl
14	525	23.8	369	10 US-09-823-114-9	Sequence 9, Appl
15	519	23.5	391	9 US-09-990-940-20	Sequence 20, Appl
16	504.5	22.8	418	9 US-09-992-331-17	Sequence 17, Appl
17	487	22.0	91	10 US-09-864-761-38421	Sequence 38421, A
18	480.5	21.7	428	9 US-09-992-331-16	Sequence 16, Appl
19	472	21.4	428	9 US-09-992-331-15	Sequence 15, Appl

20	470.5	21.3	363	9 US-09-992-331-14	Sequence 14, Appl
21	459	20.8	405	10 US-09-966-871-84	Sequence 84, Appl
22	459	20.8	405	12 US-10-039-645-84	Sequence 84, Appl
23	456.5	20.7	370	10 US-09-823-114-21	Sequence 21, Appl
24	456	20.6	362	9 US-09-992-331-13	Sequence 13, Appl
25	455	20.6	382	10 US-09-993-844-4	Sequence 4, Appl
26	453.5	20.5	390	10 US-09-761-962-25	Sequence 25, Appl
27	453.5	20.5	391	10 US-09-761-962-26	Sequence 26, Appl
28	453.5	20.5	392	10 US-09-761-962-19	Sequence 19, Appl
29	453.5	20.5	398	10 US-09-761-962-29	Sequence 29, Appl
30	453.5	20.5	398	10 US-09-966-871-83	Sequence 83, Appl
31	453.5	20.5	398	12 US-10-039-645-83	Sequence 83, Appl
32	453.5	20.5	401	10 US-09-761-962-20	Sequence 20, Appl
33	453.5	20.5	409	10 US-09-761-962-27	Sequence 27, Appl
34	453.5	20.5	438	10 US-09-761-962-17	Sequence 17, Appl
35	453.5	20.5	444	10 US-09-761-962-28	Sequence 28, Appl
36	453	20.5	372	9 US-10-112-599A-4	Sequence 4, Appl
37	453	20.5	415	10 US-09-823-114-20	Sequence 20, Appl
38	452.5	20.5	398	10 US-09-823-114-16	Sequence 16, Appl
39	452.5	20.5	398	10 US-09-966-871-1	Sequence 1, Appl
40	452.5	20.5	398	12 US-10-039-645-1	Sequence 1, Appl
41	451.5	20.4	398	10 US-09-966-871-79	Sequence 79, Appl
42	451.5	20.4	398	12 US-10-039-645-79	Sequence 79, Appl
43	449.5	20.3	372	10 US-09-966-871-80	Sequence 80, Appl
44	449.5	20.3	372	12 US-10-039-645-80	Sequence 80, Appl
45	448.5	20.3	398	10 US-09-214-904-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-885-478-27
; Sequence 27, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; PRIOR APPLICATION DATE: 2001-09-24
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 422
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-27

Query Match 100.0%; Score 2210; DB 10; Length 422;
Best local Similarity 100.0%; Pred. No. 3.7e-181;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSVGAAKKGVGRAVGLGGGSCQATEEDPLPDGACAPGCGGRMRLLPOPAWVEGSSARL 60
Db	1	MSVGAAKKGVGRAVGLGGGSCQATEEDPLPDGACAPGCGGRMRLLPOPAWVEGSSARL 60
QY	61	WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTAGSPRTGSISYINIMPSYGTIC 120
Db	61	WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTAGSPRTGSISYINIMPSYGTIC 120
QY	121	LLGIIGNSTVIFAIVVKKSKLHWCNNVPDIFIINLSYVDLFLFLGMPFIHQLMGNGVWHF 180
Db	121	LLGIIGNSTVIFAIVVKKSKLHWCNNVPDIFIINLSYVDLFLFLGMPFIHQLMGNGVWHF 180

QY 181 GETMCTLITAMDANSQFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMALS 240
Db 181 GETMCTLITAMDANSQFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMALS 240
QY 241 FISITPWLRYARLIPFPGGAVGCGIRLPNPDLDLWFTLYQFELAFALPFVVITAAVYRI 300
Db 241 FISITPWLRYARLIPFPGGAVGCGIRLPNPDLDLWFTLYQFELAFALPFVVITAAVYRI 300
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Db 301 LQRMSSVAPASQORSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
QY 361 LYNAISLGYANSCNLPFVYIVLCETFRKRLVLSVKPAAQGOLRAVSNAGTADDEERTESK 420
Db 361 LYNAISLGYANSCNLPFVYIVLCETFRKRLVLSVKPAAQGOLRAVSNAGTADDEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 2
US-09-885-478-26
; Sequence 26, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH1
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 422
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-26

Query Match 99.8%; Score 2205; DB 10; Length 422;
Best Local Similarity 99.8%; Pred. No. 9.9e-181;
Matches 421; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSVGAARKGVGRAVGLGGSGCQATEEDPLPDCGACAPGQGGRRWRLPQPAWVEGSSARL 60
Db 1 MSVGAARKGVGRAVGLGGSGCQATEEDPLPDCGACAPGQGGRRWRLPQPAWVEGSSARL 60
QY 61 WEQATGTGWADLEASLPTGPNASNTSDGPDNLTSGSPRTGSISYINITIMPSVEGTIC 120
Db 61 WEQATGTGWADLEASLPTGPNASNTSDGPDNLTSGSPRTGSISYINITIMPSVEGTIC 120
QY 121 LIGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSYVDLFLGMPFMIHQLMNGVWHF 180
Db 121 LIGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSYVDLFLGMPFMIHQLMNGVWHF 180
QY 181 GETMCTLITAMDANSQFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMALS 240
Db 181 GETMCTLITAMDANSQFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMALS 240
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Db 361 LYNAISLGYANSCNLPFVYIVLCETFRKRLVLSVKPAAQGOLRAVSNAGTADDEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 3
US-09-885-478-2
; Sequence 2, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-885-478-2

Query Match 99.5%; Score 2200; DB 10; Length 422;
Best Local Similarity 99.5%; Pred. No. 2.6e-180;
Matches 420; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAARKGVGRAVGLGGSGCQATEEDPLPDCGACAPGQGGRRWRLPQPAWVEGSSARL 60
Db 1 MSVGAARKGVGRAVGLGGSGCQATEEDPLPDCGACAPGQGGRRWRLPQPAWVEGSSARL 60
QY 61 WEQATGTGWADLEASLPTGPNASNTSDGPDNLTSGSPRTGSISYINITIMPSVEGTIC 120
Db 61 WEQATGTGWADLEASLPTGPNASNTSDGPDNLTSGSPRTGSISYINITIMPSVEGTIC 120
QY 121 LIGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSYVDLFLGMPFMIHQLMNGVWHF 180
Db 121 LIGIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSYVDLFLGMPFMIHQLMNGVWHF 180
QY 181 GETMCTLITAMDANSQFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMALS 240
Db 181 GETMCTLITAMDANSQFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMALS 240
QY 241 FISITPWLRYARLIPFPGGAVGCGIRLPNPDLDLWFTLYQFELAFALPFVVITAAVYRI 300
Db 241 FISITPWLRYARLIPFPGGAVGCGIRLPNPDLDLWFTLYQFELAFALPFVVITAAVYRI 300
QY 301 LQRMSSVAPASQORSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
Db 301 LQRMSSVAPASQORSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVY 360
QY 361 LYNAISLGYANSCNLPFVYIVLCETFRKRLVLSVKPAAQGOLRAVSNAGTADDEERTESK 420
Db 361 LYNAISLGYANSCNLPFVYIVLCETFRKRLVLSVKPAAQGOLRAVSNAGTADDEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 4


```
US-09-925-776-2
; Sequence 2, Application US/09925776
; Patent No. US20020038007A1
; GENERAL INFORMATION:
; APPLICANT: AMES, ROBERT S., JR.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: FOLEY, JAMES J.
; APPLICANT: BERGSMAN, DEBK J.
; APPLICANT: ELLIS, CATHERINE E.
; APPLICANT: CHAMBERS, JON K.
; TITLE OF INVENTION: A METHOD OF FINDING AGONIST AND
; TITLE OF INVENTION: ANTAGONIST TO HUMAN IICB SPLICE VARIANT
; FILE REFERENCE: GP-50003-D2
; CURRENT APPLICATION NUMBER: US/09/925,776
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/032,763
; PRIOR FILING DATE: 1996-12-11
; PRIOR APPLICATION NUMBER: 08/984,288
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: 60/073,747
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 09/060,504
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-925-776-2

Query Match      82.3%; Score 1819; DB 10; Length 353;
Best Local Similarity 100.0%; Pred. No. 7.1e-148;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 DLEASLPTGPNASNTSDGPDNLTSGSPRTGSIYINIMPSVFGTICLLGIGNSTV 130
    |||||||
Db 2 DLEASLPTGPNASNTSDGPDNLTSGSPRTGSIYINIMPSVFGTICLLGIGNSTV 61

QY 131 IFAVVKKSKLHMCNNVPDIFINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLITA 190
    |||||||
Db 62 IFAVVKKSKLHMCNNVPDIFINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLITA 121

QY 191 MDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWLY 250
    |||||||
Db 122 MDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWLY 181

QY 251 ARLIFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFLPFPVITAAYVRILQRTSSVAP 310
    |||||||
Db 182 ARLIFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFLPFPVITAAYVRILQRTSSVAP 241

QY 311 ASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVQLTQLSISRPTLTFVYLYNAAISLGY 370
    |||||||
Db 242 ASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVQLTQLSISRPTLTFVYLYNAAISLGY 301

QY 371 ANSCLNPFVYIVLCETFRKRLVLSVKPAAQQLRAVSNAQTADERTESKGT 422
    |||||||
Db 302 ANSCLNPFVYIVLCETFRKRLVLSVKPAAQQLRAVSNAQTADERTESKGT 353

RESULT 5
US-09-885-478-28
; Sequence 28, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH1
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
```

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; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 353
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
; US-09-885-478-28

Query Match      82.3%; Score 1819; DB 10; Length 353;
Best Local Similarity 100.0%; Pred. No. 7.1e-148;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 DLEASLPTGPNASNTSDGPDNLTSGSPRTGSIYINIMPSVFGTICLLGIGNSTV 130
    |||||||
Db 2 DLEASLPTGPNASNTSDGPDNLTSGSPRTGSIYINIMPSVFGTICLLGIGNSTV 61

QY 131 IFAVVKKSKLHMCNNVPDIFINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLITA 190
    |||||||
Db 62 IFAVVKKSKLHMCNNVPDIFINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLITA 121

QY 191 MDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWLY 250
    |||||||
Db 122 MDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWLY 181

QY 251 ARLIFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFLPFPVITAAYVRILQRTSSVAP 310
    |||||||
Db 182 ARLIFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFLPFPVITAAYVRILQRTSSVAP 241

QY 311 ASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVQLTQLSISRPTLTFVYLYNAAISLGY 370
    |||||||
Db 242 ASQSRIRLRTKRVTRTAIAICLVFVCWAPYYVQLTQLSISRPTLTFVYLYNAAISLGY 301

QY 371 ANSCLNPFVYIVLCETFRKRLVLSVKPAAQQLRAVSNAQTADERTESKGT 422
    |||||||
Db 302 ANSCLNPFVYIVLCETFRKRLVLSVKPAAQQLRAVSNAQTADERTESKGT 353

RESULT 6
US-09-895-686-2
; Sequence 2, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID NO. US20020106655A1 1459432CD1
; US-09-895-686-2

Query Match      81.6%; Score 1803; DB 10; Length 353;
Best Local Similarity 99.1%; Pred. No. 1.6e-146;
Matches 349; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 71 DLEASLPTGPNASNTSDGPDNLTSGSPRTGSIYINIMPSVFGTICLLGIGNSTV 130
    |||||||
Db 2 DLEASLPTGPNASNTSDGPDNLTSGSPRTGSIYINIMPSVFGTICLLGIGNSTV 61
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[illegible]

```

RESULT 7
US-09-885-478-4
; Sequence 4, Application US/09885478
; Patent No. US20020111306A1
;
; GENERAL INFORMATION:
;
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH1
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;
; LENGTH: 353
;
; TYPE: PRT
;
; ORGANISM: RATTUS NORVEGICUS
;
US-09-885-478-4

```

[illegible]

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RESULT 8
US-09-990-940-19
; Sequence 19, Application US/09990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiayang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupte, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030027252A1el Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 19
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human melanin-concentrating hormone receptor
; OTHER INFORMATION: (MCHR1)
US-09-990-940-19

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Query Match	76.7%;	Score 1696;	DB 9;	Length 402;
Best Local Similarity	83.2%;	Pred. No. 2.6e-137;		
Matches 341;	Conservative 7;	Mismatches 14;	Indels 48;	Gaps 4;
QY 50	PANWEGS--SARLWEQATGHWADLEASLLPTGPNASNTSDGPDN-----	92		
DB 4	PSKRWGSGHSGRIHQETHGSKRD-----KISN-SEGRENGGRGFQMGSLAE	52		
QY 93	-----LTSAGSPRTGSISYINIMPSVFETGICLIGNSTVIF	132		
DB 53	HASRMSVLRAKPMNSQRLLLLSPGSPRTGSISYINIMPSVFETGICLIGNSTVIF	112		
QY 133	AVVKKSKLHWCNVNPDIETINSVDLLFLGMPFMHQLMGVWHFGETMCTLITAMD	192		
DB 113	AVVKKSKLHWCNVNPDIETINSVDLLFLGMPFMHQLMGVWHFGETMCTLITAMD	172		
QY 193	ANSQETSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISTPWWLYAR	252		
DB 173	ANSQETSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISTPWWLYAR	232		
QY 253	LIFPPGAVGCGIRLPNPDIDLWFTLYQFFLAFLPFTVITAAVYRIIQRMTSSVAPAS	312		
DB 233	LIFPPGAVGCGIRLPNPDIDLWFTLYQFFLAFLPFTVITAAVYRIIQRMTSSVAPAS	292		
QY 313	ORSIRLRTKRVTRTAIAICLVEFVCWAPYYVLQTLQLSISRPTLTFFVYLYNNAISLGYAN	372		
DB 293	ORSIRLRTKRVTRTAIAICLVEFVCWAPYYVLQTLQLSISRPTLTFFVYLYNNAISLGYAN	352		
QY 373	SCLNPFYIIVLCETFRKRLVLSVKPAQOGQLRAVSNAGTADERTESKGT	422		
DB 353	SCLNPFYIIVLCETFRKRLVLSVKPAQOGQLRAVSNAGTADERTESKGT	402		

```
RESULT 9
US-09-864-761-38414
; Sequence 38414, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38414
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO 286090.10
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
; OTHER INFORMATION: EST_HUMAN HIT: BE701073.1, EVALU6 6.00e-44
; OTHER INFORMATION: SWISSPROT HIT: Q99705, EVALU6 0.00e+00
US-09-864-761-38414

Query Match 55.4%; Score 1224; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.7e-97;
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Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 184 MCTLTITAMDANSOFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLMAISFIS 243
Db 1 MCTLTITAMDANSOFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLMAISFIS 60
QY 244 ITPVWLARLIPFGGAVGCGIRLPNPDIDLWFTLYQFFLAFLPFWITAAVRILO 303
Db 61 ITPVWLARLIPFGGAVGCGIRLPNPDIDLWFTLYQFFLAFLPFWITAAVRILO 120
QY 304 MTSSVAPASQSRSTRLTKRVRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVLYN 363
Db 121 MTSSVAPASQSRSTRLTKRVRTAIAICLVFVCWAPYVVLQTLQLSISRPTLTFVLYN 180
QY 364 AAISLGYANSCLNDFYIIVLCETFRRKRLVSVKPAAGQLRAVSNAQTADERTESKGT 422
Db 181 AAISLGYANSCLNDFYIIVLCETFRRKRLVSVKPAAGQLRAVSNAQTADERTESKGT 239

RESULT 10
US-09-791-932-117
; Sequence 117, Application US/09791932
; Publication No. US20030003451A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayles, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huf, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030003451A1e1 G Protein-Coupled Receptors Cross-Ref
; FILE REFERENCE: 00325-US1
; CURRENT APPLICATION NUMBER: US/09/791,932
; PRIOR APPLICATION NUMBER: 2001-02-23
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/194,344
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/218,337
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 117
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-932-117
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Query Match	25.6%;	Score 565.5;	DB 9;	Length 340;	
Best Local Similarity	37.0%;	Pred. No. 6.9e-41;			
Matches 113;	Conservative 62;	Mismatches 119;	Indels 11;	Gaps 4;	
QY	110	IMPSVFGTICLIGIGNSTVIFAVVKSKSLHWCNNVPDIFITINLSVDLLELLGMPFI	169		
		: : : : : : : : : : : : : :			
Db	35	VILPSMIGIICSTGLVGNILIVETIIRSRK---KIVPDIIYNLAVADLVHIVGMPFI	90		
QY	170	HQLMGNGVWHFGETMCTLTITAMDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVA	229		
		: : : : : : : : : :			
Db	91	HQWARGGEWVFGPICIITISDTCNQFACSAIMTVMSVDRYFALVQPERLTRWRTRYKT	150		
QY	230	TLVICLLWALSFISITPWLVARLIPFPGAVGCGIRLPNPDFTDLYETLYQEFALFALP	289		
		: : : : : : :			
Db	151	IRINGLMAASFILALPWWYSKVIFKFDGESCAFDLTSPD-DVLMYTLTYLTITTTFFFP	209		
QY	290	FVVTITAAVYRIL-----QRMSSVAPASQRSI-RLRTKRVTRTALAICLVEFVWCAPYYV	343		
		: : : : : : : : : : : : : : :			
Db	210	LPILLYCYILILCYTWEMYYQNKDARCCNPSPKQRYMKLTKMVLVLVYVFILSAAPYHV	269		
QY	344	LQLTQLSISRPTLTFVYLYNNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAQGL	403		
		: : : : : : : : : : : :			
Db	270	IQLVNLQMEQPTLAFYVGYLSTICLSYASSSINPFLYILLSGNFQKRLLPQIQRATEKEI	329		
QY	404	RAVSN 408			
		:			
Db	330	NNMGN 334			

```

RESULT 11
US-09-990-940-2
; Sequence 2, Application US/099990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiayang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupta, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030027252A1e1 Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR342,
; OTHER INFORMATION: melanin-concentrating hormone receptor 2 (MCHr2)
US-09-990-940-2

```

Query Match	25.6%;	Score 565.5;	DB 9;	Length 340;
Best Local Similarity	37.0%;	Pred. No. 6.9e-41;		
Matches 113; Conservative	62;	Mismatches 119;	Indels 11;	Gaps 4;
QY 110	IMPSVEGTICLLGIIGNSTVIFAAVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMI	169		

Db	35	VILPSMIGIICSTGLVGNILIVFTIIRSK----	KTVPDLYICNLAVADLVHIVGMPELLI	90
QY	170	HOLMGNGVHGEETMCTLITAMDANSQFTSTYIL	TAMADIRLATVHPISSTFRKPSVA	229
Db	91	HQWARGGEWFGGPLCTIITS	LDTCNQACSAIMTWSVDRYFALVQPFRLTRWTRYKT	150
QY	230	TLVLCILMALSFISTITP	PWLYARLIDPPGAVGCGIRLPNBDLWFTLYQFFLAALP	289
Db	151	IRINGLMAASFIALLP	PWVWYSKVIKERDVE\$CAFDLTS\$D-DLWYTLTYLTITTFEFP	209
QY	290	FVVTAAAYVRIL----	QRM\$SSVAPASORSI-RLRTKRVTRFAIAICLVEFVCNADPYV	343
Db	210	LPILVCYLILICYTWEMYQ	QNKDARCNP\$V\$PKQVRMKLT\$KMWLVLVVVFIL\$ADPYHV	269
QY	344	LQTLQLSISRP\$TLTFV	LYLYNNAISLGYAN\$CLNP\$FVYIVLCETFERKRLVLSVKP\$PAQOL	403
Db	270	IQLVNLQMEQPTLAFYV	GYLLSICLSYASSINPFLYILL\$GNFQKRLPQIQRRATEKEI	329
QY	404	RAVSN	408	
Db	330	NNMGN	334	

```

RESULT 12
US-09-885-478-17
; Sequence 17, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 100
;
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATION CLONE
;
US-09-885-478-17

```

	Query Match	24.8%;	Score 548;	DB 10;	Length 100;	
	Best Local Similarity	100.0%;	Pred. No. 4.8e-40;			
	Matches 100;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 MSVGAAKKGVGRAVLGGSGCQATEEDPLPDCGACAPGQGGRMRLLPQPAVEGSSARL 60 					
Dd	1 MSVGAAKKGVGRAVLGGSGCQATEEDPLPDCGACAPGQGGRMRRLPQPAVEGSSARL 60 					
QY	61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSAGSP 100 					
Dd	61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSAGSP 100 					

```

RESULT 13
US-09-885-478-16
; Sequence 16, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
;

```



```

; TITLE OF INVENTION:  USES THEREOF
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 100
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATION CLONE
US-09-885-478-16
```

```

Query Match          24.3%; Score 537; DB 10; Length 100;
Best Local Similarity 98.0%; Pred. No. 4.2e-39;
Matches 98; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```

QY 1 MSVGAKKGVGRAVGLGGSGCQATEEDPLPDGACAPGQGGRRRLPQPAWEGSSARL 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MSVGAKKGVGTAVGLGGSGCQATEEDPLPDGACAPGQGGRRRLPQPAWEGSSARL 60
QY 61 WEQATGTGWADLEASLPTGPNASNTSDGPDNLTSAGSPP 100
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 WEQATGTGWADLEASLPTGPNASNTSDGPDNLTSAGSPP 100
```

RESULT 14

```

US-09-823-114-9
; Sequence 9, Application US/09823114
; Patent No. US20020061554A1
```

GENERAL INFORMATION:

APPLICANT: EVANS, CHRISTOPHER J.

KEITH, DUANE E.

TITLE OF INVENTION: OPIOID RECEPTOR GENES

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/823,114

FILING DATE: 29-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/148,351

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 22000-20526.22

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

TELEX: 90-4030 MRSNFOERSWSH

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 369 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-823-114-9

```

Query Match          23.8%; Score 525; DB 10; Length 369;
Best Local Similarity 31.5%; Pred. No. 2.2e-37;
Matches 117; Conservative 76; Mismatches 133; Indels 46; Gaps 10;
```

```

QY 62 EQATGTG-WA----DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVF 116
    ||| | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 6 EQFNGSQWTFSPFDLNGSLGPS--NGSNQTEPYDMS-----NAVLTFTY 50
QY 117 GTICLLIGTGNSTVIFAVVKKSKLWCNNVPDIFINISVDLFLGMPF-----MIH 170
    :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 51 FVVCVVGILCGNTLVIVILRYAKM--KITINIVILMLAIADELFMGLPRLAMQVALVH 107
QY 171 QLMNGVWHGETMCTLITAMDANSQFTSTYILTPAMAIDRYLATVHPISNKRKPSVAT 230
    | | | :| :| :| :| | | | | | | | | | | | | | | | | | | |
Db 108 -----WPEGKAICRVMTVDGINQFTSIFCLTVMISIDRYLAVVHPIKSAKWRPRTAK 160
QY 231 LVICLLWALSFTSTPVMLYARLIPPGAVGCGIRLPNDTDLy-WFTLYQFLAFALP 289
    :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 161 MINVAVWGVSLLVILPIMIVAGLRSNQWGRSSCTINWPEGSGAWYTGFIYAFLGLVP 220
QY 290 FVVTAAVYRILQRTSSVAPASQSRIRLTKRVTFRPAICLVFVCAWAPYVVLQTL 349
    :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 221 LTICLCYFLITIKVSSGIRVSSKRKSEKKVTRMVSIVAVFICWLPFYIFNVSSV 280
QY 350 SIS-RPTLRFVYLNAAISLGYANSCINPFYIVLCETFRKRLVLSVKPAQGOLRAVSN 408
    | :| | :| :| :| :| | | | | | | | | | | | | | | | | | |
Db 281 SVAISPTPALKMEDEFVILTYVANSKANPILYAFLLSDNFKK-----SQNVLCIVKV 332
QY 409 AQTADERTESK 420
    : | | | :| |
Db 333 SGAEDGERSDSK 344
```

RESULT 15

US-09-990-940-20

; Sequence 20, Application US/09990940

; Publication No. US20030027252A1

GENERAL INFORMATION:

APPLICANT: Tian, Hui

APPLICANT: Zhao, Jiayang

APPLICANT: Chen, Jin-Long

APPLICANT: Cutler, Gene

APPLICANT: An, Songzhu

APPLICANT: Dai, Kang

APPLICANT: Gupta, Jamila S.

APPLICANT: Tularik Inc.

TITLE OF INVENTION: No. US20030027252A1el Receptors

FILE REFERENCE: 018781-007410US

CURRENT APPLICATION NUMBER: US/09/990,940

CURRENT FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: US 60/252,841

PRIOR FILING DATE: 2000-11-22

PRIOR APPLICATION NUMBER: US 60/257,636

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 60/261,377

PRIOR FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: US 60/279,554

PRIOR FILING DATE: 2001-03-28

PRIOR APPLICATION NUMBER: US 60/280,696

PRIOR FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 20

LENGTH: 391

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: human somatostatin receptor 1 (SSTR1)

US-09-990-940-20

```

Query Match          23.5%; Score 519; DB 9; Length 391;
Best Local Similarity 30.9%; Pred. No. 7.6e-37;
```

Matches 112; Conservative 70; Mismatches 136; Indels 44; Gaps 7;

```
QY      29 PLPDCGACAPGCGGRRRRLPOPAWVEGSSARLMEQATGTGWADLEASLTPTGPNASNTSD   88
        | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      14 PSPSPSGSGEGGGSR-----GPGAGAAD---GMEPEGRNASSQNGT   50
QY      89 GPDNLTSAGSPPRTGTSISYINIMPSVFGTICLLIGIGNSTVIFAAYKKSKLHWCNVPD   148
        : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      51 LSEGQSA-----ILISFTYSVCLVGIGNSMVTIYLRIAKMKTA TN---   94
QY     149 IFIINLSVDLLELLGMPEMIHOLMGNGWHFGETMCTLLITAMDANSQFTSYILLTAMAI   208
        | : | : | : | | : | : | : | | | | | | : | : | : | | | | | | | | | |
Db      95 IYILNLAIDELMLSVFLWTSLLRH-WPFALLCRLYLSVDAVNMFTSIYCLTVLSV    153
QY     209 DRYLATVHPISSTRKFRKPSVA TLVLC LLMA LSFSITPWLYARLI PFPGAVCGGIRLP   268
        ||| : | | | | : : : | : | : | | | : | | : | | | : | | | : | | | : |
Db     154 DRYAVVHPITKAARYRPRPTAVAKVN LGWVL SLVLPLIVESRTA NSDGTVA CNMLMP    213
QY     269 NP-DTDLYWETLQEF LA FALP EVVITA AYVR ILQRMTSSVAPA SORSIRLPTRKVRTRA   327
        - | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     214 EPAQRWL VG E V L T Y FL MG FLL PG A LC L CY V LI AK MR VA L K AG W Q O R KR SER KITLMV 273
QY     328 IAICLVFEVCMAPIYVLQTLQSISRPTLLFVYLYNAAISLGANSC LNPFVYIYCETF   387
        : : : | : | | | : | : | : | | : | | | | | | | | | | | | | | | | | | |
Db     274 MMVVMMVFVICMPEFYVQLVNVFAEDDATVSQ L--SVILGYANSCANPILYGFLSDNF   330
QY     388 RK 389
        ::
Db     331 KR 332
```

Search completed: February 13, 2003, 14:10:32
Job time : 15.1019 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:56:01 ; Search time 15.1596 Seconds
(without alignments)
2676.114 Million cell updates/sec

Title: US-09-885-478-27
Perfect score: 2210
Sequence: 1 MSVGAKKGVGRAVGLGGGS.....LRVSNAGTADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2195	99.3	422	2	JC7080	melanin-concentrat
2	565.5	25.6	340	2	JC7695	G protein-coupled
3	532	24.1	369	2	D41795	somatostatin recep
4	530.5	24.0	369	2	B41795	somatostatin recep
5	525	23.8	369	2	A45291	somatostatin recep
6	524.5	23.7	369	2	JC2083	somatostatin recep
7	519	23.5	391	2	A41795	somatostatin recep
8	514	23.3	346	2	S29248	somatostatin recep
9	513.5	23.2	391	2	JN0605	somatostatin recep
10	513	23.2	391	2	C41795	somatostatin recep
11	504.5	22.8	418	2	A46226	somatostatin recep
12	500	22.6	391	2	A39297	somatostatin recep
13	494.5	22.4	384	2	A47249	brain-specific som
14	485	21.9	384	2	JC4629	somatostatin recep
15	480.5	21.7	428	2	S30508	probable G protein
16	478.5	21.7	363	2	I57955	somatostatin recep
17	478.5	21.7	364	2	JN0763	somatostatin recep
18	472	21.4	428	2	A44021	somatostatin recep
19	470.5	21.3	363	2	I57940	somatostatin recep
20	453.5	20.5	398	2	A57510	mu opioid receptor
21	453	20.5	372	2	I38532	delta opioid recep
22	452.5	20.5	398	2	I56517	mu opioid receptor
23	450.5	20.4	372	2	S34592	delta opioid recep
24	448	20.3	400	2	I56553	mu opiate receptor
25	447	20.2	392	2	S65693	opioid receptor mu
26	445.5	20.2	398	2	I56504	mu opioid receptor
27	443.5	20.1	372	2	B48227	delta opioid recep
28	440.5	19.9	380	2	JC2338	kappa opioid recep
29	432.5	19.6	380	2	A55259	kappa opioid recep

30	420.5	19.0	380	2	A48227	kappa opioid recep
31	420	19.0	328	2	I38973	G protein-coupled
32	419	19.0	380	2	S36143	kappa opioid recep
33	413	18.7	370	2	S43087	orphan opioid rece
34	410.5	18.6	367	2	I49022	kappa opioid recep
35	410.5	18.6	367	2	JC2421	opioid receptor ho
36	409.5	18.5	333	2	I38974	G protein-coupled
37	409.5	18.5	367	2	I56520	kappa opioid recep
38	409.5	18.5	380	2	JC2434	delta opioid recep
39	407	18.4	373	2	JE0087	angiotensin II rec
40	372.5	16.9	359	2	I51372	angiotensin II rec
41	368	16.7	362	2	JN0694	allatostatin recep
42	361	16.3	423	2	JC7677	probable chemotatr
43	347	15.7	371	2	JC5796	N-formyl peptide r
44	341	15.4	350	2	A42009	angiotensin II rec
45	341	15.4	359	2	A42656	

ALIGNMENTS

RESULT 1

JC7080
melanin-concentrating hormone receptor [validated] - human
N;Alternate names: MCHR; orphan somatostatin-like receptor 1 (SLC-1)
C;Species: Homo sapiens (man)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: JC7080
R;Shimomura, Y.; Mori, M.; Sugo, T.; Ishibashi, Y.; Abe, M.; Kurokawa, T.; Onda, H.; Biochem. Biophys. Res. Commun. 261, 622-626, 1999
A;Title: Isolation and identification of melanin-concentrating hormone as the endoger
A;Reference number: JC7080; MUID:99373129; PMID:10441476
A;Accession: JC7080
A;Molecule type: mRNA
A;Residues: 1-422 <SH1>
A;Note: It is uncertain wheather Met-1, Met-6 or Met-70 is the initiation codon
C;Superfamily: neurokinin 1 receptor
C;Keywords: hormone receptor; transmembrane protein

Query Match 99.3%; Score 2195; DB 2; length 422;

Best Local Similarity 99.3%; Pred. No. 1.2e-174;

Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	MSVGAKKGVGRAVGLGGSGCQATEEDPLDGCACAPGGGGRMRLLQPAPWEGSSARL 60		
Db	1	MSVGAAMKKGVGRAVGLGGSGCQATEEDPLDNCACAPGGGGRMRLLQPAPWEGSSARL 60		
QY	61	WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTASGSPRTGTSYINIMPSVFGTIC 120		
Db	61	WEQATGTGWMDEASLLPTGPNASNTSDGPDNLTASGSPRTGTSYINIMPSVFGTIC 120		
QY	121	LGIIIGNSTVIFAAYVKKSKLHWCNNVPDIFILNLSVDLLFLLGMPFMIHQLMGNGVWHF 180		
Db	121	LGIIIGNSTVIFAAYVKKSKLHWCNNVPDIFILNLSVDLLFLLGMPFMIHQLMGNGVWHF 180		
QY	181	GETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLMAIS 240		
Db	181	GETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLMAIS 240		
QY	241	FISITPVMLYARLIPPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFLPFVVITAAVRI 300		
Db	241	FISITPVMLYARLIPPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFLPFVVITAAVRI 300		
QY	301	IORMTSSVAPASQSRIRLTKRVRTAIAICLVFVCWAPYVYQLTQLSISRPTLFVY 360		
Db	301	IORMTSSVAPASQSRIRLTKRVRTAIAICLVFVCWAPYVYQLTQLSISRPTLFVY 360		
QY	361	LYNNAISLGYANSCLNDFVYIVLCETFRKRLVSVKPAAGQGLRAVSNAGTADERTESK 420		
Db	361	LYNNAISLGYANSCLNDFVYIVLCETFRKRLVSVKPAAGQGLRAVSNAGTADERTESK 420		
QY	421	GT 422		

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
C;Accession: A41795
R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of human and mouse somatost
A;Reference number: A41795; MUID:92108031; PMID:1346068
A;Accession: A41795
A;Molecule type: DNA
A;Residues: 1-391 <YAM>
A;Cross-references: GB:M81829; NID:g307433; PIDN:AAA58247.1; PID:g307434
A;Note: sequence extracted from NCBI backbone (NCBIN:74767, NCBIP:74768)
C;Genetics:
A;Gene: GDB:SSTR1
A;Cross-references: GDB:134185; OMIM:182451
A;Map position: 14q13-14q13
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; pho
F;58-84/Domain: transmembrane #status predicted <TM1>
F;95-120/Domain: transmembrane #status predicted <TM2>
F;132-153/Domain: transmembrane #status predicted <TM3>
F;173-195/Domain: transmembrane #status predicted <TM4>
F;220-250/Domain: transmembrane #status predicted <TM5>
F;269-296/Domain: transmembrane #status predicted <TM6>
F;302-326/Domain: transmembrane #status predicted <TM7>
F;4,44,48,381/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;130-208/Disulfide bonds: #status predicted
F;172/Binding site: phosphate (Thr) (covalent) (by CAMP-dependent kinase) #status predic
F;265/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predic
F;339/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 23.5%; Score 519; DB 2; Length 391;
Best Local Similarity 30.9%; Pred. No. 1.8e-35;
Matches 112; Conservative 70; Mismatches 136; Indels 44; Gaps 7;

QY 29 PLPDGACAPGOGGRWRLPQPAWVEGSSARLWEQATGTGWADLEASLLPTGPNASNTSD 88
Db 14 PSPSPGSCGEGGGR-----GPGAGAAD--GMEEPGRNASQNGT 50

QY 89 GPDLNLSAGSPRTGSISYINIMPSVEGTICLLGIIGNSTVIFAVVKSKLHMCNNVPD 148
Db 51 LSEGGSA-----ILISFIYSVCLVGLGNSMVIYVILRYAKMKTATN--- 94

QY 149 IFIINLSVVDLLFLLGMPFMIHQLMNGVWHFGETMCTLITAMDANSQFTSTYILLTAMAI 208
Db 95 IYILNLAIADLMLSVPLVTSILLRH-WPFGALLCRVLVSDAVNMFTSYCLTVLSV 153

QY 209 DRYLATVHPISSTKFRKPSVATLVICLLMALSFISTPVMYLARLIPFGAGVCGGIRLP 268
Db 154 DRYVAVHPIKAKARYRPTVAKVNLGVWVLSLVILPIVFSRTAANSDDGTACNMMLP 213

QY 269 NP-DTDLTWFTLYQFLAFALPFIYVITAAYVRILOQMTSSVAPASQSRIRLRTKRYTRTA 327
Db 214 EPAQRWLVGFLVLTFLMGFLLPVGAICLCYVLIIAKRMVALKAGWQQRKRSEKITLMV 273

QY 328 IAIQLVFVGCWAPYVYLQLTQLSISRPTLTFVYLYNAISLGYANSCLNPFVYIVLCETF 387
Db 274 MMVVMVEVLCWMPFYVVLVNVFAEQDDATVSQ--SVILGYANSCANPILYGLSDNF 330

QY 388 RK 389
Db 331 KR 332

RESULT 8
529248
somatostatin receptor 2B - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Nov-1999
C;Accession: S29248
R;Vanetti, M.; Koubda, M.; Wang, X.; Vogt, G.; Hoellt, V.
FEBS Lett. 311, 290-294, 1992
A;Title: Cloning and expression of a novel mouse somatostatin receptor (SSTR2B).

A;Reference number: S29248; MUID:93012001; PMID:1397330
A;Accession: S29248
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-346 <VAN>
A;Cross-references: EMBL:X68951; NID:g54197; PIDN:CAA48766.1; PID:g54198
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 23.3%; Score 514; DB 2; Length 346;
Best Local Similarity 31.2%; Pred. No. 4.1e-35;
Matches 115; Conservative 76; Mismatches 130; Indels 48; Gaps 11;

QY 62 EQATGTG-WA---DLEASLPTGPNASNTSDGPDNLSAGSPRTGSISYINIMPSVF 116
Db 6 EQLNGSQVWVSSPDLNGLGPS--NGSNQTEPYDMTS-----NAVLTFIY 50

QY 117 GTICLGIIGNSTVIFAIVKSKLHWCNNVPDIFIINLSVDLLFLLGMPF-----MIH 170
Db 51 FVVCVVGCLGNTLVIVILRYAKM--KITNTYILNLAIADLFLMLGLPFLAMOVALLVH 107

QY 171 QLMNGVWHFGETMCTLITAMDANSQFTSTYILLTAMAIIDRYLATVHPISSTKFRKPSVAT 230
Db 108 -----WPEGKAICRVVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRPRTAK 160

QY 231 LVICLLMALSFISTPVMYLARLIPFGAGVCGGIRLPNDTDLY-WFTLYQFLAFALP 289
Db 161 MINVAVWCVSLVLLPILMLYAGLSHNSQWRSSCTINWPGESEGAWYTGFIYAFLIGFLVP 220

QY 290 FVVITAAVYRILQMTSSVAPASQSRIRLRTKRYTRTAICLVEFVCWAPYVYLQLTQL 349
Db 221 LFTICLCYELIILIKVSSGIRVGSSKRKKSEKVTRMVSIYAVEIFCWLPIFYFNSSV 280

QY 350 SIS-RPTLTFVYLYNAISLGYANSCLNPFVYIVLCETFRRKL-VLSVKPAAQGLRAY 406
Db 281 SVAISPTPALKGMFDEVILTYANTCANPILYAFLLSDNEKKSQNVLCIVKA----- 332

QY 407 SNAQTADFE 415
Db 333 DNSQSGAED 341

RESULT 9
JN0605
somatostatin receptor 4 - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C;Accession: JN0605; JN0762; A47457
R;Xu, Y.; Song, J.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 193, 648-652, 1993
A;Title: Molecular cloning and sequencing of a human somatostatin receptor, hSSTR4.
A;Reference number: JN0605; MUID:93290656; PMID:8512564
A;Accession: JN0605
A;Molecule type: DNA
A;Residues: 1-388 <XUY>
A;Cross-references: GB:LI4856; NID:g292499; PIDN:AAA36623.1; PID:g292500
R;Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y
Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A;Title: Cloning, functional expression and pharmacological characterization of a fou
A;Reference number: JN0762; MUID:93384611; PMID:8373420
A;Accession: JN0762
A;Molecule type: DNA
A;Residues: 1-388 <YAM>
A;Cross-references: GB:D16826; NID:g693907; PIDN:BAA04106.1; PID:g693908
R;Rohrer, L.; Raulf, F.; Bruns, C.; Buettner, R.; Hofstaedter, F.; Schuele, R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
A;Title: Cloning and characterization of a fourth human somatostatin receptor.
A;Reference number: A47457; MUID:93248256; PMID:8483934
A;Accession: A47457
A;Molecule type: DNA
A;Residues: 1-82, 'T', 84-364, 'K', 366-388 <ROH>
A;Cross-references: GB:I07833; NID:g307429; PIDN:AAA60565.1; PID:g307430
A;Note: sequence extracted from NCBI backbone (NCBIN:130856, NCBIP:130858)

C;Comment: This protein mediates the diverse actions of the tetradecapeptide somatostatin.
C;Genetics:
A;Gene: GDB:SSTR4
A;Cross-references: GDB:202662; OMIM:182454
A;Map position: 20p11.2-20p11.2
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phospholipase
F;47-73/Domain: transmembrane #status predicted <TM1>
F;84-109/Domain: transmembrane #status predicted <TM2>
F;121-142/Domain: transmembrane #status predicted <TM3>
F;162-184/Domain: transmembrane #status predicted <TM4>
F;208-238/Domain: transmembrane #status predicted <TM5>
F;257-284/Domain: transmembrane #status predicted <TM6>
F;291-314/Domain: transmembrane #status predicted <TM7>
F;24/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;119-198/Disulfide bonds: #status predicted
F;161,253/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
F;327/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match	23.2%;	Score 513.5;	DB 2;	Length 388;
Best Local Similarity	31.7%;	Pred. No. 5.2e-35;		
Matches 107; Conservative	74;	Mismatches 118;	Indels 39;	Gaps 9;

```
Oy      62 EQATGTGWADLEASLLPTGPNASNTSDGPDNLTASGSPRTGSISYINIIIMPSVFETICL 121
         | : || |          | : | | | | | | | | | | | | | | | | | | | |
Db      12 EEGLGTA-----PSAANACSAPEAEAEAVAGPGDANAAGM-VAIOCIYALVCL 59
```

```
QY      122 LGIGNSTVFIAVVKKSKLHWCNNVDFIILNLSVDLFLGLGMPFI-----HQLMGN 175
      ::::: ||| ::::: |  :::::| | ||| ::::: |
Db      60 VGLVGNALVFVILRYAKMKTATN---IYLLNLAVADELFMTSVFVASSAALRH----- 111
```

QY 176 GVWHFGEINCLLITAMDANSQFTSTYLLTAMADRYLATVHPISSTKFRKPSVATVLC 235
| | | : : : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 112 --WPFGSVLCRAVLSDGLNMFSTVECLTVLSVDRYVAVYHDLRAATYRRPSVAKLNLG 169

```
QY      236 LMAISFISTPVMYLARLIPEPGG-AVCGGIRLPNPDIDLW---FTLYQFFLAFLBEV   291
           :| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      170 VMLASLTPLPIAIFADTRPARGGAVACNLQWPHP-----AMSAVFVVYTFILGLLIPVL   225
```

QY 292 VITAAYVRILOQMSTSSAPASORSITLRTKRVTRTAIACLVFFWCWAPYYVLQLQLSI 351
| : : : | : : : | : : : | : : : | : : : | : : :
Db 226 AIGICVLLIVGKMRAVALRAGWOQRRESEKKITRLVLMVVVFVLCMPFYVVOQLNLVY 285

```
QY      352 SREPLTFVLYLYNNAISLGYANSCNPFVYIVLCETFRK 389
      :      |      :      :      :      :      :      :      :
Db      286 TSLDAT--VNHSLSLTSYANSCNPILYGLFSLDNRR 320
```

RESULT 10
C41795

somatostatin receptor 1 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
 C:Accession: C41795
 R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
 Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
 A:Title: Cloning and functional characterization of a family of human and mouse somatostatin receptors
 A:Reference number: A41795; MUID:92108031; PMID:1346068
 A:Accession: C41795
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-391 <YAM>
 A:Cross-references: GB:M81831; NID:g201058; PIDN:AAA58255.1; PID:g201059
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match	23.2%;	Score 513;	DB 2;	Length 391;
Best Local Similarity	30.9%;	Pred. No. 5.7e-35;		
Matches 112;	Conservative 73;	Mismatches 133;	Indels 44;	Gaps 8;

QY 29 PLEDCGACAPGGGRWRRLPQPAWVESSARLMEQATGTGNADLEASLLPTGPNASNTSD 88
| | : | || : : | : | | |

```
Db      14  PSPSPGSCG-----EGACSR---GPGSGAAD---GMEEPGRNASQNGT  50
```

```

QY      89  GPDNLTSA GSPPRIGSISYINIMPSVEGTICLLGIIGNSTVYFAVVKSKLHWCNNVPD 148
      :  ||  ||::: ||||: ||| ||: ::: ||:  |
Db      51  LSEGQGS A-----ILISFTYVCLVGLGCSNMTYIVILRYAKMKTATN--- 94

```

Qy 149 IFIINLSVVDLLEFLGMPFEMIHQLMGNGVWHEFGETMCTLIITANDANSOFTSTYILTAMAI 208
|::|::| | | ::|::| : | | ::|::| : ||| | | ::
Db 95 IYIINLAIDELMLSVPLVTSTLRH-WPGALLCRVLSDAVNMFTSIYCLTVLSV 153

```
OY      209 DRILATVHPRISSIKRKRPVSVALVICLIALMSFISITPVMVLARLIPEPGAVGCCIRLP   268
|||:|||:::||::||:| ||:| |::|| ||:| |::||
Db     154 DRYVAVVHPIKARYRKPRTVAKVAVNLGWAYLSLVILPIVESFTANSDDGTACNNMLMP   213
```

```

QY      269  NP-DTDLWTFLELYOEFLAFALPEFVVTAAVVRILQRMSTSSVAPASQSRIRLRTKRYRTA 327
          | | | | | : | | | | | | | | | | : : : : |
Db      214  EPAQRWLVGFEVLYTFLEMGFLLPVGATCICVYLIIAKMRMAADKAGWOQRKRSEKRTIMV 273

```

```

OY      328  IALCLVEFVCADPYVLQTLQLSISRPLTFVLYLNAASISGYANCLNPFVYIYLCET 387
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      274  MAMVVMFEVICMDEYVQLVNFEAEDDATVSOL--SVIIGYANSCANPIYLGTSDFN 330

```

QY	388	RK	389
		∴	
Db	331	KR	332

RESULT 11
A46226

somatostatin receptor 3 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A46226; S32501
R:Yamada, Y.; Reisine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Selino, M.,
Mol. Endocrinol. 6, 2136-2142, 1992
A:Title: Somatostatin receptors, an expanding gene family: cloning and functional char
A:Reference number: A46226; MUID:93149123; PMID:1337145
A:Accession: A46226
A:Molecule type: DNA
A:Residues: 1-418 <YAM>
A:Cross-references: GB:M96738; NID:q338498; PIDN:AAA60592.1; PID:q338499
A:Note: sequence extracted from NCBI backbone (NCBIN:123685, NCBIPI:123690)
R:Corrness, J.D.; Demchyshyn, L.L.; Seeman, P.; van Tol, H.H.M.; Srikant, C.B.; Kent,
FEBS Lett. 321, 279-284, 1993
A:Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays pr
A:Reference number: S32501; MUID:93238970; PMID:8097479

```
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-418 <COR>
```

A:Gene: GDB:SSTR3
A:Cross-references: GDB:134187; OMIM:182453
A:Map position: 22q13.1-22q13.1
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F:44-70/Domain: transmembrane #status predicted <TM1>
F:81-106/Domain: transmembrane #status predicted <TM2>
F:118-139/Domain: transmembrane #status predicted <TM3>
F:159-181/Domain: transmembrane #status predicted <TM4>
F:203-233/Domain: transmembrane #status predicted <TM5>
F:255-282/Domain: transmembrane #status predicted <TM6>
F:289-316/Domain: transmembrane #status predicted <TM7>
F:17,30/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:116-191/Disulfide bonds: #status predicted

Query Match	22.8%;	Score 504.5;	DB 2;	Length 418;
Best Local Similarity	32.5%;	Pred. No.3.1e-34;		
F:151,251,317,332/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #sta				
F:251/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre				
F:256/Binding site: phosphate (Thr) (covalent) (by CAMP-dependent kinase) #status pre				
F:412/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predi				

Matches	118;	Conservative	76;	Mismatches	134;	Indels	35;	Gaps	11;
QY	81	PNASNTSDGPDNLTAGSP-----	PRTGISISYINIMPSVEFTICLLGIIGNSTV	130					
Db	6	PSSVSTTSEPENASSAWPPDALTGNVSAGSP	PAGLAVSGVLIPLVYLVCVVGILGNSLV	65					
QY	131	IFAVVKRSKLMWCNNVPDIFILINSVDLFL	LGMPFMHQLMNGV--WHEGFTMCTLI	188					
Db	66	IYVVLRHRTA---SPSVTNVYLMLADELF	MLGLPFLAAO---NALSYWPFGLMCRLV	119					
QY	189	TAMDANSQFTSTYILTAAMADRILATVHP	ISSTKFRKPSVATLVICLLMALSFISITP	248					
Db	120	MAVDGINQFTSIFCLTVMSSVDRLAVYH	PTRSARWRTAPARTVSAAVWVASAVVLP	179					
QY	249	LYARLPPFGAVGCGIRLPNPDILYW--	FTLYQFLAFALPEFVITAAYVRILQRM	305					
Db	180	VFSGV---PRGMSTCHMQWPEPAA--	AMRAGFIITYAALGFEGPLLVICLCYLL	234					
QY	306	SS---VAPASQSRISRLRTKRVTRTA	IAICLVFVCWAPYYVQLTQLSISRP-TL	360					
Db	235	SAGRRWAPSCQRR-RRSERRVTRMVA	VALFVLCWMPFYVLINIVNVCPLPEE	293					
QY	361	LYNMAISLGYANSCLNPFYIVLCETFR	--KRLVLSVKPAQGQLRAVSNQTADE	417					
Db	294	LYFLVALPYANSCANPILYGLFLSYR	KQGFRRVLLRPSRRVRSQEPVTGPPE	353					
QY	418	ESK 420							
Db	354	EEE 356							

RESULT 12
A39297
somatostatin receptor - rat
N;Alternate names: probable G-protein-coupled receptor; SRIF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 24-Nov-1999
C;Accession: A39297; A45102; S20088
R;Meyerhof, W.; Paust, H.J.; Schoenrock, C.; Richter, D.
DNA Cell Biol. 10, 689-694, 1991
A;Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expressed
A;Reference number: A39297; MUID:92096119; PMID:1661599
A;Accession: A39297

A;Molecule type: mRNA
A;Residues: 1-391 <MEY>
A;Cross-references: GB:X62314; GB:X61630; NID:g56309; PIDN:CAA44193.1; PID:g56310
A;Experimental source: brain
A;Note: it is uncertain whether Met-1 is the initiator or whether translation is initiated
R;Li, X.J.; Forte, M.; North, R.A.; Ross, C.A.; Snyder, S.H.
J. Biol. Chem. 267, 21307-21312, 1992
A;Title: Cloning and expression of a rat somatostatin receptor enriched in brain.
A;Reference number: A45102; MUID:93016064; PMID:1400442
A;Accession: A45102
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-391 <LIL>
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:116692)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

Query Match 22.6%; Score 500; DB 2; Length 391;
Best Local Similarity 31.2%; Pred. No. 6.9e-34;
Matches 105; Conservative 73; Mismatches 134; Indels 24; Gaps 6;

QY	55	GSSARLMEQATGTGWADLEASLLPTGPNASNTSDGPDNLT	SAGSPRTGISISYINIIMPS	114					
Db	20	GCGEVCSRPGSGAAD---GMEEPGRNSSQNGTLSEGGSA-	-----ILISF	63					
QY	115	VEGTICLLGIGNSTVIFAVVKSKLMWCNNVPDIFILINS	VDLFLLGMPFMHQLMG	174					
Db	64	ITSVCLVGLCGNSMVTIYLIRYAKMKTATN--IYLINL	IAIDELMLSVFVLVTSTLL	120					

QY	175	NGVWHFETMCTLITAMDANSQFTSTYILTAAMADR	ILATVHPISSTKFRKPSVATLVIC	234					
Db	121	RH-WPFGALICRLVLSVDVANNMFTSICLTVLSVDR	YAAVVAHPIKARYRRPTVAKVYNL	179					
QY	235	LLWALSFSITPWWLYARLIPFGAVGCGIRLPN-D	TDLYWFTLYQFLAFALPEVVI	293					
Db	180	GVWVLSLVLIPDIVESRTAANSDDGYACNMMLPE	PAQRMVGVGYLTFLMGFLIPGAI	239					
QY	294	TAAYVRILQRMSSVAPASQSRISRLRTKRVTRTA	IAICLVFVCWAPYYVQLTQLSISR	353					
Db	240	CLCYVLLIAKMMVALKAGWQQRKRSEKKITLMVM	MMVMVMEVIGMMPFYVQLVNVFAEQ	299					
QY	354	PTLTFVLYNMAISLGYANSCLNPFYIVLCETFR	K 389						
Db	300	DDATVSQL--SVILGYANSCANPILYGLFLSDN	FKR 332						

RESULT 13
A47249
brain-specific somatostatin receptor SSNR-4 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A47249
R;Bruno, J.F.; Xu, Y.; Song, J.; Berelowitz, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 11151-11155, 1992
A;Title: Molecular cloning and functional expression of a brain-specific somatostatin
A;Reference number: A47249; MUID:93087484; PMID:1360663
A;Accession: A47249
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-384 <BRU>
A;Cross-references: GB:M96544; NID:g207072; PIDN:AAA42180.1; PID:g207073
A;Note: sequence extracted from NCBI backbone (NCBIN:119731, NCBIP:119732)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 22.4%; Score 494.5; DB 2; Length 384;
Best Local Similarity 33.0%; Pred. No. 1.9e-33;
Matches 104; Conservative 66; Mismatches 116; Indels 29; Gaps 8;

QY	85	NTSDGPDNLTAGSPRTGISISYINIIMPSVEFTICLL	GIGNSTVIFAVVKSKLMWCN	144					
Db	21	NASWAPDEEDAVRSDGTGTAGMVTI--QCITAV	CLVGLGVGNALVIEYILLRYAKMKTAT	78					
QY	145	NVPDIFILINSVDLFLLGMPFMI-----	HQLMNGVWHFETMCTLITAMDANSQFT	198					
Db	79	N---IYLLNAVADLEMLSVPFVASAALRH-----	WPFGAVLCRAVISVDGLNMT	128					
QY	199	STYILTAAMADRILATVHPISSTKFRKPSVATLVIC	LLMALSFISITPWWLYARLIPFG	258					
Db	129	SVFCLTVLSVDRYAAVVAHDLRAATYRRPSVAKLIN	GWLASLVTLPYAFADTRPARG	188					
QY	259	G-AVGCGRLPNPDFTLYW--FTLYQFLAFALPE	FVITAAAYVRILQRMSSVAPASQ	314					
Db	189	GEAVACNLHMPHP---AMSAVFVIYTFILGFLP	YLAIGLCYLLIVGKMRVALRAGWQ	244					
QY	315	SIRLTKRVTRTAIAICLVFVCWAPYYVQLTQLS	ISRPTLTFFVLYNMAISLGYANSC	374					
Db	245	QRRSEKKITRLVLMVVEFVLCWMPFYVQLLN	LEVTSLDAT---VNHVSILISYANSC	301					
QY	375	LNPFYIVLCETFRK 389							
Db	302	ANPILYGLFLSDNFKR 316							

RESULT 14
JC4629
somatostatin receptor type-4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 24-Nov-1999
C;Accession: JC4629
R;Schwabe, W.; Brennan, M.B.; Hochgeschwender, U.
Gene 168, 233-235, 1996

A:Title: Isolation and characterization of the mouse (Mus musculus) somatostatin receptor
A:Reference number: JC4629; MUID:96194903; PMID:8654950
A:Accession: JC4629
A:Molecule type: DNA
A:Residues: 1-384 <SCH>
A:Cross-references: GB:U26176; NID:g833840; PIDN:AAA67561.1; PID:g833841
C:Comment: This protein works through the G-proteins and plays a role in mediating inter
C:Genetics:
A:Gene: sstr4
C:Superfamily: vertebrate rhodopsin
C:Keywords: receptor; transmembrane protein
F:46-349/Domain: transmembrane #status predicted <TMM>

Query Match 21.9%; Score 485; DB 2; Length 384;
Best Local Similarity 29.9%; Pred. No. 1.2e-32;
Matches 102; Conservative 69; Mismatches 134; Indels 36; Gaps 8;

QY 53 VEGSSARLMEQATGTGWADLEASLLPTGPNASNTSDGPDNLTSGSPPRGTSISYINIM 112
DB 8 LRGVEDTTWTPGINASWA-----PEQEDAMGSDGTAGM-----VTI 46
QY 113 PSVEFTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQ 172
DB 47 QCIYALVCLVGLVGNALVIEYLRYAKMTATN---IYLLNLAVADELFMLSVPE-VRSA 102
QY 173 MNGVWHFGETMCTLTITAMDANSQFTSTYILTAMADRYLATVHPISSTFKRKPVSATLV 232
DB 103 AALRHWPFCAVLCRAVLSDVGNLMTSVFCLTVLSVDRYVAVVHPLRTATYRPSVAKLI 162
QY 233 ICLLWALSFISITPVMLYARLIPPPGG-AVGCGRLPNDPDTLYW--FTLYQFFLAFAL 288
DB 163 NLGVWLASLLVTLPIAVFADTRPARGEAVACNLHMPHP---AWSAVEVLYTFLLGFLP 218
QY 289 PFVVTITAAVVRILQRMSSVAPASQRSIRLRTRKRVFRTAIAICLVFVCWAPYYVQLTQ 348
DB 219 PVLAIGLCYLLIVGKMRVALRGWQQRSEKKITRLVLMVTVFVLCWMPFYYVQLLN 278
QY 349 LSI SRPTLTFVYLYNAISLGYANSCLNPFVYIVLCETFRK 389
DB 279 LFTVSLDAT---VNHVSLILSYANSCANPILYGFISDNFRR 316

RESULT 15
S30508
probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
C:Accession: S30508
R:Meyerhof, W.; Wulfsen, I.; Schoenrock, C.; Fehr, S.; Richter, D.
Proc. Natl. Acad. Sci. U.S.A. 89, 10267-10271, 1992
A:Title: Molecular cloning of a somatostatin-28 receptor and comparison of its expressio
A:Reference number: S30508; MUID:93066220; PMID:1279674
A:Accession: S30508
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-428 <MEY>
A:Cross-references: EMBL:X63574; NID:g56315; PIDN:CAA45130.1; PID:g56316
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 21.7%; Score 480.5; DB 2; Length 428;
Best Local Similarity 31.3%; Pred. No. 3.2e-32;
Matches 118; Conservative 73; Mismatches 143; Indels 43; Gaps 11;

QY 75 SLUPTGPNASNTSDG---PDNLTSGSPPRGTSISYINIMPSVEFTICLLGIGNSTVI 131
DB 8 SSVPTTLDPGNASSAWPLDTSIGNASAGTSLAGLAVSGILISLYLVVCVVGGLGNSLVI 67
QY 132 FAVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGV--WHFGETMCTLIT 189
DB 68 YVVLRRHTS---SPSVTSVYILNLALADELFMLGLPFLAAQ--NALSYWPFGLMGRLYM 121
QY 190 AMDANSQFTSTYIILTAMADRYLATVHPISSTFKRKPVSATLVICLLWALSFISITPVL 249

DB 122 AVDGINQFTSICLTVMASVDRYLAAVHPTRSARWRRTAPVARMVSAAVVASAVVLPVV 181
QY 250 YARLIPFPGAGVCGIRLPNPDITLYW--FTLYQFFLAFALPFVVTITAAVYRILQRM 306
DB 182 FSGV--PRGMSTCHMQWPEPAA--AWRTAFIITYAALGFEGDPLVICLCYLLIVKVR 236
QY 307 SV-----APASQSRIRLRKRVTRTAIAICLVFVCWAPYYVQLTQLSISRP 354
DB 237 TTRRVRAPSCQWQAPACQRR-RRSERVTRMVAVVALFVLCWMPFYLLNIVNVCP 295
QY 355 -TLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRK-----RLVLSVKPAAQGL 403
DB 296 EEPAFFGLYFLVVALPYANSCANPILYGFLSYRFKQGFRRILLRPSRRVRSQEPGSP 355
QY 404 RAVSNAQTADERTESK 420
DB 356 KTEEEDEEEERREE 372

Search completed: February 13, 2003, 14:01:06
Job time : 16.1596 secs

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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:50:36 ; Search time 13.7494 Seconds
(without alignments)
1273.004 Million cell updates/sec

Title: US-09-885-478-27
Perfect score: 2210
Sequence: 1 MSVGAKKGVGRAVGLGGGS.....LRVSNAGTADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1758	79.5	353	1 GP24_RAT	P97639 rattus norv
2	1696	76.7	402	1 GP24_HUMAN	Q99705 homo sapien
3	532	24.1	369	1 SSR2_MOUSE	P30875 mus musculu
4	530.5	24.0	369	1 SSR2_HUMAN	P30874 homo sapien
5	525	23.8	369	1 SSR2_RAT	P30680 rattus norv
6	524.5	23.7	369	1 SSR2_PIG	P34994 sus scrofa
7	523.5	23.7	368	1 SSR2_BOVIN	P34993 bos taurus
8	519	23.5	391	1 SSR1_HUMAN	P30872 homo sapien
9	513.5	23.2	388	1 SSR4_HUMAN	P31391 homo sapien
10	513	23.2	391	1 SSR1_MOUSE	P30873 mus musculu
11	504.5	22.8	418	1 SSR3_HUMAN	P32745 homo sapien
12	500	22.6	391	1 SSR1_RAT	P28646 rattus norv
13	494.5	22.4	384	1 SSR4_RAT	P30937 rattus norv
14	485	21.9	384	1 SSR4_MOUSE	P49660 mus musculu
15	480.5	21.7	428	1 SSR3_RAT	P30936 rattus norv
16	478.5	21.7	364	1 SSR5_HUMAN	P35346 homo sapien
17	472	21.4	428	1 SSR3_MOUSE	P30935 mus musculu
18	470.5	21.3	363	1 SSR5_RAT	P30938 rattus norv
19	458	20.7	401	1 OPRM_BOVIN	P79350 bos taurus
20	456	20.6	362	1 SSR5_MOUSE	O08858 mus musculu
21	453.5	20.5	398	1 OPRM_MOUSE	P42866 mus musculu
22	453	20.5	401	1 OPRM_PIG	O95247 sus scrofa
23	451.5	20.4	372	1 OPRD_HUMAN	P41143 homo sapien
24	451.5	20.4	398	1 OPRM_RAT	P33535 rattus norv
25	451	20.4	400	1 OPRM_MACMU	Q9myw9 macaca mula
26	450.5	20.4	372	1 OPRD_RAT	P33533 rattus norv
27	448	20.3	400	1 OPRM_HUMAN	P35372 homo sapien
28	443.5	20.1	372	1 OPRD_MOUSE	P32300 mus musculu
29	440.5	19.9	380	1 OPRK_HUMAN	P41145 homo sapien
30	432.5	19.6	380	1 OPRK_CAVPO	P41144 cavia porce
31	426	19.3	370	1 OPRX_CAVPO	P47748 cavia porce
32	420.5	19.0	380	1 OPRK_MOUSE	P33534 mus musculu
33	420	19.0	328	1 GPR7_HUMAN	P48145 homo sapien

34	419	19.0	380	1 OPRK_RAT	P34975 rattus norv
35	413	18.7	370	1 OPRX_HUMAN	P41146 homo sapien
36	410.5	18.6	367	1 OPRX_MOUSE	P35377 mus musculu
37	409.5	18.5	333	1 GPR8_HUMAN	P48146 homo sapien
38	409.5	18.5	367	1 OPRX_RAT	P35370 rattus norv
39	398	18.0	370	1 OPRX_PIG	P79292 sus scrofa
40	372.5	16.9	359	1 AG2R_CHICK	P79785 gallus gall
41	372.5	16.9	359	1 AG2R_MEIGA	P33396 meleagris g
42	370	16.7	363	1 AG2S_XENLA	P35373 xenopus lae
43	368	16.7	362	1 AG2R_XENLA	P32303 xenopus lae
44	359.5	16.3	352	1 P2Y7_HUMAN	O15722 homo sapien
45	350	15.8	353	1 CKR8_MOUSE	P56484 mus musculu

ALIGNMENTS

RESULT 1					
GP24_RAT					
ID	GP24_RAT	STANDARD;	PRT;	353 AA.	
AC	P97639;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Probable G protein-coupled receptor GPR24 (SLC-1).				
GN	GPR24 OR SLC1.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=98193144; PubMed=9531978;				
RA	Lakaye B., Minet A., Zorzi W., Grisar T.;				
RT	"Cloning of the rat brain cDNA encoding for the SLC-1 G protein-				
RT	coupled receptor reveals the presence of an intron in the gene.";				
RL	Biochim. Biophys. Acta 1401:216-220(1998).				
RN	[2]				
RP	SEQUENCE OF 143-300 FROM N.A.				
RX	MEDLINE=97131607; PubMed=8977118;				
RA	Kolakowski L.F. Jr., Jung B.P., Nguyen T., Johnson M.P., Lynch K.R.,				
RA	Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;				
RT	"Characterization of a human gene related to genes encoding				
RT	somatostatin receptors.";				
RL	FEBS Lett. 398:253-258(1996).				
CC	-1- FUNCTION: ORPHAN RECEPTOR. DOES NOT SEEM TO BIND TO SOMATOSTATIN.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	SIMILAR TO SOMATOSTATIN RECEPTORS.				
CC	-----				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AF008650; AAC27977.1; -				
DR	EMBL; U77953; AAC14588.1; -				
DR	InterPro; IPR000276; GPCR_Rhodpsn.				
DR	InterPro; IPR004047; MCH1receptor.				
DR	Pfam; PF00001; 7tm_1; 1.				
DR	PRINTS; PR00237; GPCR_RHODPSN.				
DR	PRINTS; PR01507; MCH1RECEPTOR.				
DR	PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; FALSE_NEG.				
DR	PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.				
KW	G-protein coupled receptor; Transmembrane.				
FT	DOMAIN 1 45				
FT	TRANSMEM 46 66				
FT	DOMAIN 67 79				
FT	TRANSMEM 80 100				
FT	EXTRACELLULAR (POTENTIAL).				
FT	CYTOPLASMIC (POTENTIAL).				
FT	2 (POTENTIAL).				

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FT DOMAIN 101 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 139 3 (POTENTIAL).
FT DOMAIN 140 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 182 4 (POTENTIAL).
FT DOMAIN 183 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 225 5 (POTENTIAL).
FT DOMAIN 226 256 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 277 6 (POTENTIAL).
FT DOMAIN 278 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 315 7 (POTENTIAL).
FT DOMAIN 316 353 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 353 AA; 39063 MW; F6EEB2DF381084A9 CRC64;

Query Match 79.5%; Score 1758; DB 1; length 353;
Best Local Similarity 96.0%; Pred. No. 4e-91;
Matches 338; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 71 DLEASLLPTGNASNTSDGPDNLTSAGSPPTGSGISYINIMPSVFGTICLLGIGNSTV 130
||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 DLQTSLLSTGNASNISDGQDNLTLPSSPPRTGVSYSINIMPSVFGTICLLGIVGNSIV 61

QY 131 IFAVVKSSKLMHCNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLITA 190
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 IFAVVKSSKLMHCNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHFGETMCTLITA 121

QY 191 MDANSQFTSTYLLTAMADRYLATVHPISSTKFKRPSVATLVICLMAISFISITPWLY 250
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 MDANSQFTSTYLLTAMTIDRYLATVHPISSTKFKRPSMATLVICLMAISFISITPWLY 181

QY 251 ARLIPEPGAVGCGIRLPNDTDLXWFTLYQFELAFALPFVVTAAVRILOMTSSVAP 310
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 ARLIPEPGAVGCGIRLPNDTDLXWFTLYQFELAFALPFVVTAAVRILOMTSSVAP 241

QY 311 ASQSRIRLTKRVTRTAIAICLVFVCWAPYVYLQTLQSLISRPITLFFVYLYNNAISLGY 370
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 ASQSRIRLTKRVTRTAIAICLVFVCWAPYVYLQTLQSLISRPITLFFVYLYNNAISLGY 301

QY 371 ANSCLNPFVYIVLCETFRKRRLVSVKPAAGQLRAVSNAGTADERTESKGT 422
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 ANSCLNPFVYIVLCETFRKRRLVSVKPAAGQLRTVSNAGTADERTESKGT 353

RESULT 2
GP24_HUMAN STANDARD; PRT; 402 AA.
ID GP24_HUMAN
AC Q99705;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor GPR24 (SLC-1).
GN GPR24 OR SLC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
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RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclell J., McLaren S., McMuray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., MitsuYama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shaikh T., Kurahashi H., Saita S., Budarf M.L.,
RA Mcdermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edlmann L.,
RA Kim U.J., Shizuya H., Simon M.I., Dumaniski J.P., Peyrard M., Kedra D.,
RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tilahun Y., Wright H.,
RT "The DNA sequence of human chromosome 22." ;
RL Nature 402:489-495(1999).
CC -!- FUNCTION: ORPHAN RECEPTOR. DOES NOT SEEM TO BIND TO SOMATOSTATIN.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: GREATEST ABUNDANCE IN BRAIN, PARTICULARLY IN
CC THE FRONTAL CORTEX AND HYPOTHALAMUS. A LOWER LEVEL EXPRESSION IS
CC SEEN IN THE LIVER AND HEART.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC SIMILAR TO SOMATOSTATIN RECEPTORS.
CC -----
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CC -----
CC EMBL; U71092; AAC14587.1; -
CC EMBL; Z86090; CAB62943.1; -
CC Genew; HGNC:4479; GPR24.
CC MIM; 601751; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC InterPro; IPR004047; MCH1receptor.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCR_RHODOPSIN.
CC PRINTS; PR01507; MCH1RECEPTOR.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR.
CC PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane.
CC DOMAIN 1 94
CC TRANSMEM 95 115 1 (POTENTIAL).
CC DOMAIN 116 128 2 (POTENTIAL).
CC TRANSMEM 129 149 2 (POTENTIAL).
CC DOMAIN 150 167 3 (POTENTIAL).
CC TRANSMEM 168 188 3 (POTENTIAL).
CC DOMAIN 189 210 4 (POTENTIAL).
CC TRANSMEM 211 231 4 (POTENTIAL).
CC DOMAIN 232 253 EXTRACELLULAR (POTENTIAL).
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FT	TRANSMEM	254	274	5 (POTENTIAL).
FT	DOMAIN	275	305	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	306	326	6 (POTENTIAL).
FT	DOMAIN	327	343	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	344	364	7 (POTENTIAL).
FT	DOMAIN	365	402	CYTOPLASMIC (POTENTIAL).
SO	SEQUENCE	402 AA;	44454 MW;	5D24B72E76CF4F82 CRC64;

Query Match	76.7%;	Score 1696;	DB 1;	Length 402;
Best Local Similarity	83.2%;	Pred. No. 1.2e-87;		
Matches 341;	Conservative	7;	Mismatches 14;	Indels 48;
				Gaps 4;

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QY 50 PAWVEGS--SARLMEQATGTGMADLEASLLPTGPNASNTSDGPDN----- 92
      1:  :||  |  :  :  |  |  |
Db 4 PSKTDGSGHSGRIHQETHGEKKRD-----KISN-SEGRENGGGRFQMNGGSLAE 52
      93 -----LTSAGSPRTGSIYINIMPSVEGTICLLGIIGNSTVIIF 132
      53 HASRMSVLRAPMSNSQORLLLSPGSPRTGISISYINIMPSVEGTICLLGIIGNSTVIIF 112
QY 133 AVVKKSKLHWCNNVPDIFIINLSVVDLLELLGMPFMIHQLMGNGVWHFGETMCTLLTAMD 192
      |||||||
Db 113 AVVKKSKLHWCNNVPDIFIINLSVVDLLELLGMPFMIHQLMGNGVWHFGETMCTLLTAMD 172
      |||||||
QY 193 ANSQFTSTYILTAMAIIDRYLATVHPISSTKERRKPSVATLVICLLMAISFISITPWWLYAR 252
      |||||||
Db 173 ANSQFTSTYILTAMAIIDRYLATVHPISSTKERRKPSVATLVICLLMAISFISITPWWLYAR 232
      |||||||
QY 253 LIPEFGAGVGCGIRLPNPDIDLWFTLLYQFELAFALPEVVIITAAVYRILQRMSTSSVAPAS 312
      |||||||
Db 233 LIPEFGAGVGCGIRLPNPDIDLWFTLLYQFELAFALPEVVIITAAVYRILQRMSTSSVAPAS 292
      |||||||
QY 313 QRSIRLRTKRVRTAIAIACLVFEVCWADPYVVLQTLQLSISRPLTLFVYLYNNAISLGAN 372
      |||||||
Db 293 QRSIRLRTKRVRTAIAIACLVFEVCWADPYVVLQTLQLSISRPLTLFVYLYNNAISLGAN 352
      |||||||
QY 373 SCLNPFVYIYLCETFRKRLVLSVKKPAAGQLRAVSNMAQTADERTESKGT 422
      |||||||
Db 353 SCLNPFVYIYLCETFRKRLVLSVKKPAAGQLRAVSNMAQTADERTESKGT 402

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RESULT 3
SSR2_MOUSE
ID      SSR2_MOUSE      STANDARD;      PRT;      369 AA.
AC      P30875; P30934;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, last sequence update)
DT      15-JUN-2002 (Rel. 41, last annotation update)
DE      Somatostatin receptor type 2 (SS2R) (SRIF-1) (SS2RA and SS2RB) .
GN      SS2R2 OR SMSTR2.
OS      Mus musculus (Mouse) .
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92108031; PubMed=1346068;
RA      Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;
RT      "Cloning and functional characterization of a family of human and
RT      mouse somatostatin receptors expressed in brain, gastrointestinal
RT      tract, and kidney.";
RL      Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93012001; PubMed=1397330;
RA      Vanetti M., Kouba M., Wang X., Vogt G., Hoellt V.;
RT      "Cloning and expression of a novel mouse somatostatin receptor
RT      (SS2RB)." ;
RL      FEBS Lett. 311:290-294(1992).
RN      [3]
RP      SEQUENCE OF 99-309 FROM N.A.
RX      MEDLINE=94300079; PubMed=7913111;
RA      Elliott D.E., Metwalli A., Blum A.M., Sandor M., Lynch R.,

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RA Weinstock J.V.;
RT "T lymphocytes isolated from the hepatic granulomas of schistosoma-
RT infected mice express somatostatin receptor subtype II (sstr2)
RT messenger RNA.";
RL J. Immunol. 153:1180-1186(1994).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=93387480; PubMed=8104154;
RA Vanetti M., Hoellt V.;
RT "The two isoforms of the mouse somatostatin receptor (mstr2a and
RT mstr2b) differ in coupling efficiency to adenylate cyclase and in
RT agonist-induced receptor desensitization.";
RL FEBS Lett. 331:260-266(1993).
CC -I- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
CC PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CC CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC -I- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (By
CC similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SS2RA (SHOWN HERE) AND SS2RB;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -I- TISSUE SPECIFICITY: CEREBRUM AND KIDNEY.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC
DR EMBL; M81832; AAA58256.1; -.
DR EMBL; X68951; CAA48766.1; -.
DR EMBL; S71756; -; NOT_ANNOTATED_CDS.
DR PIR; D41795; D41795.
DR PIR; S29248; S29248.
DR HSSP; P02699; IBOJ.
DR MGD; MGI:98328; Smstr2.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate; Alternative splicing.
KW DOMAIN 1 43
FT TRANSMEM 44 67
FT DOMAIN 68 78
FT TRANSMEM 79 103
FT DOMAIN 104 118
FT TRANSMEM 119 138
FT DOMAIN 139 161
FT TRANSMEM 162 181
FT DOMAIN 182 207
FT TRANSMEM 208 229
FT DOMAIN 230 253
FT TRANSMEM 254 278
FT DOMAIN 279 288
FT TRANSMEM 289 303
FT DOMAIN 304 369
FT CARBOHYD 9 9
FT CARBOHYD 22 22
FT CARBOHYD 29 29
FT CARBOHYD 32 32
FT DISULFID 115 193
FT LIPID 328 328
FT VARSPPLIC 332 369
FT CONFLICT 179 179
FT I -> I (IN REF. 2).

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FT CONFLICT 305 305 S -> T (IN REF. 2).
SQ SEQUENCE 369 AA; 41221 MW; A78845AF74823039 CRC64;
Query Match 24.1%; Score 532; DB 1; Length 369;
Best Local Similarity 31.7%; Pred. No. 3.4e-23;
Matches 118; Conservative 76; Mismatches 132; Indels 46; Gaps 10;
QY 62 EQATGTG-WA---DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVF 116
Db 6 EQLNGSOYVWSSPFDLNGSLGPS--NGSNQTEPYDMTS-----NAVLTFIY 50
QY 117 GTICLLGIIGNSTVIFAIVKSKLHWCNNVPDIFINLSVDDLFLGMPF-----MIH 170
Db 51 FVVCYVGLCGNTLVIVILRYAKM--KTITNITLNLAIADLFMLGLPFLAMQVALVH 107
QY 171 QLMNGVWHFGETMCTLTITAMDANSQFTSTYILTAMADRYLATVHPISSTKRRKPSVAT 230
Db 108 -----WPFGKAICRVVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRPRPTAK 160
QY 231 LVICLLMALSFISITPVMWLYARLIPPGAVGCGIRLPNDTDLY-WFTLYQFLAFLP 289
Db 161 MINVAVWCYSLVLVLPIMIVAGLSNQWRSSCTINWPGESGAWYTGFIYAFILGLVP 220
QY 290 FVVITAAVYRILQRMTSVAPASQSRIRLRTKRVTRTAICLVEFVCWAPYVYLQTL 349
Db 221 LTITCLCYLFIILIKVSSGIRVSSKRKKSEKVTBMVSIVAVEIFCWLPEYIFNVSSV 280
QY 350 SIS-RPTLTFVYLYNNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSN 408
Db 281 SVAISPPTALKGMFDEVILTYANSCANPILYAFLSDNFKK-----SFQNVLCIVKY 332
QY 409 AQTADERTESK 420
Db 333 SGTEDGERSDSK 344
RESULT 4
SSR2_HUMAN
ID SSR2_HUMAN STANDARD; PRT; 369 AA.
AC P30874;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor type 2 (SS2R) (SRIF-1).
GN SSR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92108031; PubMed=1346068;
RA Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;
RT "Cloning and functional characterization of a family of human and
RT mouse somatostatin receptors expressed in brain, gastrointestinal
RT tract, and kidney."
RL Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=93236586; PubMed=8386508;
RA Patel Y.C., Greenwood M., Kent G., Panetta R., Srikanth C.B.;
RT "Multiple gene transcripts of the somatostatin receptor SSR2: tissue
RT selective distribution and cAMP regulation."
RL Biochem. Biophys. Res. Commun. 192:288-294(1993).
RN [3]
RP INTERACTION WITH SHANK1.
RX MEDLINE=20020275; PubMed=10551867;
RA Zitzer H., Hoenck H.-H., Baechner D., Richter D., Kreienkamp H.-J.;
RT "Somatostatin receptor interacting protein defines a novel family of
RT multidomain proteins present in human and rodent brain."
RL J. Biol. Chem. 274:32997-33001(1999).
CC -!- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF

CC ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
CC PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CC CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC -!- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: CEREBRUM AND KIDNEY. IN LESSER AMOUNTS IN
CC JEJUNUM, COLON, AND LIVER.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL; M81830; AAA58248.1; -.
CC PIR; B41795; B41795.
CC HSSP; P02699; IBOJ.
CC Genew; HGNC:11331; SSR2.
CC MIM; 182452; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_RHODOPSIN.
CC PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; 1.
CC DR PROSITE; PS50262; G_PROTEIN_RECPE_F1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family; Lipoprotein; Palmitate; Alternative splicing.
FT DOMAIN 1 43
FT TRANSMEM 44 67
FT DOMAIN 68 78
FT TRANSMEM 79 103
FT DOMAIN 104 118
FT TRANSMEM 119 138
FT DOMAIN 139 161
FT TRANSMEM 162 181
FT DOMAIN 182 207
FT TRANSMEM 208 229
FT DOMAIN 230 253
FT TRANSMEM 254 278
FT DOMAIN 279 288
FT TRANSMEM 289 303
FT DOMAIN 304 369
FT CARBOHYD 9 9
FT CARBOHYD 22 22
FT CARBOHYD 29 29
FT CARBOHYD 32 32
FT DISULFID 115 193
FT LIPID 328 328
FT VARSPLIC 332 369
SQ SEQUENCE 369 AA; 41332 MW; 3B5D7D8A9AC246C6 CRC64;
Query Match 24.0%; Score 530.5; DB 1; Length 369;
Best Local Similarity 31.8%; Pred. No. 4.2e-23;
Matches 114; Conservative 75; Mismatches 128; Indels 41; Gaps 8;
QY 71 DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVGTICLLGIIGNSTV 130
Db 20 DLNGSVYST--NTSNQTEPYDULTS-----NAVLTFIYFVVCILGCGNTLV 64
QY 131 IEAVVKKSKLHWCNNVPDIFINLSVDDLFLGMPF-----MIHQLMGVWHFGETM 184
Db 65 IYVILRYAKM--KTITNITLNLAIADLFMLGLPFLAMQVALVH-----WPFGKAI 114
QY 185 CTLITAMDANSQFTSTYILTAMADRYLATVHPISSTKRRKPSVATLVICLLMALSFISI 244
Db 115 CRVVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRPRPTAKMITMAVWGVSLLVI 174

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QY    245 TPVWLYARLIPPGGAVCGCIRLPNDPTDLY-WETLIYQFFLAFLPFVVITAAVRILOR 303
      | : ||| |   |   |   |   |   |   |   |   |   |   |   |   |   | : :
Db    175 LPIMIYAGLRSNOWGNSSCTINWPGESGAWMTGTFTTYTIFLGVLPLTTICLCYEFTIK 234

QY    304 MTSSVPASQRSLRLTKRVTRTAIAICLVFEVCWADPYVLQLTOLIS-RPITIIFYLY 362
      : | | : ||| |   | : ||| |   | | | | : | : : : : | : :
Db    235 VKSSGIRVGSSKRKKSEKKTVMVSIVAVAFIEFCMLPEYIFNVSVSMAISPFBALKGWF 294
      : : | |||| | : | : | : | : | : | : | : | : | : | : | : | : | :
      295 DFVVLLTYANSCANPIIYAFLSDNFKF-----SFQNVLCIVKVSGTDGERDSK 344

RESULT 5
SSR2_RAT
ID     SSR2_RAT           STANDARD;          PRT;       369 AA.
AC     P30680;
DT     01-APR-1993 (Rel. 25, Created)
DT     01-APR-1993 (Rel. 25, last sequence update)
DT     15-JUN-2002 (Rel. 41, last annotation update)
DE     Somatostatin receptor type 2 (SS2R) (SRIF-1).
GN     SSTR2.
OS     Rattus norvegicus (Rat).
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN     NCBI_TaxId=10116;
      [1]
RP     SEQUENCE FROM N.A.
RC     TISSUE=Brain;
RX     MEDLINE=92262491; Pubmed=1374909;
RA     Kluxen F.-W., Bruns C., Luebbert H.;
RT     "Expression cloning of a rat brain somatostatin receptor cDNA.";
RL     Proc. Natl. Acad. Sci. U.S.A. 89:4618-4622(1992).
      [2]
RP     SEQUENCE OF 76-81; 179-189; 294-320 AND 350-358.
RC     TISSUE=pituitary;
RX     MEDLINE=92231915; Pubmed=1348934;
RA     Hulmes J.D., Corbett M., Zysk J.R., Boehlen P., Eppler C.M.;
RT     "Partial amino acid sequence of a somatostatin receptor isolated from
      RL     GH4Cl pituitary cells.";
      Biochem. Biophys. Res. Commun. 184:131-136(1992).
      [3]
RP     ALTERNATIVE SPLICING.
RX     MEDLINE=93236586; Pubmed=8386508;
RA     Patel Y.C., Greenwood M., Kent G., Panetta R., Srikanth C.B.;
RT     "Multiple gene transcripts of the somatostatin receptor SSTR2: tissue
      RT     selective distribution and CAMP regulation.";
      Biochem. Biophys. Res. Commun. 192:288-294(1993).
      -|- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
      CC     COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
      CC     ADENYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSIENE
      CC     PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSSENSITIVE AS WELL AS
      CC     SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
      CC     CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
      CC     -|- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (by
      CC     similarity).
      CC     -|- SUBCELLULAR LOCATION: Integral membrane protein.
      CC     -|- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
      CC     PRODUCED BY ALTERNATIVE SPLICING.
      CC     -|- TISSUE SPECIFICITY: CORTEX, HIPPOCAMBUS, PITUITARY GLAND, COLON
      CC     ADRENALS, PANCREAS-DERIVED CELL LINE, AND PANCREATIC TUMOR.
      CC     -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
      CC     -----
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      CC     or send an email to license@isb-sib.ch).
      -----
DR     EMBL; M96817; AAAA2166.1; -.
DR     EMBL; M93273; AAAA2165.1; -.

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[illegible]


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DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Somatostatin receptor type 2 (SS2R) (SRIF-1).
GN STR2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
ON NCBI_TaxID=9823;
RX MEDLINE=94168590; PubMed=8123027;
RA Matsumoto K., Yokogoshi Y., Fujinaka Y., Zhang C., Saito S.;
RT "Molecular cloning and sequencing of porcine somatostatin receptor
  2."
RL Biochem. Biophys. Res. Commun. 199;298-305(1994).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLATE CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
CC PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CC CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC -1- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D21338; BAA04810.1; -.
DR PIR: JC2083; JC2083.
DR HSSP: P02699; IBOJ.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 67 1 (POTENTIAL).
FT DOMAIN 68 78 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 79 103 2 (POTENTIAL).
FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 138 3 (POTENTIAL).
FT DOMAIN 139 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 181 4 (POTENTIAL).
FT DOMAIN 182 207 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 208 229 5 (POTENTIAL).
FT DOMAIN 230 253 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 254 278 6 (POTENTIAL).
FT DOMAIN 279 288 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 289 303 7 (POTENTIAL).
FT DOMAIN 304 369 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 9 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 115 193 BY SIMILARITY.
FT LIPID 328 PALMITATE (POTENTIAL).
SQ SEQUENCE 369 AA; 41218 MW; C4C8347764EA2E70 CRC64;

Query Match 23.7%; Score 524.5; DB 1; Length 369;
Best Local Similarity 31.6%; Pred. No. 8.9e-23;
Matches 113; Conservative 75; Mismatches 129; Indels 41; Gaps 8;
OY 71 DLEASLLPTGPNASNTSDGPDNLTSAGSPRTGISIYINIIIMPVFGTCLLGIIGNSTV 130
  |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 20 DLNGSVATA--NSSNQTEPYDLTS-----NAVLFTFYFVVCIIIGLCGNTLV 64

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[illegible]

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RESULT 7
SSR2__BOVIN          STANDARD;          PRT;          368 AA.
ID      SSR2_BOVIN
AC      P34993;
DT      01-FEB-1994 (Rel. 28, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Somatostatin receptor type 2 (SS2R) (SRIF-1).
GN      SSTR2.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      Xin W.W., Wong M.-L., Rumlund J., Nestler E.J., Duman R.S.;
RL      Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
CC      -|- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC      COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC      ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
CC      PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC      SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CC      CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC      -|- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (By
CC      similarity).
CC      -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; L06613; AAA30764.1; -.
DR      HSSP; P02699; LBOJ.
DR      InterPro; IPR000276; GPCR_Rhodpsn.
DR      pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRHRDOPSN.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein;
KW      Multigene family; Lipoprotein; Palmitate.
FT      DOMAIN          1          42      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM          43          66      1 (POTENTIAL).
FT      DOMAIN          67          77      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM          78          102      2 (POTENTIAL).

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FT	DOMAIN	103	117	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	118	137	3 (POTENTIAL).
FT	DOMAIN	138	160	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	161	180	4 (POTENTIAL).
FT	DOMAIN	181	206	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	207	228	5 (POTENTIAL).
FT	DOMAIN	229	252	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	253	277	6 (POTENTIAL).
FT	DOMAIN	278	287	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	288	302	7 (POTENTIAL).
FT	DOMAIN	303	368	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	8	8	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	21	21	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	28	28	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	31	31	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	114	192	BY SIMILARITY.
FT	LIPID	327	327	PALMITATE (POTENTIAL).
SQ	SEQUENCE	368 AA;	41133 MW;	B5852262A6BB080B CRC64;

Query Match	23.7%;	Score 523.5;	DB 1;	Length 368;
Best Local Similarity	31.6%;	Pred. No. 1e-22;		
Matches 112; Conservative	74;	Mismatches 131;	Indels 37;	Gaps 8;

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QY      79 TGPNASNETDEGPDNLTSAGSPRTGISISYI---NIMDSVEGTICLLGIIGNSTVIEAV 134
        | | | | | : : : | | : : : : : : : : : : : : : : : : : : : : : : : :
Db      15 TTPFDLNGSVGANISNOTEP-----YYDLASNVLTFIFYFVCIIIGLCGNLTVIYVI 67

QY      135 VKKSKLHMCNNVPDIFIINLSVVDLEFLGMPE----MIHQLMGNGVWHFGTMTCTLI 188
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      68 LRYAKM--KTITNIYIILMAIDELFMLGLPFAMQVALDH-----WPEGKAICRVV 117

QY      189 TAMDANSOFTSTVILTAMAIIDRYLATVHPISSTKERKPSVATLVICLLMALSFISTIPWV 248
        : | : | | : | | : | | | | | | | | | | : : : : : : : : : : : : : :
Db      118 MTVDDINGOFTSIFCLTWMSIDRYLAHVPHIKSAKWRRPRAKMINVAWGVSLVLIPIM 177

QY      249 LYARLIPEPGCAVGCGIRLPNDPDLX-WFTLYQEFALAPFEVVITAAYVRILQMSTSS 307
        : | | | | | | | | | | | | | | | | | | | | | | : : : : : : : : : :
Db      178 IYAGLRSNQWRSSSCTINWPGESGAWYTGFIIYAFIGLVLPLTIICLCYLFILTKVKS 237

QY      308 VAPASQSRIRLTKRVRTAIAICLVEFCWAPRYVLQLTQLSIS-RPTLTFVLYLNAAI 366
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      238 GIRVGSSKKRKSEKKVTBMVSIVAVFIQCWLPIYIFNVSSVSVAISPALKMGHDFV 297

QY      367 SLGYANSCINPEVYIVLCETFRKRRLVLSVKPAOGQLRAVNAQTADERTESK 420
        | | | | | | | | | | : : : : : : : : : : : : : : : : : : : : : : : :
Db      298 VLTYSANCANPLIYAFLSDNEFK-----SFQNVLCIAKVSGTDGERSDSK 343
```

RESULT 8	
SSR1_HUMAN	
ID	SSR1_HUMAN
STANDARD;	PRT;
	391 AA.

DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Somatostatin receptor type 1 (SSTR) (SRIF-2).
GN SSTR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92108031; PubMed=1346068;
RA Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Selino S.;
RT "Cloning and functional characterization of a family of human and
RT mouse somatostatin receptors expressed in brain, gastrointestinal
tract, and kidney.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR
CC SOMATOSTATIN-14 THAN -28. THIS RECEPTOR IS COUPLED VIA PERTUSSIS
CC TOXIN SENSITIVE G PROTEINS TO INHIBITION OF ADENYLYL CYCLASE. IN
CC ADDITION IT STIMULATES PHOSPHOTYROSINE PHOSPHATASE AND NA+/H+
CC

```

CC EXCHANGER VIA PERTUSSIS TOXIN INSENSITIVE G PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: FETAL KIDNEY, FETAL LIVER, AND ADULT PANCREAS,
CC BRAIN, LUNG, JEJUNUM, AND STOMACH.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M81829; AAA58247.1; -.
CC PIR; A41795; A41795.
CC Genew; HGNC:11330; SSTR1.
CC MIM; 182451; -.
CC DR InterPro; IPR000276; GPCR_Rhodpsn.
CC DR Pfam; PR00001; 7tm_1; 1.
CC DR PRINTS; PR00237; GPCR_RHODPSN.
CC DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
CC DR PROSITE; PS0262; G_PROTEIN_REC_P1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family; Lipoprotein; Palmitate.
CC KW DOMAIN 1 56 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 57 84 1 (POTENTIAL).
CC FT DOMAIN 85 94 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 95 120 2 (POTENTIAL).
CC FT DOMAIN 121 131 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 132 153 3 (POTENTIAL).
CC FT DOMAIN 154 175 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 176 196 4 (POTENTIAL).
CC FT DOMAIN 197 219 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 220 244 5 (POTENTIAL).
CC FT DOMAIN 245 270 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 271 296 6 (POTENTIAL).
CC FT DOMAIN 297 303 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 304 327 7 (POTENTIAL).
CC FT DOMAIN 328 391 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT DISULFID 130 208 BY SIMILARITY.
CC FT LIPID 339 339 PALMITATE (POTENTIAL).
CC SEQUENCE 391 AA; 42686 MW; 85C99AFFF339A43D CRC64;

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[illegible]

Db 274 MMVWVEVICMMPFYVQLVNVEAQDDATVSQ_L---SVILGYANSCANPILYGLSDNF 330
OY 388 RK 389
Db 331 KR 332

RESULT 9

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SSR4_HUMAN          STANDARD;          PRT;          388 AA.
ID   SSR4_HUMAN
AC   P31391; Q9UIY1;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Somatostatin receptor type 4 (SS4R).
GN   SSR4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;

[1]
RN   RP
RP   MEDLINE=93290656; PubMed=8512564;
RX   Xu Y., Song J., Bruno J.F., Berelowitz M.;
RT   "Molecular cloning and sequencing of a human somatostatin receptor,
RT   hsstr4."
RL   Biochem. Biophys. Res. Commun. 193:648-652(1993).

[2]
RN   RP
RP   MEDLINE=93248256; PubMed=8483934;
RX   Rohrer L., Raulf F., Bruns C., Buettner R., Hofstaedter F.,
RT   Schuele R.;
RT   "Cloning and characterization of a fourth human somatostatin
RT   receptor."
RL   Proc. Natl. Acad. Sci. U.S.A. 90:4196-4200(1993).

[3]
RN   RP
RP   MEDLINE=93384611; PubMed=8373420;
RX   Yamada Y., Kagimoto S., Kubota A., Yasuda K., Masuda K., Someya Y.,
RT   Ihara Y., Li Q., Imura H., Seino S., Seino Y.;
RT   "Cloning, functional expression and pharmacological characterization
RT   of a fourth (hsstr4) and a fifth (hsstr5) human somatostatin receptor
RT   subtype."
RL   Biochem. Biophys. Res. Commun. 195:844-852(1993).

[4]
RN   RP
RP   MEDLINE=93302729; PubMed=8100352;
RX   Demchyshyn L.L., Srikant C.B., Sunahara R.K., Kent G., Seeman P.,
RT   van Tol H.H.M., Panetta R., Patel Y.C., Niznik H.B.;
RT   "Cloning and expression of a human somatostatin-14-selective receptor
RT   variant (somatostatin receptor 4) located on chromosome 20."
RL   Mol. Pharmacol. 43:894-901(1993).

[5]
RN   RP
RP   MEDLINE=21638749; PubMed=11780052;
RX   Deloukas P., Mathews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RT   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RT   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RT   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RT   Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RT   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RT   Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RT   Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RT   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RT   Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
RT   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RT   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RT   Kay M.P., Kimberley A.M., King A., Knights K., Laird G.K., Lawlor S.,
RT   Lehtvasialho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RT   Marsh V.L., Martin S.L., McConnachie L.J., McIay K., McMurray A.A.,
RT   Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RT   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.L.,
RT   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
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RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Wittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20."
RL   Nature 414:865-871(2001).
CC   -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS
CC   RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
CC   CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF
CC   ADENYLYL CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE
CC   RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
CC   MEDIATES ANTIPROLIFERATIVE ACTION OF SOMATOSTATIN IN TUMOR CELLS.
CC   -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN FETAL AND ADULT
CC   BRAIN, LUNG TISSUE, STOMACH, AND IN LESSER QUANTITIES IN THE
CC   KIDNEY, PITUITARY, AND ADRENALS.
CC   -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   -----
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; D16826; BAA04106.1; -.
DR   EMBL; L14856; AAA36623.1; -.
DR   EMBL; L07833; AAA60565.1; -.
DR   EMBL; L07061; -; NOT ANNOTATED_CDS.
DR   EMBL; AL049651; CAB51953.1; -.
DR   PIR; JN0605; JN0605.
DR   PIR; JN0762; JN0762.
DR   HSSP; P02699; 1BOJ.
DR   Genew; HGNC:11333; SSTR4.
DR   MIM; 182454; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRHOPOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Lipoprotein; Palmitate; Phosphorylation;
KW   Polymorphism.
KW   DOMAIN
FT   1 46 EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM 47 73 1 (POTENTIAL).
FT   DOMAIN 74 83 CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM 84 104 2 (POTENTIAL).
FT   DOMAIN 105 120 EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM 121 142 3 (POTENTIAL).
FT   DOMAIN 143 161 CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM 162 185 4 (POTENTIAL).
FT   DOMAIN 186 208 EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM 209 232 5 (POTENTIAL).
FT   DOMAIN 233 260 CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM 261 280 6 (POTENTIAL).
FT   DOMAIN 281 291 7 (POTENTIAL).
FT   TRANSMEM 292 314 EXTRACELLULAR (POTENTIAL).
FT   DOMAIN 315 388 7 (POTENTIAL).
FT   CARBOHYD 24 24 CYTOPLASMIC (POTENTIAL).
FT   DISULFID 119 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   LIPID 327 327 PALMITATE (POTENTIAL).
FT   VARIANT 83 83 /FTID=VAR_011703.
FT   CONFLICT 284 284 V -> F (IN REF. 4 AND 5).
FT   CONFLICT 321 321 S -> F (IN REF. 5).
FT   CONFLICT 365 365 P -> K (IN REF. 2).
SQ   SEQUENCE 388 AA; 41894 MW; 8BCDC69B5F3BC2F5 CRC64;
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Query Match

23.2%; Score 513.5; DB 1; Length 388;

RX MEDLINE=93149123; PubMed=1337145; Ihara Y., Kubota A., Kagimoto S.,
RA Yamada Y., Reisine T., Law S.F.,
RA Sano M., Sano Y., Bell G.I., Sano S.;
RT "Somatostatin receptors, an expanding gene family: cloning and
RT functional characterization of human SSTR3, a protein coupled to
RT adenylyl cyclase.";
RL Mol. Endocrinol. 6:2136-2142(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93238970; PubMed=8097479;
RA Corness J.D., Demchyshyn L.L., Seeman P., van Tol H.H.M.,
RA Srikant C.B., Kent G., Patel Y.C., Niznik H.B.;
RT "A human somatostatin receptor (SSTR3), located on chromosome 22,
RT displays preferential affinity for somatostatin-14 like peptides.";
RL FEBS Lett. 321:279-284(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiwich R., Beare D.M.,
RA Clamp M., Smink L.J., Alnscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burdill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grahm D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Mala J.E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier A., Mardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shaikh T., Kurahashi H., Salita S., Budarf M.L.,
RA Mcdermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tlahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
CC -!- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: BRAIN, PITUITARY AND PANCREAS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; M96738; AAA60592.1; -;
DR EMBL; 282188; CAB45263.1; -;
DR PIR; S32501; S32501.
DR PIR; A46226; A46226.
DR HSSP; P34996; 1DD.
DR Genew; HGNC:11332; SSTR3.
DR MIM; 182453; -;
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Polymorphism.
KW DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 69 1 (POTENTIAL).
FT DOMAIN 70 79 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 80 101 2 (POTENTIAL).
FT DOMAIN 102 116 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 117 138 3 (POTENTIAL).
FT DOMAIN 139 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 181 4 (POTENTIAL).
FT DOMAIN 182 205 5 (POTENTIAL).
FT TRANSMEM 206 231 6 (POTENTIAL).
FT DOMAIN 232 257 7 (POTENTIAL).
FT TRANSMEM 258 279 8 (POTENTIAL).
FT DOMAIN 280 293 9 (POTENTIAL).
FT TRANSMEM 294 316 10 (POTENTIAL).
FT DOMAIN 317 418 11 (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 116 191 BY SIMILARITY.
FT DOMAIN 346 360 GLU-RICH (ACIDIC).
FT VARIANT 411 411 S->T (IN DBSNP:229568).
FT SQ SEQUENCE 418 AA; 45847 MW; 1227095F801190C4 CRC64;
Query Match 22.8%; Score 504.5; DB 1; Length 418;
Best Local Similarity 32.5%; Pred. No. 1.3e-21;
Matches 118; Conservative 76; Mismatches 134; Indels 35; Gaps 11;
QY 81 PNASNTSDGPDNLTASGSP-----PRTSISYINIMPSVFGTICLIGNSTV 130
DB 6 PSSVSTSEPENASSAWPPDATLGNVSAGSPAGLAVSGVLLPLVLYVVCVGLGNSLV 65
QY 131 IFAYVKKSKLHWCNNVPDIFINLSVDDLFLGMPFMHQMGNGV--WHFGETMCTLI 188
DB 66 IYVVLRHFA---SPSVTVNYILNLADLEFLMLGLPFLAQ---NALSYWFGSLMCRLV 119
QY 189 TAMDANSQFTSTYILFTAMAIDRYLATVHPISSTKFRKPSVATLVICLMLALSFISTPFW 248
DB 120 MAVDGINQFTSIFCLTMSVDRLAVVHPTRSARWRTPAVRTVSAAVWVASAVVLPVV 179
QY 249 LYARLPPFGAGVCGIRLPNPDLDLXW---FTLYQFLAFALPFVITAAYVRILQRMF 305
DB 180 VFSGV---PRGMSSTCHMQWPEPA--AMRAGFIITYAALGFRGPLLVICLCYLLIVKVR 234
QY 306 SS---VAPASQSRIRLRTKRVTRFAAICLVFVCWAPRYVQLTOLISRP-TLTFVY 360
DB 235 SAGRVRWAPSCQRR-RRSERATRVAVVAVLFLCWMPEFYLVNIVNVCPPLPEEPARFG 293
QY 361 LYNAISLIGVANSCLNPFVYIVLCETFR---KRLVLSVKPAAGQLRAVSNAGTADERT 417
DB 294 LYFLVVALPFRVANSCLNPFVYIVLCETFR---KRLVLSVKPAAGQLRAVSNAGTADERT 353
QY 418 ESK 420
DB 354 EEE 356

RESULT 12			
ID	SSRL_RAT	STANDARD;	PRT; 391 AA.
AC	P28646;		
DT	01-DEC-1992 (Rel. 24, Created)		
DT	01-DEC-1992 (Rel. 24, Last sequence update)		
DT	01-FEB-1996 (Rel. 33, Last annotation update)		
DE	Somatostatin receptor type 1 (SS1R) (SRIF-2).		
GN	SSRL.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxId=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Wistar; TISSUE=Brain;		
RX	MEDLINE=92096119; PubMed=1661599;		
RA	Meyerhof W., Paust H.J., Schoenrock C., Richter D.;		
RT	"Cloning of a cDNA encoding a novel putative G-protein-coupled		
RT	receptor expressed in specific rat brain regions.";		
RL	DNA Cell Biol. 10:689-694(1991).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=93016064; PubMed=1400442;		
RA	Li X.-J., Forte M., North R.A., Ross C.A., Snyder S.H.;		
RT	"Cloning and expression of a rat somatostatin receptor enriched in		
RT	brain.";		
RL	J. Biol. Chem. 267:21307-21312(1992).		
CC	-1- FUNCTION: RECEPTOR FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR		
CC	SOMATOSTATIN-14 THAN -28. THIS RECEPTOR IS COUPLED TO		
CC	PHOSPHORYLASE PHOSPHATASE AND NA+/H+ EXCHANGER VIA PERTUSSIS		
CC	TOXIN INSENSITIVE G PROTEINS.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- TISSUE SPECIFICITY: BRAIN, PITUITARY, ISLET, JEJUNUM, STOMACH,		
CC	HEART, SPLEEN.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	-----		
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CC	or send an email to license@lsb-sib.ch).		
CC	-----		
DR	EMBL; X62314; CAA44193.1; -.		
DR	EMBL; M97656; -; NOT_ANNOTATED_CDS.		
DR	PIR; A39297; A39297.		
DR	PIR; A45102; A45102.		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCR_RHODOPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.		
DR	PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;		
KW	Multigene family; Lipoprotein; Palmitate.		
FT	DOMAIN 1	56	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 57	84	1 (POTENTIAL).
FT	DOMAIN 85	94	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 95	120	2 (POTENTIAL).
FT	DOMAIN 121	131	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 132	153	3 (POTENTIAL).
FT	DOMAIN 154	175	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 176	196	4 (POTENTIAL).
FT	DOMAIN 197	219	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 220	244	5 (POTENTIAL).
FT	DOMAIN 245	270	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 271	296	6 (POTENTIAL).
FT	DOMAIN 297	303	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 304	327	7 (POTENTIAL).
FT	DOMAIN 328	391	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD 4	4	N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD      44       44    N-LINKED (GLUCNAC. .) (POTENTIAL).
FT CARBOHYD     48       48    N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID     130      208        BY SIMILARITY.
FT LIPID         339      339        PALMITATE (POTENTIAL).
SQ SEQUENCE     391 AA;   42746 MW;  28ED6E894B72FB B7 CRC64;

Query Match          22.6%; Score 500; DB 1; Length 391;
Best Local Similarity 31.2%; Pred. No. 2,le-21;
Matches 105; Conservative 73; Mismatches 134; Indels 24; Gaps

QY 55 GSSARLMEQATGTGWADLEASLLPTGPNASNSTSDGPNLTSAGSPRTGISIINIIMPS 114
DB 20 GCGEVGSRGGPGSGAAD--GMEEPRGNSSQGNTLSSEGOSA-----ILISF 63
QY 115 VEGTICLIIGNSTVFIAVVKKSKLHWCMNNVPDIETINLSVDLLFLLGPMPIHQLMG 174
DB 64 IYSVCVLGCNGNSMVIIVLYLKAKMTATN--ITLNLAIDEMLMSVPELVLTSTLL 120
QY 175 NGVMHEGETMCCTLITAMDANSOFTSYILLTAIDAIRLATVHPISSTKFRPSVATLYIC 234
DB 121 RH-WPFALLCRLVLSVDAYNMFTSICYCLTVLSVDRIYAAPHIKARYRPPTYAAKVNL 179
QY 235 LLWALSFSITPVWLRYARLRPPFGAVCGGIRLPNP-DTDLYWFLLYOFFALPALPEVVI 293
DB 180 GWVWSLLLVLPLIVEFSRTAANDSGTVA CNMMPAPORFWLVGFVLYTFELMGFLLPVGAI 239
QY 294 TAAVYRIQRMTSSVAPASQRSIRLTRVTARTAITACLVEFCWAPYYVLDTQLSISR 353
DB 240 CLCYVLIIAKRMVALKAGMQQKRSEKITLMVMVMVYVICWPMPFYVOLVNFAEQ 299
QY 354 PTLTEVYLNAAISLGYANSCNDPEVYIVLCETFRRK 389
DB 300 DDATAVSQ---SVILGYANSCANPDILYGFLSDNFKR 332

RESULT 13
SSRA_RAT ID SSRA_RAT STANDARD; PRT; 384 AA.
AC P30937;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DN Somatostatin receptor type 4 (SS4R).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93087484; PubMed=1360663;
RA Bruno J.F., Xu Y., Song J., Berelowitz M.;
RT "Molecular cloning and functional expression of a brain-specific somatostatin receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:11151-11155(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Hippocampus;
RX MEDLINE=94230347; PubMed=8175684;
RA Bito H., Mori M., Sakanaka C., Takano T., Honda Z., Gotoh Y.,
RA Nishida E., Shimizu T.;
RT "Functional coupling of SST4, a major hippocampal somatostatin receptor, to adenylylate cyclase inhibition, arachidonate release and activation of the mitogen-activated protein kinase cascade.";
RL J. Biol. Chem. 269:12722-12730(1994).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF ADENYLYATE CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, LUNGS, HEART AND ISLETS. MODERATE
```


QY 113 PSVFGTICLLGIGNSTYIFAVVKKSKLHMCNNVPDIFIINLSVVDLLFLLGMPFMIHQI 172
Db 47 OCTYALVCLVGLVGNALVIFVILRYAKMKATN---IYLLNLAVADELFMLSVPF-VRSA 102
QY 173 MGNVWHFGETMCTLTITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLV 232
Db 103 AALRHWPFGAVLCRAVLSVDGLNMTSVFCLTYLSVDRYAVAVHPLRTATYRRPSVAKLI 162
QY 233 ICLLMALSFISITPWLTKARLIPFPGG-AVGGCIRLPNPDITLYW---FTLYQFFLAFLAL 288
Db 163 NLGVWLASLVTLPFAVFADTRPARGGEAVACNLHWPHP---AMSAVFVITYTFLGLFLP 218
QY 289 PEVYITAAVYRILQRMSSVAPASQSRIRLRTKRVTRTAIAICLVFFVCWAPYVVLQITQ 348
Db 219 PVLAIGLCYLLIVGKMAVALRGWQQRKRSEKKITRLVLMVYVFLCWMPEYVVLQILN 278
QY 349 LSIISRPITLTFVYLYNNAISLGYANSCLNPEFYIIVLCETFRK 389
Db 279 LEVTSIDAT---VNHVSLILSYANSCANPILYGLFSLDNFRK 316

RESULT 15

SSR3_RAT STANDARD; PRT; 428 AA.
AC P30936;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Somatostatin receptor type 3 (SS3R) (SSR-28).
GN SSR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=93066220; PubMed=1279674;
RA Meyerhof W., Wulfsen I., Schoenrock C., Fehr S., Richter D.;
RT "Molecular cloning of a somatostatin-28 receptor and comparison of
its expression pattern with that of a somatostatin-14 receptor in rat
brain."
RL Proc. Natl. Acad. Sci. U.S.A. 89:10267-10271(1992).
CC -!- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
ADENYLYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: DENSELY EXPRESSED IN CEREBELLUM AND IN MODERATE
LEVELS IN THE AMYGDALA, CORTEX, STRIATUM, SPLEEN, LIVER,
PITUITARY.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X63574; CAA45130.1; .
DR PIR; S30508; S30508.
DR HSSP; P34996; 1DD.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 71 1 (POTENTIAL).
FT DOMAIN 72 81 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 82 103 2 (POTENTIAL).
FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 140 3 (POTENTIAL).
FT DOMAIN 141 162 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 163 182 4 (POTENTIAL).
FT DOMAIN 183 206 5 (POTENTIAL).
FT TRANSMEM 207 232 5 (POTENTIAL).
FT DOMAIN 233 266 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 267 288 6 (POTENTIAL).
FT DOMAIN 289 302 7 (POTENTIAL).
FT TRANSMEM 303 325 7 (POTENTIAL).
FT DOMAIN 326 428 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 117 192 BY SIMILARITY.
FT DOMAIN 358 373 POLY-GLU.
SQ SEQUENCE 428 AA; 47151 MW; BE0AA948840A9E9D CRC64;

Query Match 21.7%; Score 480.5; DB 1; Length 428;
Best Local Similarity 31.3%; Pred. No. 2.8e-20;
Matches 118; Conservative 73; Mismatches 143; Indels 43; Gaps 11;

QY 75 SLPTGPNASNTSDG---PDNLTSAGSPPRTGISYINIMPSVFGTICLLGIGNSTVI 131
Db 8 SSVPTTLDPGNASSAMPPLDTSLGNASAGTSLAGLAVSGILISLVYLVVCVVGIGNSLVI 67
QY 132 FAVVKKSKLHMCNNVPDIFIINLSVVDLLFLLGMPFMIHQMGNGV--WHFGETMCTLTIT 189
Db 68 YVVLNRHTS---SPSVTSVYIINLADELFLMLGLPFLAQ---NALSYWPFSGSLMCRLYM 121
QY 190 AMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPWL 249
Db 122 AVDGINQFTSIFCLTVMSVDRYLAHVHPTRSARWRTAPVARMVSAAVVASAVVVLPPVV 181
QY 250 YARLIPPGAVCGCIRLPNPDITLYW---FTLYQFFLAFLALPFVYITAAVYRILQRM 306
Db 182 FSGV--PRGMSTCHMOWPEPAA--AWRTAFIITYTALGFHGPBLVLVTCYLLIVVKVS 236
QY 307 SV-----APASQSRIRLRTKRVTRTAIAICLVFFVCWAPYVVLQITQISIRP 354
Db 237 TTRRVRAPSCQWQAPACQRR-RRSERVRTMVAVVALFVLCWMPFYLLNIVVVCPLP 295
QY 355 -TLTFVYLYNNAISLGYANSCLNPEFYIIVLCETFRK-----RLVLSYKPAAGQL 403
Db 296 EEPAFFGLYFLVVALPYANSCANPILYGLFSLYRKQGFRIILRPSRVRVRSQEPGSGPPE 355
QY 404 RAVSNAQTADERTESK 420
Db 356 KTEEEDEDEEERREE 372

Search completed: February 13, 2003, 13:58:47
Job time : 15.7494 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:55:16 ; Search time 29.2615 Seconds
(without alignments)
2971.547 Million cell updates/sec

Title: US-09-885-478-27

Perfect score: 2210

Sequence: 1 MSVGAARKGVGRAVGLGGGS.....LRAVSNAGTADERTESKGT 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2200	99.5	422	4 Q9BV08	Q9bv08 homo sapien
2	2195	99.3	422	4 Q96S47	Q96s47 homo sapien
3	601	27.2	121	6 Q9MZ01	Q9mz01 sus scrofa
4	565.5	25.6	340	4 Q969V1	Q969v1 homo sapien
5	559.5	25.3	340	4 Q9BXA8	Q9bxa8 homo sapien
6	559.5	25.3	340	6 Q8SQ54	Q8sq54 macaca fasc
7	523	23.7	370	13 Q8UWL5	Q8uw15 fugu rubrip
8	521.5	23.6	346	4 Q96GE0	Q96ge0 homo sapien
9	515.5	23.3	356	4 Q96TF2	Q96tf2 homo sapien
10	515	23.3	346	11 Q91Y73	Q91y73 mus musculu
11	502.5	22.7	367	13 Q9PVG0	Q9pvq0 carassius a
12	502	22.7	315	6 Q9GKP7	Q9gkp7 sus scrofa
13	499.5	22.6	367	13 Q9PVF9	Q9pvf9 carassius a
14	494.5	22.4	346	6 Q95KS6	Q95ks6 ovis aries
15	487	22.0	380	13 Q9DGO6	Q9dgo6 carassius a
16	469	21.2	390	13 Q8QGQ4	Q8qqq4 carassius a

17	457	20.7	385	11 Q9JK40	Q9jk40 mus musculu
18	453.5	20.5	390	11 Q8VI71	Q8vi71 mus musculu
19	453.5	20.5	391	11 Q8VI70	Q8vi70 mus musculu
20	453.5	20.5	393	11 Q9R1M0	Q9r1m0 mus musculu
21	453.5	20.5	401	11 Q9R1L9	Q9r1l9 mus musculu
22	453.5	20.5	409	11 Q8VI69	Q8vi69 mus musculu
23	453.5	20.5	438	11 Q9R0D1	Q9r0d1 mus musculu
24	453.5	20.5	444	11 Q9J1Y1	Q9jiy1 mus musculu
25	448	20.3	454	4 Q9H573	Q9h573 homo sapien
26	443	20.0	400	6 Q95M54	Q95m54 macaca fasc
27	435	19.7	383	13 Q42324	Q42324 catostomus
28	423.5	19.2	377	13 Q98U14	Q98u14 brachydanio
29	422	19.1	384	13 Q98UH1	Q98uh1 brachydanio
30	411	18.6	451	5 Q9VWQ1	Q9vvq1 drosophila
31	407	18.4	373	13 Q57585	Q57585 brachydanio
32	402.5	18.2	272	4 Q9BWH1	Q9bwh1 homo sapien
33	392	17.7	362	11 Q8VI74	Q8vi74 mus musculu
34	391	17.7	362	11 Q9J1N4	Q9jin4 rattus norv
35	373.5	16.9	380	5 Q9NEV2	Q9nfv2 lymnaea sta
36	370.5	16.8	393	5 Q9VWV0	Q9vvq0 drosophila
37	367	16.6	291	11 Q91Z24	Q91zz4 mus musculu
38	367	16.6	325	11 Q8VIN4	Q8vin4 mus musculu
39	367	16.6	330	11 Q8VIP1	Q8vip1 mus musculu
40	367	16.6	370	11 Q8VIP0	Q8vip0 mus musculu
41	366.5	16.6	380	5 Q9NEV1	Q9nfv1 lymnaea sta
42	364.5	16.5	380	5 Q9NEV3	Q9nfv3 lymnaea sta
43	363.5	16.4	380	5 Q9NEV0	Q9nfv0 lymnaea sta
44	361.5	16.4	359	13 Q9PVY7	Q9pv7 anguilla an
45	361	16.3	423	5 Q964D4	Q964d4 periplaneta

ALIGNMENTS

RESULT 1

ID	Q9BV08	PRELIMINARY;	PRT;	422 AA.
AC	Q9BV08;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Similar to G protein-coupled receptor 24 (Hypothetical 46.0 kDa protein).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRAIN;			
RA	Strausberg R.;			
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRAIN;			
RA	Strausberg R.;			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC001736; AAH01736.1; -			
DR	EMBL; BC021146; AAH21146.1; -			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PRO1559; DUFFYANTIGEN.			
DR	PRINTS; PRO0237; GPCR_RHODOPSN.			
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.			
KW	Receptor; Hypothetical protein.			
SQ	SEQUENCE 422 AA; 45963 MW; 86A9F398B5D5F397 CRC64;			

QY	1 MSVGAARKGVGRAVGLGGSCQATEEDPLPDGACAPGQGGRRRLPQPAWYEGSSARL 60
	Query Match 99.5%; Score 2200; DB 4; Length 422;
	Best Local Similarity 99.5%; Pred. No. 2e-179;
	Matches 420; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLDCCACAPGGGRRMRLPQPAWEGSSARL 60

QY 61 WEQATGTGWADLEASLLPTGPNASNTSDGDNLTAGSPPRTGISYINIIIMPSVFGTIC 120

Db 61 WEQATGTGWMDLASLLPTGPNASNTSDGPDNLTAGSPPRTGISYINIIIMPSVFGTIC 120

QY 121 LLGIIGNSTVIFAAVVKSKLHWCNNVPDIFILINSVDLLFLLGMPFMHQLMGNGVWHF 180

Db 121 LLGIIGNSTVIFAAVVKSKLHWCNNVPDIFILINSVDLLFLLGMPFMHQLMGNGVWHF 180

QY 181 GETMCTLITAMDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240

Db 181 GETMCTLITAMDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240

QY 241 FISITPWLVARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFALEFVVITAAVYRI 300

Db 241 FISITPWLVARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFALEFVVITAAVYRI 300

QY 301 LQRMSSVAPASQSRIRLTKRVTRTAIAICLVFVCWAPYYVLQLTQLSISRPTLTFVY 360

Db 301 LQRMSSVAPASQSRIRLTKRVTRTAIAICLVFVCWAPYYVLQLTQLSISRPTLTFVY 360

QY 361 LYNAISLGYANSCINPFYIIVLCETFRRKRLVSVKPAQOQLRAVSNAGTADERTESK 420

Db 361 LYNAISLGYANSCINPFYIIVLCETFRRKRLVSVKPAQOQLRAVSNAGTADERTESK 420

QY 421 GT 422

Db 421 GT 422

RESULT 2

ID Q96S47 PRELIMINARY; PRT; 422 AA.

AC Q96S47;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Somatostatin receptor-like protein.

GN SLC-1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Sugo T., Mori M.;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99373129; PubMed=10441476;

RA Shimomura Y., Mori M., Sugo T., Ishibashi Y., Abe M., Kurokawa T.,

RA Onda H., Nishimura O., Sumino Y., Fujino M.;

RT "Isolation and identification of melanin-concentrating hormone as the

RT endogenous ligand of the SLC-1 receptor.";

RL Biochem. Biophys. Res. Commun. 261:622-626(1999).

DR EMBL; AB063174; BAB60890.1; -.

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PRO1559; DUFFYANTIGEN.

DR PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

SQ SEQUENCE 422 AA; 45962 MW; 3986919A18183818 CRC64;

Query Match 99.3%; Score 2195; DB 4; Length 422;

Best local Similarity 99.3%; Pred. No. 5.4e-179;

Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAAKKGVGRAVGLGGSGCQATEEDPLPDGACAPGGGRRMRLPQPAWEGSSARL 60

Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPNCGACAPGGGRRMRLPQPAWEGSSARL 60

QY 61 WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTAGSPPRTGISYINIIIMPSVFGTIC 120

Db 61 WEQATGTGWMDLASLLPTGPNASNTSDGPDNLTAGSPPRTGISYINIIIMPSVFGTIC 120

QY 121 LLGIIGNSTVIFAAVVKSKLHWCNNVPDIFILINSVDLLFLLGMPFMHQLMGNGVWHF 180

Db 121 LLGIIGNSTVIFAAVVKSKLHWCNNVPDIFILINSVDLLFLLGMPFMHQLMGNGVWHF 180

QY 181 GETMCTLITAMDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240

Db 181 GETMCTLITAMDANSQFTSTYILTAMAIIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240

QY 241 FISITPWLVARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFALEFVVITAAVYRI 300

Db 241 FISITPWLVARLIPFPGGAVGCGIRLPNPDLDLYWFTLYQFFLAFALEFVVITAAVYRI 300

QY 301 LQRMSSVAPASQSRIRLTKRVTRTAIAICLVFVCWAPYYVLQLTQLSISRPTLTFVY 360

Db 301 LQRMSSVAPASQSRIRLTKRVTRTAIAICLVFVCWAPYYVLQLTQLSISRPTLTFVY 360

QY 361 LYNAISLGYANSCINPFYIIVLCETFRRKRLVSVKPAQOQLRAVSNAGTADERTESK 420

Db 361 LYNAISLGYANSCINPFYIIVLCETFRRKRLVSVKPAQOQLRAVSNAGTADERTESK 420

QY 421 GT 422

Db 421 GT 422

RESULT 3

ID Q9M201 PRELIMINARY; PRT; 121 AA.

AC Q9M201;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE Melanin-concentrating hormone receptor (Fragment).

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN; HYPOTHALAMUS;

RA Matteri R.L.;

RT "Sus scrofa melanin-concentrating hormone (MCH) receptor.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF273611; AAF81827.1; -.

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PRO0237; GPCR_RHODOPSIN.

DR PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

FT NON_TER 1 1

FT NON_TER 121 121

SQ SEQUENCE 121 AA; 13583 MW; 884D8268B6F9F010 CRC64;

Query Match 27.2%; Score 601; DB 6; Length 121;

Best local Similarity 99.2%; Pred. No. 9.7e-44;

Matches 120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 294 TAAVYRIQRMSTSSVAPASQSRIRLTKRVTRTAIAICLVFVCWAPYYVLQLTQLSISR 353

Db 1 TAAVYRIQRMSTSSVAPASQSRIRLTKRVTRTAIAICLVFVCWAPYYVLQLTQLSISR 60

QY 354 PTLTFVLYNAAISLGYANSCINPFYIIVLCETFRRKRLVSVKPAQOQLRAVSNAGTAD 413

Db 61 PTLTFVLYNAAISLGYANSCINPFYIIVLCETFRRKRLVSVKPAQOQLRAVSNAGTAE 120

QY 414 E 414

Db 121 E 121

```
RESULT 4
Q969V1 ID Q969V1 PRELIMINARY; PRT; 340 AA.
AC Q969V1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE G protein-coupled receptor (Melanin-concentrating hormone 2 receptor)
DE (Melanin-concentrating hormone receptor MCH-R2) (GPRV17).
GN SLT OR GPRV17.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21255282; PubMed=11355873;
RA Mori M., Harada M., Terao Y., Sugo T., Watanabe T., Shimomura Y.,
RA Abe M., Shintani Y., Onda H., Nishimura O., Fujino M.;
RT "Cloning of a novel g protein-coupled receptor, slt, a subtype of the
RT melanin-concentrating hormone receptor."
RT Biochem. Biophys. Res. Commun. 283:1013-1018(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21309932; PubMed=11404457;
RA Sailer A.W., Sano H., Zeng Z., McDonald T.P., Pan J., Pong S.-S.,
RA Feighner S.D., Tan C.P., Fukami T., Iwasa H., Hreniuk D.L.,
RA Morin N.R., Sadowski S.J., Ito M., Ito M., Bansal A., Ky B.,
RA Figueroa D.J., Jiang Q., Austin C.P., MacNeil D.J., Ishihara A.,
RA Ihara M., Kanatani A., Van der Ploeg L.H.T., Howard A.D., Liu Q.;
RT "Identification and characterization of a second melanin-concentrating
RT hormone receptor, MCH-2R."
RT Proc. Natl. Acad. Sci. U.S.A. 98:7564-7569(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21433976; PubMed=11459838;
RA Wang S., Behan J., O'Neill K., Weig B., Fried S., Laz T., Bayne M.,
RA Gustafson E., Hawes B.E.;
RT "Identification and pharmacological characterization of a novel human
RT melanin-concentrating hormone receptor, MCH-R2."
RL J. Biol. Chem. 276:34664-34670(2001).
RN [4]
RP SEQUENCE FROM N.A.
RA Kurama T., Matsumoto S., Takasaki J., Terai K., Matsumoto M.,
RA Kamohara M., Saito T., Soga T., Saito Y., Oda T., Masuho Y.,
RA Furuichi K.;
RT "Molecular characterization of a novel melanin-concentrating hormone
RT receptor: Evidence of its expression in lateral hypothalamus."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB060151; BAB55677.1; -.
DR EMBL; AY029596; AAK38157.1; -.
DR EMBL; AF399937; AAL05528.1; -.
DR EMBL; AB058849; BAB87842.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 340 AA; 38849 MW; 754A302BB951FAC6 CRC64;

Query Match 25.6%; Score 565.5; DB 4; Length 340;
Best Local Similarity 37.0%; Pred. No. 3.6e-40;
Matches 113; Conservative 62; Mismatches 119; Indels 11; Gaps 4;
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QY 230 TLVICLWALSISTPVMLYARLIPFGAVGCGIRLPNDTDLWFTLYQFFLAFLP 289
DB 151 IRINGLWMAASFILALPVMVYSKVIFKDGVESECAFDLTSPD-DVLWYTLVLTITTEFFP 209
QY 290 FVVTAAVVRIL-----QRMSSVAPASQRSI-RLRTKRVRTAIAICLVFVCAPIYV 343
DB 210 LPLILVCYLILICYTWEMYQONKDARCCNPSPVKQRYMKLTKMVLVYVFIISAAPYHV 269
QY 344 LQLTQLSIRPTLTFVYLYNMAISLGYANSCLNPFVYIVLCETFRKRLVLSVPAAGQL 403
DB 270 IQLVNLQMEQPTLAFYVGYLLSTCLSYASSINPFLYILSGNFQKRLPQIQRRATEKEI 329
QY 404 RAVSN 408
DB 330 NMMGN 334

RESULT 5
Q9BXA8 ID Q9BXA8 PRELIMINARY; PRT; 340 AA.
AC Q9BXA8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE G protein-coupled receptor MCH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21282939; PubMed=11274220;
RA Hill J., Duckworth M., Murdock P., Rennie G., Sabido-David C.,
RA Ames R.S., Szekeres P., Wilson S., Bergsma D.J., Gloger I.S.,
RA Levy D.S., Chambers J.K., Muir A.I.;
RT "Molecular Cloning and Functional Characterization of MCH2, a Novel
RT Human MCH Receptor."
RT J. Biol. Chem. 276:20125-20129(2001).
RL J. Biol. Chem. 276:20125-20129(2001).
DR EMBL; AF347063; AAK32193.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 340 AA; 38803 MW; 95A43ECB57511ACC CRC64;

Query Match 25.3%; Score 559.5; DB 4; Length 340;
Best Local Similarity 36.7%; Pred. No. 1.2e-39;
Matches 112; Conservative 62; Mismatches 120; Indels 11; Gaps 4;
```

Db 330 NNMGN 334

RESULT 6

Q8SQ54 PRELIMINARY; PRT; 340 AA.

AC Q8SQ54; 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)

DE GPRV17.

GN GPRV17.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopithecinae; Macaca.

OC NCBI_TaxID=9541;

OX NCBI_TaxID=9541;

RP [1]

RA SEQUENCE FROM N.A.

RA Kurama T., Matsumoto S., Takasaki J., Terai K., Matsumoto M., Kamohara M., Saito T., Soga T., Saito Y., Oda T., Masuho Y., Furuichi K.;

RA "Molecular characterization of a novel melanin-concentrating hormone receptor : Evidence of its expression in lateral hypothalamus.";

RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; AB058850; BAB87843.1; "

DR SEQUENCE 340 AA; 38769 MW; BD22CF1972332439 CRC64;

SQ

Query Match 25.3%; Score 559.5; DB 6; Length 340;

Best Local Similarity 36.7%; Pred. No. 1.2e-39;

Matches 112; Conservative 60; Mismatches 122; Indels 11; Gaps 4;

QY 110 IMPSVFGTICLLIGNSTVIFAVVKSKLHWCNVDPDIFINLSVVDLFLGMPFMI 169

Db 35 VILPSMIGIICSTGLVGNILIVFTIIRSRK---KTVPDITYICNLAVADLVHIIGMPFLI 90

QY 170 HQLMNGVWHFGETMCTLITAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVA 229

Db 91 HQWARGGEWVFGPLCTIITSIDTCNQFACSAIMTVMSVDRYFALVQPFRLTSWRTRYKT 150

QY 230 TLVICLLMALSFISTPVMYLARLIPFGGAVGCGIRLPNDPDLVWFTLYQFLAFALP 289

Db 151 IRINGLMAASFILALPWIYKSKVIKFDGESCAFDLSPD-DVLWYTLVLTITTFEFP 209

QY 290 FVVTATAYVRIL-----QRMSSVAPASQRSI-RLRTKRVTRTAIAICLVFVCWAPYYV 343

Db 210 LPLILVCYLILCYTWEMTQONKDARCCNPSPVKQRMKLTKMVLVLAVFILLSAAPHYV 269

QY 344 LQLTQLSISRPTLTFVLYLNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAQGL 403

Db 270 IQLVNLQMEQPTLAFYGVYGLISCLSYASSSINPFLYIILSGNFQKRLPOLQRVTDKEI 329

QY 404 RAVSN 408

Db 330 NNMGN 334

RESULT 7

Q8UWL5 PRELIMINARY; PRT; 370 AA.

AC Q8UWL5; 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)

DE Somatostatin receptor 2.

GN SSTR2.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.

OC NCBI_TaxID=31033;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21564205; PubMed=11707075;

RA Bagheri-Fam S., Ferraz C., Demaille J., Scherer G., Pfeifer D.;

RT "Comparative Genomics of the SOX9 Region in Human and Fugu rubripes: Conservation of Short Regulatory Sequence Elements within Large Intergenic Regions.";

RL Genomics 78:73-82(2001).

DR EMBL; AF329945; AAL32173.1; "

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCR_RHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

SQ SEQUENCE 370 AA; 41364 MW; 420BD12F204946B6 CRC64;

Query Match 23.7%; Score 523; DB 13; Length 370;

Best Local Similarity 32.9%; Pred. No. 1.7e-36;

Matches 128; Conservative 74; Mismatches 131; Indels 56; Gaps 13;

QY 45 WRLPQPAWEGSSARLW--EQATGTGWADLEASLPTGPNASNTSDGPDNLTSAGSPR 101

Db 4 WILP-PSPLNSDLHLVDGFEQANG--SDLHA-----NRIHSLNKTS----- 43

QY 102 TGSISYINIIMPSVEGTICLLIGNSTVIFAVVKSKLHWCNVDPDIFINLSVDLFL 161

Db 44 -----TVVITCMYFLVCAVGLCGNALVIYILRYAKM---KTVTNIIYILNLAVADVLF 93

QY 162 LIGMPEMIHQLMNGVWHFGETMCTLITAMDANSQFTSTYILTAMADRYLATVHPISST 221

Db 94 MGLPFIATIQ-LALVHMPFGPVLGRVMTVDSLNGFTSIFCLMWSIDRYLAVHPIKST 152

QY 222 KFRKPSVATLVICLLMALSFISTPVMYLARLIPFGGAVGCGIRLPNDPDLVW-FTLY 280

Db 153 KWKRPRAKTIINAVMGASLVNLPVIVYSGITRKQDGF-CTIVWPEPEAYYTAFMIX 211

QY 281 QFLAFALPFWVTATAYVRILQRMSSVAPASQRSIRLRTKRVTRTAIAICLVFVCWAP 340

Db 212 TFLIGFPLPLVLSLCYVFLIIVKSSGIRVSSKRRKSEKVTIRMVSIYAVFVLCWLP 271

QY 341 YVYIQLTQLS-----ISRPTLTFVLYLNAISLGYANSCLNPFVYIVLCETFRKRL-- 391

Db 272 FYVFNVTSVTGISATHYLRSTFAFV-----VLGYANSCANPILYAFLSGNPKKSFQN 325

QY 392 VLSVKPAAQGLRAVSNAGTADDEERTESK 420

Db 326 VLCLQ-----KVGGLDEAERSDSRQDKSR 349

RESULT 8

Q96GE0 PRELIMINARY; PRT; 346 AA.

AC Q96GE0; 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)

DE Unknown (Protein for IMAGE:3354783) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RA SEQUENCE FROM N.A.

RP TISSUE=EYE;

RC Strausberg R.;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC009522; AAH09522.1; "

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm.1; 1.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

FT NON_TER 1

SQ SEQUENCE 346 AA; 38790 MW; EA073A6CC05FEB72 CRC64;

Query Match	23.6%;	Score 521.5;	DB 4;	Length 346;
Best Local Similarity	31.7%;	Pred. No. 2.1e-36;		
Matches 110;	Conservative 73;	Mismatches 125;	Indels 39;	Gaps 77;

[illegible]

RESULT	9
ID	Q96TF2
AC	Q96TF2;
DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE	Somatostatin receptor 2B.
GN	SSTR2.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euthalia; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=20084417; PubMed=10619399;
RA	Petersen S., Rasch A.C., Presch S., Bell F.U., Schulte H.M.;
RT	"Genomic structure and transcriptional regulation of the human
RT	somatostatin receptor type 2.";
RT	Mol. Cell. Endocrinol. 157:75-85(1999).
DR	EMBL; AF184174; AAF42810.1; -.
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PROSITE; PS00237; G_PROTEIN_REC_P1_1; UNKNOWN_1.
DR	PROSITE; PSS0262; G_PROTEIN_REC_P1_2; 1.
SO	SEQUENCE 356 AA; 4006 MW; D10FA237FAED61F3 CRC64;

Query Match	23.3%;	Score 515.5;	DB 4;	Length 356;
Best Local Similarity	31.0%;	Pred. No. 7e-36;		
Matches 110; Conservative	77;	Mismatches 123;	Indels 45;	Gaps 9;

```

QY      71 DLEASLLPTGNASNTSDGPDNLTSAGSPPRGTGISYINIMPSVEFTICLLGIIGNSTV 130
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      20 DLNGSVST--NTSNQTEPYDLTS-----NAVLFTFYFVVCIIIGLCGNLTV 64

QY      131 IFAVVKKSKLHWCNNVPDIFIINLSVDLLELGMPE-----MIHQLMGNGVHFEETM 184
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      65 IYVILRYAKM--KTITNIIYILNLAIDELLEMLGLPELMAQVALVH-----WPEFKAI 114

QY      185 CTLITAMDANSOFTSTYIILTAMAIIDRLATVHPISSTKFKRPSVALTVICLLMALSFISI 244
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      115 CRVVMTVVDGINOFTSIFCLTVMSIDRYLAVVHPKSAKWRRPRTAKMTIMAVWGVSLLVI 1744

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```
QY      245 TPVWLRYARLIPFPGGAVGCCGIRLPNDPIDLY-WETLYQGFLEAFALPFWVITAAVRILOR 303
        : : : | | - - - | | | - - - | : | : | : | : : :
Db      175 LPIMITYAGLRSMQGRSSCTINWPGESGAWYTGFIIYTFILGEFLVPLTIICLCYFLIITK 234
QY      304 MTSSVAPASQRSRIRLTRKVRTTAIAICIEFFVCWAPYYVLQTQLSIS-RPTLFVEVLY 362
        : | | : : | : | | : | | : | : : : : : : :
Db      235 VKSSGIRVGSSSKRKKSEKKVTIRMVSIVAAVFICWLPFIYFNVSYSMAISPPTALKGMF 294
QY      363 NAAISLGYANSCLNPFVYIVLCETERK--RLVLSVKPPAOGQLRAYSNAQTAD E 414
        : : | | | | | | : : | : | : : : : : : : :
Db      295 DFVVVLTYANSCLNPDILYAFLSDNFKKSFQNVLCLVK-----VDNSKSGEE 340
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RESULT	ID	Q01Y73	PRELIMINARY;	PRT;	346 AA.
10	Q01Y73	Q01Y73			
AC	Q01Y73;				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)				
DE	Somatostatin receptor type 2.				
GN	SMSTR2 OR SST2.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=129; TISSUE=LIVER;				
RX	MEDLINE=21201198; PubMed=11278805;				
RA	Puente E., Saint-Laurent N., Torrisani J., Furet C., Schally A.V.,				
RA	Vaysse N., Buscail L., Susini C.;				
RT	"Transcriptional Activation of Mouse sst2 Somatostatin Receptor				
RT	Promoter by Transforming Growth Factor-beta. Involvement of Smad4.";				
RL	J. Biol. Chem. 276:13461-13468(2001).				
DR	EMBL: AF008914; AAD01420.1; -.				
DR	MGD: GGI:98328; Smstr2.				
DR	InterPro: IPR000276; GPCR_Rhodpsn.				
DR	Pfam: PF00001; 7tm_1; 1.				
DR	PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.				
KW	PROSITE, PS50262; G_PROTEIN_RECEP_F1_2; 1.				
DR	Receptor.				
SEQ	SEQUENCE 346 AA; 38586 MW; D7A20AE1371C400 CRC64;				

Query Match	23.3%;	Score 515;	DB 11;	Length 346;
Best Local Similarity	31.2%;	Pred. No. 7.5e-36;		
Matches 115;	Conservative 76;	Mismatches 130;	Indels 48;	Gaps 11;

QY	62	EQATGTG-WA----	DLEASLPTGPNASNSDGDPNLTSAGSPPRIGSISYINIMP	SVF	116
		: : :			
Db	6	EQLNGSQVWVSSPFDLNGLGPS--	NGSNQTEPYD	MTS-----	NAVLTFY 50
QY	117	G7ICLLGIGNSTVIFA	VVKKSKLHWCNNVDFI	INLSVVDLEFLGMPF-----	MH 1700
		: : : : : : : : : : : :			
Db	51	FVVCVGLCGNTLV	IYILRYAKM--	KTITNITILNLAIDELFMGLPFLAMQ	VALVH 1077
QY	171	QLMNGVWHFGETMCTLT	AMDANSQFTSTYLLTAMAIDRYL	ATVADPISSTKFRKPSVAT	2300
		: : : : : : : : : : : :			
Db	108	-----WPF	GKAICRYVMTVDGINQFTSIFCLTVMSIDRYL	VAVHPIKSAKMRRPR	IRIAK 1600
QY	231	LVICLLWALSFISITP	WMLYARLIPFGAGVCGIRLPNP	DTDL-WFTLYQF	FLAFALP 2899
		: : : : : : : : : : : :			
Db	161	MINVAVWCVSLVILP	IMITYAGLRSNQWGRSSCTINWPGESGAWY	IGFI	IYAFILGLVP 2200
QY	290	FVVTITAAVVRILQ	RMITSSVAPASQSRISIRLPRKRV	TRTITAIAICLVFV	CWAPYVLQTLQ 3499
		: : : : : : : : : : :			
Db	221	LTITCLCYLFI	IIIKVXSSGIRVGS	SKRKKSEKRVTRMVSIVAV	VFIFCWLPIFYIFNVSSV 2800
QY	350	SIS-RPTLTFVYLY	NAAISLGYANSCLNPFVYIVLC	ETFRKL--VLSVKP	PAQGLRAV 4066
		: : : : : : : : : : :			
Db	281	SVAISFTPALKGM	DFVYVILTYANSCANPILYAFLSDN	EKKSFQNYCLVKA-----	3322
QY	407	SNAQTADDEE	415		

RA Lin X., Janovick J.A., Brothers S., Conn P.M., Peter R.E.;
RT "Molecular cloning and expression of two type one somatostatin
receptors in goldfish brain."
RL Endocrinology 140:5211-5219(1999).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF097727; AAF08614.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 367 AA; 41614 MW; A5BA0AE68D47C455 CRC64;

Query Match 22.6%; Score 499.5; DB 13; Length 367;
Best Local Similarity 30.1%; Pred. No. 1.7e-34;
Matches 97; Conservative 80; Mismatches 120; Indels 25; Gaps 6;

QY 71 DLEASLLPTGPNASNTSDGPDNLTSGSPRTGSISYINIMPSVFGTICLLIGNSTV 130
DB 9 NLEDGLYLNFSSNETHNGDSHGSSA-----IFISFISVCLVGLCGNSMV 55
QY 131 IFAVVKKSKLHWCNVNDIFIIINLSVDLLELLGMPEMIHQLMNGVWHFGETMCTLTAA 190
DB 56 IYVIFRYAKMKTATN---IYILNLAIADDLMLSVPLVTSLSLHH-WPFGSLICRLVLS 111
QY 191 MDANSQETSTYILTAADRYLATVHPISSTKFRKPSVATLVICLLMAISFISITPVWLY 250
DB 112 VDAINMFTSYCLVLSIDRYISVHPKARYRRPTIAKMVNLGVMFISILVLPITIF 171
QY 251 ARLPEPGAVGCGIRLPNPDTLVW---FTLYQFLAFALPFVVITAAVVRILQRMWSS 307
DB 172 STTAPNSDGSVACNMQMEPERQ--WMAVEVYIAFLMGFLFPVIALCMCYILLIVKMRV 229
QY 308 VAPASQSRISRLTKRVTATAICLVFVCMAPYVYLQTLQLSISRPTLTFVLYNNAIS 367
DB 230 ALKAGWQQRKKSEKRTLMVMVTVFVICMRFHIVQLVSVEVQHNST---LSQLAVI 286
QY 368 LGYANSCINPFVYIVLCETFRK 389
DB 287 LGYANSCANPILYGFLSDNFR 308

RESULT 14
Q95KS6 PRELIMINARY; PRT; 346 AA.

AC Q95KS6; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Somatostatin receptor subtype 1 (Fragment).
GN SST1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PIUTITARY;
RA Debuss N., Dutour A., Vnaroqueaux V., Oliver C., Ouafik L.;
RT "The ovine somatostatin receptor subtype 1 (osstl): Partial cloning
and tissue distribution."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PIUTITARY;
RA Debuss N.;
RL Thesis (1999),
RL Department of Intercellular communications in Endocrinology,
RL University of Aix-Marseilles II, Marseilles, France.
DR EMBL; AJ314853; CAC69545.1; -.

DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 346 AA; 38479 MW; 65547713CF2CA5C6 CRC64;

Query Match 22.4%; Score 494.5; DB 6; Length 346;
Best Local Similarity 33.3%; Pred. No. 4.2e-34;
Matches 98; Conservative 69; Mismatches 116; Indels 11; Gaps 5;

QY 100 PRGTSISY---INIMPSVEGTICLLIGNSTVIFAVVKKSKLHWCNVNDIFIIINLSV 156
DB 1 PONGTISEGOGSAILISFISVCLVGLCGNSMVIYILRYAKMKTATN---IYILNLAI 57
QY 157 VDLEFLGMPEMIHQLMNGVWHFGETMCTLTITAMDANSQETSTYILTAADRYLATVH 216
DB 58 ADELMLSVPLVTSLLRH-WPFGALLCRLVLSVDVNMFTSYCLVLSYDRYAVVH 116
QY 217 PISSTKFRKPSVATLVICLLMAISFISITPVWLYARLIPPGAVGCGIRLPN-DTDLV 275
DB 117 PIKARYRRPTVAKVNLGVWVLSLLVLPVVFSTRANSDDGTACNMMEPEAQRWLV 176
QY 276 WFTLYQFLAFALPFVVITAAVVRILQRMWSSVAPASQSRISRLTKRVTATAICLVF 335
DB 177 GFVLTFELMGFLLPVGAICLCYVLIIAKRMVALKAGWQQRNGSEKRTLMVMVTVFV 236
QY 336 VCMAPYVYLQTLQLSISRPTLTFVLYNNAISLGYANSCINPFVYIVLCETFRK 389
DB 237 ICWMPFYVQLVNVFAEQDAIVSOL---SVILGYANSCANPILYGFLSDNFR 287

RESULT 15
Q9DGQ6 PRELIMINARY; PRT; 380 AA.

AC Q9DGQ6; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Somatostatin receptor type two.
GN SST2.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20453044; Pubmed=10996426;
RA Lin X., Janovick J.A., Cardenas R., Conn P.M., Peter R.E.;
RT "Molecular cloning and expression of a type-two somatostatin receptor
in goldfish brain and pituitary."
RL Mol. Cell. Endocrinol. 166:75-87(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF139597; AAF98367.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 380 AA; 43146 MW; CE897FE7537CFA30 CRC64;

Query Match 22.0%; Score 487; DB 13; Length 380;
Best Local Similarity 31.8%; Pred. No. 2e-33;
Matches 108; Conservative 71; Mismatches 147; Indels 14; Gaps 6;

QY 67 TGMADLEASLLPTGPNASNTSDGPDNLTSG-----SPRTGSISYINIMPSVFGTIC 120
DB 3 TKWTFMPNSNMLPDRLLNDSFFPGNESDGLEMPYPHNSHTPGFDQTSSVYITFYVYVVC 62

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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:56:21 ; Search time 12.3392 Seconds
(without alignments)
1006.264 Million cell updates/sec

Title: US-09-885-478-27
Perfect score: 2210
Sequence: 1 MSVGAKKGVGRAVGLGGGS.....LRVSNACQADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2200	99.5	422	4	US-09-224-426-2 Sequence 2, Appl1
2	2200	99.5	422	4	US-09-478-601-2 Sequence 2, Appl1
3	2200	99.5	422	4	US-09-478-602-2 Sequence 2, Appl1
4	1819	82.3	353	3	US-08-984-288-2 Sequence 2, Appl1
5	1819	82.3	353	4	US-09-218-467B-2 Sequence 2, Appl1
6	1758	79.5	353	4	US-09-224-426-4 Sequence 4, Appl1
7	1758	79.5	353	4	US-09-478-601-4 Sequence 4, Appl1
8	1758	79.5	353	4	US-09-478-602-4 Sequence 4, Appl1
9	1691	76.5	402	3	US-08-602-809-2 Sequence 2, Appl1
10	1680	76.0	400	5	PCT-US95-16472-2 Sequence 2, Appl1
11	533	24.1	369	4	US-08-120-601B-9 Sequence 9, Appl1
12	532	24.1	369	1	US-07-816-283-8 Sequence 8, Appl1
13	532	24.1	369	1	US-08-417-103-8 Sequence 8, Appl1
14	530.5	24.0	369	1	US-07-816-283-6 Sequence 6, Appl1
15	530.5	24.0	369	1	US-08-417-103-6 Sequence 6, Appl1
16	530.5	24.0	369	1	US-08-417-103-16 Sequence 16, Appl1
17	525	23.8	369	2	US-08-411-859-3 Sequence 3, Appl1
18	525	23.8	369	4	US-08-387-707-9 Sequence 9, Appl1
19	525	23.8	369	4	US-08-405-271A-9 Sequence 2, Appl1
20	519	23.5	391	1	US-07-816-283-2 Sequence 2, Appl1
21	519	23.5	391	1	US-08-417-103-2 Sequence 2, Appl1
22	519	23.5	391	1	US-08-417-103-14 Sequence 14, Appl1
23	513	23.2	391	1	US-07-816-283-4 Sequence 4, Appl1
24	513	23.2	391	1	US-08-417-103-4 Sequence 4, Appl1
25	504.5	22.8	418	1	US-07-816-283-10 Sequence 10, Appl1
26	504.5	22.8	418	1	US-08-417-103-10 Sequence 10, Appl1
27	502	22.7	391	4	US-08-120-601B-8 Sequence 8, Appl1

28	501.5	22.7	389	4	US-08-430-286A-7	Sequence 7, Appl1
29	494.5	22.4	384	3	US-09-071-434-3	Sequence 3, Appl1
30	472	21.4	428	1	US-07-816-283-12	Sequence 12, Appl1
31	472	21.4	428	1	US-08-417-103-12	Sequence 12, Appl1
32	456.5	20.7	370	4	US-08-405-271A-21	Sequence 21, Appl1
33	453	20.5	400	4	US-08-188-275A-2	Sequence 2, Appl1
34	453	20.5	400	4	US-09-351-198-2	Sequence 2, Appl1
35	453	20.5	400	4	US-09-113-426-2	Sequence 2, Appl1
36	453	20.5	415	4	US-08-405-271A-20	Sequence 20, Appl1
37	452.5	20.5	398	1	US-08-149-093A-5	Sequence 5, Appl1
38	452.5	20.5	398	2	US-08-911-245-5	Sequence 5, Appl1
39	452.5	20.5	398	4	US-08-889-108-2	Sequence 2, Appl1
40	452.5	20.5	398	4	US-08-120-601B-2	Sequence 2, Appl1
41	452.5	20.5	398	4	US-08-387-707-16	Sequence 16, Appl1
42	452.5	20.5	398	4	US-09-510-473-5	Sequence 5, Appl1
43	452.5	20.5	398	4	US-08-405-271A-16	Sequence 16, Appl1
44	452.5	20.5	398	5	PCT-US94-10358-2	Sequence 2, Appl1
45	451.5	20.4	391	2	US-08-454-549-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-224-426-2
; Sequence 2, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salon, John A
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453/JPW/JHB
; CURRENT APPLICATION NUMBER: US/09/224,426
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-224-426-2

Query Match	99.5%;	Score 2200;	DB 4;	Length 422;
Best Local Similarity	99.5%;	Pred. No. 2.1e-172;		
Matches 420;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY 1	MSVGAKKGVGRAVGLGGSGCQATEEDPLDPCGACAPGGGRRRLPQPAWEGSSARL 60			
DB 1	MSVGAMKKGVGRAVGLGGSGCQATEEDPLDPCGACAPGGGRRRLPQPAWEGSSARL 60			
QY 61	WEQATGTGWADLEASLPTGPNASNTSDGPDNLTSGSPPRGTGISYINIMPSVFGTIC 120			
DB 61	WEQATGTGWMDLEASLPTGPNASNTSDGPDNLTSGSPPRGTGISYINIMPSVFGTIC 120			
QY 121	LGIGNSTVIFAIVKRSKLMWCNNVPDIFILNSVVDLFLGMPFMIHQLMGNGVWHF 180			
DB 121	LGIGNSTVIFAIVKRSKLMWCNNVPDIFILNSVVDLFLGMPFMIHQLMGNGVWHF 180			
QY 181	GETMCTLITAMDANSQFTSTYILTAMADRYLATVHPISSTKFKRPSVATLVICLMALS 240			
DB 181	GETMCTLITAMDANSQFTSTYILTAMADRYLATVHPISSTKFKRPSVATLVICLMALS 240			
QY 241	FISITPVMLYARLIPPGGAVGCGIRLPNDTDLWFTLYQFELAFALPFVITAAYVRI 300			
DB 241	FISITPVMLYARLIPPGGAVGCGIRLPNDTDLWFTLYQFELAFALPFVITAAYVRI 300			
QY 301	IQRMSSVAPASQSRIRLRTKRVTRTAICIVFVCWAPYYVQLTQLSISRPTLFVY 360			
DB 301	IQRMSSVAPASQSRIRLRTKRVTRTAICIVFVCWAPYYVQLTQLSISRPTLFVY 360			

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OY      361  LYNAAISLGYANSCLNPFVYIVLCETFFKRRLVSVKPPAAGQGLRAVSNACOTADEERTESK  4200
      |||
      361  LYNAAISLGYANSCLNPFVYIVLCETFFKRRLVSVKPPAAGQGLRAVSNACOTADEERTESK  4200
Db

OY      421  GT  422
      ||
Db      421  GT  422

RESULT 2
US-09-478-601-2
; Sequence 2, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453z\JFW
; CURRENT APPLICATION NUMBER: US/09/478,601
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-478-601-2

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Query Match	99.5%;	Score 2200;	DB 4;	Length 422;
Best Local Similarity	99.5%;	Pred. No. 2.1e-172;		
Matches 420; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

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RESULT 3
US-09-478-602-2
; Sequence 2, Application US/09478602

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; Patent No. 6291195
;
; GENERAL INFORMATION:
;
; APPLICANT: Salon, John A.
;
; APPLICANT: Laz, Thomas M.
;
; APPLICANT: Nagorny, Raisa
;
; APPLICANT: Wilson, Amy E.
;
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
;
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
;
; FILE REFERENCE: 57453Y\JPW
;
; CURRENT APPLICATION NUMBER: US/09/478, 602.
;
; CURRENT FILING DATE: 2000-01-06
;
; EARLIER APPLICATION NUMBER: 09/224, 426
;
; EARLIER FILING DATE: 1998-12-31
;
; NUMBER OF SEQ ID NOS: 15
;
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 2
;
; LENGTH: 422
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
US-09-478-602-2

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Query Match	99.5%	Score 2200;	DB 4;	Length 422;
Best Local Similarity	99.5%;	Pred. No. 2.1e-172;		
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Db	1	MSVGAMKKGVGRAVGLGGGSGCOATEEDPLPDCGACAPGQGGRRWRLPOPAVEGSSARL	60
QY	61	WEQATGTGWADLEASLLPTGPNASNTSDGPDNLTASGSPRTGISISYINIMPSVFCTIC	120
Db	61	WEQATGTGWMDLEASLLPTGPNASNTSDGPDNLTASGSPRTGISISYINIMPSVFCTIC	120
QY	121	LLGIIGNSTVTEFAVVKKSKLHWCNNVPDIFIINLSVVDLFLFLGMPFMIHQLMNGVWHE	180
Db	121	LLGIIGNSTVTEFAVVKKSKLHWCNNVPDIFIINLSVVDLFLFLGMPFMIHQLMNGVWHE	180
QY	181	GETMCTLITAMDANSQFTSTYILTAAMADRYLATVHPISSTFKRKPVSATLVICLMAWS	240
Db	181	GETMCTLITAMDANSQFTSTYILTAAMADRYLATVHPISSTFKRKPVSATLVICLMAWS	240
QY	241	FISITPWLRYARLTPFPGAVGCGIRLPNDTDLWFTLYQFLAFALPFVVITAAYVRI	300
Db	241	FISITPWLRYARLTPFPGAVGCGIRLPNDTDLWFTLYQFLAFALPFVVITAAYVRI	300
QY	301	LQRMSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPRYVYLQTLQLSISRPTLFVY	360
Db	301	LQRMSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPRYVYLQTLQLSISRPTLFVY	360
QY	361	LYNAAISLGYANSCLPFVYIVLCETFRRRLVLSVKPAAQGLRAVSNQOTADEERTESK	420
Db	361	LYNAAISLGYANSCLPFVYIVLCETFRRRLVLSVKPAAQGLRAVSNQOTADEERTESK	420
QY	421	GT 422	
Db	421	GT 422	

RESULT 4
US-08-984-288-2
; Sequence 2, Application US/08984288
; Patent No. 603872
; GENERAL INFORMATION:
; APPLICANT: BERGSMÄ, DERK
; APPLICANT: ELIIS, CATHERINE
; TITLE OF INVENTION: NOVEL HUMAN 11CB SPLICED
; TITLE OF INVENTION: ARIANT
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RÄTNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA

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; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,288
; FILING DATE: 03-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,763
; FILING DATE: 11-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: P50599
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-984-288-2
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Query Match      82.3%; Score 1819; DB 3; Length 353;
Best Local Similarity 100.0%; Pred. No. 2.5e-141;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 131 IFAVVKKSKLHWCNNVPDIFINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLITA 190
Db 62 IFAVVKKSKLHWCNNVPDIFINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLITA 121
QY 191 MDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFSITPVWLY 250
Db 122 MDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFSITPVWLY 181
QY 251 ARLIPEPGGAVGCGIRLPNPDIDLYWFTLYQFFLAFLAPFVVITAAVYRILOQMTSSVAP 310
Db 182 ARLIPEPGGAVGCGIRLPNPDIDLYWFTLYQFFLAFLAPFVVITAAVYRILOQMTSSVAP 241
QY 311 ASQRSIRLRTKRVTRTAIAICLVFVCWAPYVYLQTLQSLISRPDLTFVLYNNAISLGY 370
Db 242 ASQRSIRLRTKRVTRTAIAICLVFVCWAPYVYLQTLQSLISRPDLTFVLYNNAISLGY 301
QY 371 ANSCLNPFVYIYVLCETFRKRLVLSVKPAAQGLRAVSNAQTADERTESKGT 422
Db 302 ANSCLNPFVYIYVLCETFRKRLVLSVKPAAQGLRAVSNAQTADERTESKGT 353
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RESULT 5
US-09-218-467B-2
; Sequence 2, Application US/09218467B
; Patent No. 6362326
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: HALSEY, WENDY
; APPLICANT: BERGMA, DERK
; TITLE OF INVENTION: 11cby Genomic Sequence
; FILE REFERENCE: GP-50010
; CURRENT APPLICATION NUMBER: US/09/218,467B
; CURRENT FILING DATE: 2001-06-22
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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-218-467B-2
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Query Match      82.3%; Score 1819; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 2.5e-141;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 71 DLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFGTICLLIGNSTV 130
Db 2 DLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFGTICLLIGNSTV 61
QY 131 IFAVVKKSKLHWCNNVPDIFINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLITA 190
Db 62 IFAVVKKSKLHWCNNVPDIFINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLITA 121
QY 191 MDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFSITPVWLY 250
Db 122 MDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFSITPVWLY 181
QY 251 ARLIPEPGGAVGCGIRLPNPDIDLYWFTLYQFFLAFLAPFVVITAAVYRILOQMTSSVAP 310
Db 182 ARLIPEPGGAVGCGIRLPNPDIDLYWFTLYQFFLAFLAPFVVITAAVYRILOQMTSSVAP 241
QY 311 ASQRSIRLRTKRVTRTAIAICLVFVCWAPYVYLQTLQSLISRPDLTFVLYNNAISLGY 370
Db 242 ASQRSIRLRTKRVTRTAIAICLVFVCWAPYVYLQTLQSLISRPDLTFVLYNNAISLGY 301
QY 371 ANSCLNPFVYIYVLCETFRKRLVLSVKPAAQGLRAVSNAQTADERTESKGT 422
Db 302 ANSCLNPFVYIYVLCETFRKRLVLSVKPAAQGLRAVSNAQTADERTESKGT 353
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RESULT 6
US-09-224-426-4
; Sequence 4, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Ralsia
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453/JPW/JHB
; CURRENT APPLICATION NUMBER: US/09/224,426
; CURRENT FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: rat
; US-09-224-426-4
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Query Match      79.5%; Score 1758; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 2.4e-136;
Matches 338; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
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Db 2 DLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFGTICLLIGNSTV 61
QY 131 IFAVVKKSKLHWCNNVPDIFINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLITA 190
Db 62 IFAVVKKSKLHWCNNVPDIFINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLITA 121
QY 191 MDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFSITPVWLY 250
Db 302 MDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFSITPVWLY 250
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Db 122 MDANSQFTSTYILTAMTIDRYLATVHPISSTKFRKPSMATLVICLLMALSFISITPVWLY 181
QY 251 ARLIPEPGGAVGCGIRLPNDPDTLWFTLYQFFLAFLPFWVITAAYVRILOMTSSVAP 310
Db 182 ARLIPEPGGAVGCGIRLPNDPDTLWFTLYQFFLAFLPFWVITAAYVKILQMTSSVAP 241
QY 311 ASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNNAISLGY 370
Db 242 ASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNNAISLGY 301
QY 371 ANSCINPFVYIVLCETFRKRLVLSVKPAAQGOLRTVSNQOTADEERTESKGT 422
Db 302 ANSCINPFVYIVLCETFRKRLVLSVKPAAQGOLRTVSNQOTADEERTESKGT 353

RESULT 7
US-09-478-601-4
; Sequence 4, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453z\JPW
; CURRENT APPLICATION NUMBER: US/09/478, 601
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224, 426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-478-601-4

Query Match 79.5%; Score 1758; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 2.4e-136;
Matches 338; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 71 DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSYFGTICLLGIIGNSTV 130
Db 2 DLQTSLSLTGPNASNISDGQDNLTLPGSPRTGSVSYINIMPSYFGTICLLGIIGNSTV 61
QY 131 IFAVVKKSKLHMCNVPDIFIINLSVVDLFLGLMPFMIHQLMGVWHFGETMCTLITA 190
Db 62 IFAVVKKSKLHMCNVPDIFIINLSVVDLFLGLMPFMIHQLMGVWHFGETMCTLITA 121
QY 191 MDANSQFTSTYILTAMTIDRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWLY 250
Db 122 MDANSQFTSTYILTAMTIDRYLATVHPISSTKFRKPSMATLVICLLMALSFISITPVWLY 181
QY 251 ARLIPEPGGAVGCGIRLPNDPDTLWFTLYQFFLAFLPFWVITAAYVRILOMTSSVAP 310
Db 182 ARLIPEPGGAVGCGIRLPNDPDTLWFTLYQFFLAFLPFWVITAAYVKILQMTSSVAP 241
QY 311 ASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNNAISLGY 370
Db 242 ASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNNAISLGY 301
QY 371 ANSCINPFVYIVLCETFRKRLVLSVKPAAQGOLRAVSNQOTADEERTESKGT 422
Db 302 ANSCINPFVYIVLCETFRKRLVLSVKPAAQGOLRTVSNQOTADEERTESKGT 353

RESULT 8
US-09-478-602-4
; Sequence 4, Application US/09478602
; Patent No. 6291195
; GENERAL INFORMATION:

; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453y\JPW
; CURRENT APPLICATION NUMBER: US/09/478, 602
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224, 426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-478-602-4

Query Match 79.5%; Score 1758; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 2.4e-136;
Matches 338; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 71 DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSYFGTICLLGIIGNSTV 130
Db 2 DLQTSLSLTGPNASNISDGQDNLTLPGSPRTGSVSYINIMPSYFGTICLLGIIGNSTV 61
QY 131 IFAVVKKSKLHMCNVPDIFIINLSVVDLFLGLMPFMIHQLMGVWHFGETMCTLITA 190
Db 62 IFAVVKKSKLHMCNVPDIFIINLSVVDLFLGLMPFMIHQLMGVWHFGETMCTLITA 121
QY 191 MDANSQFTSTYILTAMTIDRYLATVHPISSTKFRKPSVATLVICLLMALSFISITPVWLY 250
Db 122 MDANSQFTSTYILTAMTIDRYLATVHPISSTKFRKPSMATLVICLLMALSFISITPVWLY 181
QY 251 ARLIPEPGGAVGCGIRLPNDPDTLWFTLYQFFLAFLPFWVITAAYVRILOMTSSVAP 310
Db 182 ARLIPEPGGAVGCGIRLPNDPDTLWFTLYQFFLAFLPFWVITAAYVKILQMTSSVAP 241
QY 311 ASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNNAISLGY 370
Db 242 ASQRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNNAISLGY 301

RESULT 9
US-08-602-809-2
; Sequence 2, Application US/08602809
; Patent No. 6008012
; GENERAL INFORMATION:
; APPLICANT: BERGMA, DERK
; APPLICANT: ELLIS, CATHERINE
; TITLE OF INVENTION: HUMAN SOMATOSTATIN-LIKE R
; TITLE OF INVENTION: ECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: US
; ZIP: 19482-0980
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; APPLICATION DATA:
; APPLICATION NUMBER: US/08/602, 809
; FILING DATE: 13-JUN-1997


```

; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16472
; FILING DATE: 15-DEC-1995
; APPLICATION NUMBER: US 08/357,675
; FILING DATE: 16-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: P50277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 601-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-602-809-2
```

```

Query Match          76.5%; Score 1691; DB 3; Length 402;
Best Local Similarity 82.9%; Pred. No. 8.5e-131;
Matches 340; Conservative 7; Mismatches 15; Indels 48; Gaps 4;
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QY 50 PAWEGS--SARLMEQATGTGWADLEASLLPTGPNASNTSDGPDN----- 92
   |:||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 4 PSKTDGSGHSGRIHQETHGEGRD-----KISN-SEGRENGGRGFQMGSLAE 52
QY 93 -----LTSAGSPRTGSIYINIMPSVFGTICLLIGNSTVIF 132
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 53 HASRMSVLRAPKPMNSQRLLLCPGSPRTGISYINIMPSVFGTICLLIGNSTVIF 112
QY 133 AVVKKSKLHCNNVDFIINLSVVDLFLGMPFIHQLMGNGVWHFGETMCTLTAMD 192
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 113 AVVKKSKLHCNNVDFIINLSVVDLFLGMPFIHQLMGNGVWHFGETMCTLTAMD 172
QY 193 ANSOFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFSITPVWLYAR 252
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 173 ANSOFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFSITPVWLYAR 232
QY 253 LIPEPGAVGCGIRLPNPDTLWFTLYQFELAFALPFVVTAAVRILOQMTSSVAPAS 312
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 233 LIPEPGAVGCGIRLPNPDTLWFTLYQFELAFALPFVVTAAVRILOQMTSSVAPAS 292
QY 313 QRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNAAISLGYAN 372
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 293 QRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNAAISLGYAN 352
QY 373 SCLNPFVYIVLCETFRKRLVLSVKPAAOGQLRAVSNAQTADERTESKGT 422
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 353 SCLNPFVYIVLCETFRKRLVLSVKPAAOGQLRAVSNAQTADERTESKGT 402
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RESULT 10
PCT-US95-16472-2
; Sequence 2, Application PC/TUS9516472
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk J
; APPLICANT: Ellis, Catherine E
; TITLE OF INVENTION: Human Somatostatin Receptor
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation/Corporate
; ADDRESSEE: Intellectual Proper
; STREET: P. O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
;
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16472
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5024
; TELEFAX: 610 270 5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; PCT-US95-16472-2
```

```

Query Match          76.0%; Score 1680; DB 5; Length 400;
Best Local Similarity 82.8%; Pred. No. 6.7e-130;
Matches 338; Conservative 7; Mismatches 15; Indels 48; Gaps 4;
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QY 50 PAWEGS--SARLMEQATGTGWADLEASLLPTGPNASNTSDGPDN----- 92
   |:||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 4 PSKTDGSGHSGRIHQETHGEGRD-----KISN-SEGRENGGRGFQMGSLAE 52
QY 93 -----LTSAGSPRTGSIYINIMPSVFGTICLLIGNSTVIF 132
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 53 HASRMSVLRAPKPMNSQRLLLCPGSPRTGISYINIMPSVFGTICLLIGNSTVIF 112
QY 133 AVVKKSKLHCNNVDFIINLSVVDLFLGMPFIHQLMGNGVWHFGETMCTLTAMD 192
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 113 AVVKKSKLHCNNVDFIINLSVVDLFLGMPFIHQLMGNGVWHFGETMCTLTAMD 172
QY 193 ANSOFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFSITPVWLYAR 252
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 173 ANSOFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFSITPVWLYAR 232
QY 253 LIPEPGAVGCGIRLPNPDTLWFTLYQFELAFALPFVVTAAVRILOQMTSSVAPAS 312
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 233 LIPEPGAVGCGIRLPNPDTLWFTLYQFELAFALPFVVTAAVRILOQMTSSVAPAS 292
QY 313 QRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNAAISLGYAN 372
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 293 QRSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLTFVYLYNAAISLGYAN 352
QY 373 SCLNPFVYIVLCETFRKRLVLSVKPAAOGQLRAVSNAQTADERTESK 420
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 353 SCLNPFVYIVLCETFRKRLVLSVKPAAOGQLRAVSNAQTADERTESK 400
```

```

RESULT 11
US-08-120-601B-9
; Sequence 9, Application US/08120601B
; Patent No. 6235496
; GENERAL INFORMATION:
; APPLICANT: Yu, lei
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSOTIONS AND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
;
; COMPUTER READABLE FORM:
```


ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-417-103-8

Query Match 24.18; Score 532; DB 1; Length 369;
Best Local Similarity 31.7%; Pred. No. 4.9e-36;
Matches 118; Conservative 76; Mismatches 132; Indels 46; Gaps 10;

QY 62 EQATGTG-WA----DLEASLPTGPNASNTSDGPDNLTSAGSPPTGTSISYINIMPSVF 116
DB 6 EQLNGSQVWSSPFDLNGSLGPS--NGSNQTEPYDMTS-----NAVLTFTY 50
QY 117 GTICLLGIIGNSTVIFAVVKKSKLHWCNNVDPDIFINLSVVDLFLGMPE-----MIH 170
DB 51 FVVCVVGLCGNTLVIYVILRYAKM--KTITNIIYILNLAIADLEFLMLGLPFLAMQVALVH 107
QY 171 QLMGNGVWHFEGTCTLTITAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVAT 230
DB 108 -----WPFKAICRVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRPRRTAK 160
QY 231 LVICLLMALSEISTPVPVLYARLIPPEGAVGCGIRLPNPDLDLY-WETLYQFLAFALP 289
DB 161 MINVAVWCVSLVILPIMITYAGLRSNQWGRSSCTINWPGESGAWYTGFTIYAFILGFLVP 220
QY 290 FVVITAAVRIQMTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPYVYQLTQL 349
DB 221 LTIICLCYLFILIKVSSGIRVGSSKRKKSEKVTRMVSIYAVEIFCWLPEYIFNVSSV 280
QY 350 SIS-RPTLTFVYLYNAISLGYANSCINPFEVYIVLCETFRKRLVLSVKPAAQGLRAVSN 408
DB 281 SVAISPTPALKGMPDEFVILTYANSKANPILYAFLSDNFKK-----SFQNVLCIVKV 332
QY 409 AQTADERTESK 420
DB 333 SGTEDGERSDSK 344

RESULT 14
US-07-816-283-6
; Sequence 6, Application US/07816283
; Patent No. 5436155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee

STREET: PO Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/816,283
FILING DATE: 19911231
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-816-283-6

Query Match 24.0%; Score 530.5; DB 1; Length 369;
Best Local Similarity 31.8%; Pred. No. 6.5e-36;
Matches 114; Conservative 75; Mismatches 128; Indels 41; Gaps 8;

QY 71 DLEASLPTGPNASNTSDGPDNLTSAGSPPTGTSISYINIMPSVFGTICLLGIIGNSTV 130
DB 20 DLNGSVYST--NTSNQTEPYDLS-----NAVLTFTYFVVCITIGLCGNTLV 64
QY 131 IFVAVVKKSKLHWCNNVDPDIFINLSVVDLFLGMPE-----MIHQLMGNGVWHFETM 184
DB 65 IYVILRYAKM--KTITNIIYILNLAIADLEFLMLGLPFLAMQVALVH-----WPFKA 114
QY 185 CULITAMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSEISI 244
DB 115 CRVAVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRPRRTAKMITMAVWCVSLVI 174
QY 245 TPVWLYARLIPPEGAVGCGIRLPNPDLDLY-WETLYQFLAFALPFEVITAAVRIQOR 303
DB 175 LPIMITYAGLRSNQWGRSSCTINWPGESGAWYTGFTIYFILGFLVPLTIICLCYLFIIK 234
QY 304 MTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCWAPYVYQLTQLSIS-RPTLTFVYLY 362
DB 235 VKSSGIRVGSSKRKKSEKVTRMVSIYAVEIFCWLPEYIFNVSSVMAISPTPALKGMP 294
QY 363 NAAISLGYANSCINPFEVYIVLCETFRKRLVLSVKPAAQGLRAVSNQADERTESK 420
DB 295 DEVVVLTLYANSKANPILYAFLSDNFKK-----SFQNVLCIVKSGTDDGERSDSK 344

RESULT 15
US-08-417-103-6
; Sequence 6, Application US/08417103
; Patent No. 5723299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America

```
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,103
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/816,283
; FILING DATE: 01-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-417-103-6
```

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Query Match 24.0%; Score 530.5; DB 1; Length 369;
Best Local Similarity 31.8%; Pred. NO. 6.5e-36;
Matches 114; Conservative 75; Mismatches 128; Indels 41; Gaps 8;
```

```
OY 71 DLEASLPTGPNASNTSDGPDNLTSGSPRTGISYINIMPSVFGTICLLIGIGNSTV 130
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 20 DLNGSVST--NTSNQTEPYDLS-----NAVLTIFYFVVCIIIGCNTLV 64

OY 131 IEAVVKKSKLHWCNNVPDIFITNLVVDLLFLGMPF-----MIHQLMGVWHFGETM 184
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 65 IYVILRYAKM---KITNTIYILNLAIADLFMLGLPFLAMQVALVH-----WPGKAI 114

OY 185 CTLITAMDANSQFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLWALSFISI 244
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 115 CRVVMIVDGINQFTSIFCLTVMGSDRYLAVVHPIKSAKWRPRRTAKMITMAVWGVSLLVI 174

OY 245 TPVWLYARLIPFPGGAVGCGIRLPNDTDLV-WFTLYQFLAFALPFVVITAAYVRIQR 303
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 175 LPIMTYAGLRSNQWGRSSCTINWPGESGAWYTGFIITYFIIIGFLVPLTIICLCYLIIRK 234

OY 304 MTSSVAPASQSRIRLTKRVRTALICLVFVVCWAPYYVLQTLQLSIS-RPTLTFVYLY 362
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 235 VKSSGIRVGSSKRKKSEKVTBMVSIYVAVFIFCWLPEYIFENVSSVSMASISPTPALKGMF 294

OY 363 NAAISLGYANSCINPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAQTADERTESK 420
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 295 DFVVVLTYANSCANPILYAFLSDNEFK-----SFQNVLCIVKVSGETDGERSDSK 344
```

Search completed: February 13, 2003, 14:01:48
Job time : 13.3392 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2003, 13:55:16 ; Search time 29.2615 Seconds
(without alignments)
2971.547 Million cell updates/sec

Title: US-09-885-478-2
Perfect score: 2212
Sequence: 1 MSVGAMKKGVGRAVGLGGS.....LRVSNAGTADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_21:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2212	100.0	422	4 Q9BV08	Q9bv08 homo sapien
2	2207	99.8	422	4 Q96S47	Q96s47 homo sapien
3	601	27.2	121	6 Q9MZ01	Q9mz01 sus scrofa
4	565.5	25.6	340	4 Q969V1	Q969v1 homo sapien
5	559.5	25.3	340	4 Q9BXA8	Q9bxa8 homo sapien
6	559.5	25.3	340	6 Q8SQ54	Q8sq54 macaca fasc
7	523	23.6	370	13 Q8UWL5	Q8uw15 fugu rubrip
8	521.5	23.6	346	4 Q96GE0	Q96ge0 homo sapien
9	516.5	23.3	356	4 Q96TF2	Q96tf2 homo sapien
10	516	23.3	346	11 Q91Y73	Q91y73 mus musculu
11	502.5	22.7	367	13 Q9PVG0	Q9pvg0 carassius a
12	499.5	22.6	367	13 Q9PVF9	Q9pvf9 carassius a
13	497	22.5	315	6 Q9GKP7	Q9gkp7 sus scrofa
14	494.5	22.4	346	6 Q95KS6	Q95ks6 ovis aries
15	487	22.0	380	13 Q9DGO6	Q9dgo6 carassius a
16	469	21.2	390	13 Q8QGQ4	Q8qgq4 carassius a

17	457	20.7	385	11 Q9JK40	Q9jk40 mus musculu
18	453.5	20.5	390	11 Q8VI71	Q8vi71 mus musculu
19	453.5	20.5	391	11 Q8VI70	Q8vi70 mus musculu
20	453.5	20.5	393	11 Q9R1M0	Q9rlm0 mus musculu
21	453.5	20.5	401	11 Q9R1L9	Q9rl19 mus musculu
22	453.5	20.5	409	11 Q8VI69	Q8vi69 mus musculu
23	453.5	20.5	438	11 Q9R0D1	Q9r0d1 mus musculu
24	453.5	20.5	444	11 Q9JTY1	Q9jiy1 mus musculu
25	448	20.3	454	4 Q9H573	Q9h573 homo sapien
26	443	20.0	400	6 Q95M54	Q95m54 macaca fasc
27	435	19.7	383	13 Q42324	Q42324 catostomus
28	422.5	19.1	377	13 Q98U14	Q98u14 brachydanio
29	422	19.1	384	13 Q98UH1	Q98uh1 brachydanio
30	412	18.6	451	5 Q9VVO1	Q9vvq1 drosophila
31	407	18.4	373	13 Q57585	Q57585 brachydanio
32	402.5	18.2	272	4 Q9BWH1	Q9bwh1 homo sapien
33	393	17.8	362	11 Q8VI74	Q8vi74 mus musculu
34	392	17.7	362	11 Q9JIN4	Q9jin4 rattus norv
35	373	16.9	380	5 Q9NEV2	Q9nfv2 lymnaea sta
36	370.5	16.7	393	5 Q9VVO0	Q9vvq0 drosophila
37	367	16.6	291	11 Q91Z24	Q91zz4 mus musculu
38	367	16.6	325	11 Q8VIN4	Q8vin4 mus musculu
39	367	16.6	330	11 Q8VIP1	Q8vip1 mus musculu
40	367	16.6	370	11 Q8VIP0	Q8vip0 mus musculu
41	366	16.5	380	5 Q9NEV1	Q9nfv1 lymnaea sta
42	364.5	16.5	380	5 Q9NEV3	Q9nfv3 lymnaea sta
43	363	16.4	380	5 Q9NEV0	Q9nfv0 lymnaea sta
44	361.5	16.3	359	13 Q9PVY7	Q9pvy7 anguilla an
45	361	16.3	423	5 Q964D4	Q964d4 periplaneta

ALIGNMENTS

RESULT 1

Q9BV08 PRELIMINARY; PRT; 422 AA.

AC Q9BV08; 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Similar to G protein-coupled receptor 24 (Hypothetical 46.0 kDa protein).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RA Strausberg R.;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RA Strausberg R.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC001736; AAH01736.1; -.

DR EMBL; BC021146; AAH21146.1; -.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PRO1559; DUFFYANTIGEN.

DR	PRINTS; PRO0237; GPCR_RHODPSN.
DR	PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
KW	Receptor; Hypothetical protein.
SQ	SEQUENCE 422 AA; 45963 MW; 86A9F398B5D5F397 CRC64;

Query Match 100.0%; Score 2212; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 4.3e-183;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVGRAVGLGGSGQATEEDPLPDGCACAPGQGRRWRLPPAWEGSSARL 60
|||||

Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDGCACAPGQGGRRWRLPQPAWVEGSSARL 60
QY 61 WEQATGTGWMDLASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVEGTIC 120
Db 61 WEQATGTGWMDLASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVEGTIC 120
QY 121 LGGTGNSTVIFAIVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHF 180
Db 121 LGGTGNSTVIFAIVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHF 180
QY 181 GETMCTLITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240
Db 181 GETMCTLITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240
QY 241 FISITPVWLYARLIPFPGAVGCGIRLPNPDLDLYWFTLYQFFLAFALPFVVITAAVRI 300
Db 241 FISITPVWLYARLIPFPGAVGCGIRLPNPDLDLYWFTLYQFFLAFALPFVVITAAVRI 300
QY 301 LQRMSSVAPASQORSIRLRTKRVTRTAIAICLVFVWCWAPYVYLQTLQLSISRPTLTFVY 360
Db 301 LQRMSSVAPASQORSIRLRTKRVTRTAIAICLVFVWCWAPYVYLQTLQLSISRPTLTFVY 360
QY 361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPPAOGQLRAVSNAQTADDEERTESK 420
Db 361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPPAOGQLRAVSNAQTADDEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 2

Q96S47 PRELIMINARY; PRT; 422 AA.
AC Q96S47;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Somatostatin receptor-like protein.
GN SLC-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sugo T., Mori M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99373129; PubMed=10441476;
RA Shimomura Y., Mori M., Sugo T., Ishibashi Y., Abe M., Kurokawa T.,
RA Onda H., Nishimura O., Sumino Y., Fujino M.;
RT "Isolation and identification of melanin-concentrating hormone as the
RT endogenous ligand of the SLC-1 receptor.";
RL Biochem. Biophys. Res. Commun. 261:622-626(1999).
DR EMBL; AB063174; BAB60890.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01559; DUFFYANTIGEN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 422 AA; 45962 MW; 3986919A18183818 CRC64;

Query Match 99.8%; Score 2207; DB 4; Length 422;
Best Local Similarity 99.8%; Pred. No. 1.2e-182;
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDGCACAPGQGGRRWRLPQPAWVEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDGCACAPGQGGRRWRLPQPAWVEGSSARL 60
QY 61 WEQATGTGWMDLASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVEGTIC 120

Db 61 WEQATGTGWMDLASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVEGTIC 120
QY 121 LGGTGNSTVIFAIVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHF 180
Db 121 LGGTGNSTVIFAIVVKKSKLHWCNNVPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHF 180
QY 181 GETMCTLITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240
Db 181 GETMCTLITAMDANSQFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLLMALS 240
QY 241 FISITPVWLYARLIPFPGAVGCGIRLPNPDLDLYWFTLYQFFLAFALPFVVITAAVRI 300
Db 241 FISITPVWLYARLIPFPGAVGCGIRLPNPDLDLYWFTLYQFFLAFALPFVVITAAVRI 300
QY 301 LQRMSSVAPASQORSIRLRTKRVTRTAIAICLVFVWCWAPYVYLQTLQLSISRPTLTFVY 360
Db 301 LQRMSSVAPASQORSIRLRTKRVTRTAIAICLVFVWCWAPYVYLQTLQLSISRPTLTFVY 360
QY 361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPPAOGQLRAVSNAQTADDEERTESK 420
Db 361 LYNAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPPAOGQLRAVSNAQTADDEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 3

Q9MZ01 PRELIMINARY; PRT; 121 AA.
AC Q9MZ01;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Melanin-concentrating hormone receptor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN; HYPOPHALAMUS;
RA Matteri R.L.;
RT "Sus scrofa melanin-concentrating hormone (MCH) receptor.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF273611; AAF81827.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13583 MW; 884D8268B6F9F010 CRC64;

Query Match 27.2%; Score 601; DB 6; Length 121;
Best Local Similarity 99.2%; Pred. No. 1.9e-44;
Matches 120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 294 TAAVYRILQRMSSVAPASQORSIRLRTKRVTRTAIAICLVFVWCWAPYVYLQTLQLSISR 353
Db 1 TAAVYRILQRMSSVAPASQORSIRLRTKRVTRTAIAICLVFVWCWAPYVYLQTLQLSISR 60
QY 354 PTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPPAOGQLRAVSNAQTAD 413
Db 61 PTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPPAOGQLRAVSNAQTAE 120
QY 414 E 414
Db 121 E 121

Db 330 NMGN 334

RESULT 6

Q8S054 PRELIMINARY; PRT; 340 AA.

AC Q8S054; 01-JUN-2002 (TReMBLrel. 21, Created)

DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)

DE GPRV17. 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

GN GPRV17.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

OC Cercopitheciinae; Macaca.

OX NCBI_TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RA Kurama T., Matsumoto S., Takasaki J., Terai K., Matsumoto M.,

RA Kamohara M., Saito T., Soga T., Saito Y., Oda T., Masuno Y.,

RA Furutachi K.;

RT "Molecular characterization of a novel melanin-concentrating hormone

RT receptor : Evidence of its expression in lateral hypothalamus.";

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB058850; BAB87843.1; "

SQ SEQUENCE 340 AA; 38769 MW; BD22CF1972332439 CRC64;

Query Match 25.3%; Score 559.5; DB 6; Length 340;

Best Local Similarity 36.7%; Pred. No. 2.6e-40;

Matches 112; Conservative 60; Mismatches 122; Indels 11; Gaps 4;

QY 110 IMPSVFGTICLLGIGNSTVIFAIVKSKRLHWCNNVPDIFINLSVVDLLFLGMPPI 169

Db 35 VILPSMIGIICSTGLVGNILIVFTIIRSRK---KTVPDITICMLAVADLVHIIIGMPFLI 90

QY 170 HOLMGNGVWHFGEYMCITLTAMDANSQFTSTYIITAMAIDRYLATVHPISSTKFRKPSVA 229

Db 91 HOWARGGEWVFGPCLCTITITSLDTCNQFACSAIMTVMSVDRYPALVQPRLTSMWRPYKT 150

QY 230 TLVICLLWALSFISITPVWLYARLIPPGGAVGCGIRLPNPDIDLWFTLYQEFALP 289

Db 151 IRINLGLWASFILALPVWYISKVIFKDGVECAFDLTSPD-DVLWYTLTYLTITPFPFP 209

QY 290 FVVTAAVYRIL-----QRMTSVAPASQRSI-RLRTKRVTRTAIAICLVFVVCWAPYV 343

Db 210 IPLIVCYILILCYWEMYQONKDARCCNSVPKQRMKLTVMYLVLVAVFILSAAPYHV 269

QY 344 LQLTQLSISRPTLTFVYLYNNAISLGYANSCINPEVYIVLCETFRKRLVLSVKPAAGOL 403

Db 270 IQLVNLQMEOPTLAFVGYYSICLSYASSINPFLYILLSGNFQKRLPQIQRRVTDKEI 329

QY 404 RAVSN 408

Db 330 KNMGN 334

RESULT 7

Q8UWL5 PRELIMINARY; PRT; 370 AA.

AC Q8UWL5; 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DE Somatostatin receptor 2.

GN SSTR2.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Takifugu.

OX NCBI_TaxID=31033;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21564205; Pubmed=11707075;

RA Bagheri-Fam S., Ferraz C., Demaille J., Scherer G., Pfeifer D.;

RT "Comparative Genomics of the SOX9 Region in Human and Fugu rubripes:

RT Conservation of Short Regulatory Sequence Elements within Large

RT Intergenic Regions.";

RL Genomics 78:73-82(2001).

DR EMBL; AF329945; AAL32173.1; "

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_RHODPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

SQ SEQUENCE 370 AA; 41364 MW; 420BH12F204946B6 CRC64;

Query Match 23.6%; Score 523; DB 13; Length 370;

Best Local Similarity 32.9%; Pred. No. 4.2e-37;

Matches 128; Conservative 74; Mismatches 131; Indels 56; Gaps 13;

QY 45 WRLPQPAWVEGSSARLW---EQATGTGWMMDLEASLLPTGPNASNTSDGPDNLTSAGSPR 101

Db 4 WILP-PSPLNLSDDLHYDGFEGANGS---DLHA-----NRTDHLNKTG----- 43

QY 102 TGSISYINIMPSVEGTICLLGIGNSTVIFAIVKSKRLHWCNNVPDIFINLSVVDLLF 161

Db 44 -----TVVITCMFLVCAGVLCGNALVTVILRYAKM---KTVTNITILNLAVADVLF 93

QY 162 LLGMPFMIHOLMGNGVWHFGEYMCITLTAMDANSQFTSTYIITAMAIDRYLATVHPISST 221

Db 94 MLGLPFLAIQL-ALVHWPFPGVLCRVMTVDSLNDFTSIFCLMVMSIDRYLAVVHPIKST 152

QY 222 KFRKPSVALTVICLLWALSFISITPVWLYARLIPPGGAVGCGIRLPNPDIDLW-FTLY 280

Db 153 KWRKPRVAKTINVAVWGASLVVNDPIVIYSGITRKODCF-CTIWWPEPEAYTAFMIT 211

QY 281 QEFALPAPFVVTAAVYRIQRMTSVAPASQRSIRLRTKRVTRTAIAICLVFVVCWAP 340

Db 212 TFLGFPLPLLVISLCYVFITVYKSSGIRVGSKRKRSEKVTVMYSIVAVFVLCWLP 271

QY 341 YVYLQLTQDS-----ISRPTLTFVYLYNNAISLGYANSCINPEVYIVLCETFRKRL-- 391

Db 272 FYVENVTSTGTSISATHVLRSTFAFV-----VVLGYANSCANPILYAFUSENFKKSQN 325

QY 392 VLSVKPAAGQLRAVSNACQTADERTESK 420

Db 326 VLCLQ-----KVGGLDEAERSDSRQDKSR 349

RESULT 8

Q96GEO PRELIMINARY; PRT; 346 AA.

AC Q96GEO; 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DE Unknown (Protein for IMAGE:3354783) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC009522; AAH09522.1; "

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

FT NON_TER 1 1

SQ SEQUENCE 346 AA; 38790 MW; EA073A6CC05FEB72 CRC64;

Query Match	23.6%;	Score 521.5;	DB 4;	Length 346;
Best Local Similarity	31.7%;	Pred. NO. 5.2e-37;		
Matches 110;	Conservative 73;	Mismatches 125;	Indels 39;	Gaps 7;

[illegible]

RESULT 9

ID Q96TF2 PRELIMINARY; PRT; 356 AA.

DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Somatostatin receptor 2B.
GN SSTR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
RX MEDLINE=20084417; Pubmed=10619399;
RA Petersenn S., Rasch A.C., Presch S., Beil F.U., Schulte H.M.;
RT "Genomic structure and transcriptional regulation of the human
RT somatostatin receptor type 2."
RL Mol. Cell. Endocrinol. 157:75-85(1999).
DR EMBL; AF184174; AAF42810.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PSS0262; G_PROTEIN_RECEP_FL_2; 1.
SQ SEQUENCE 356 AA; 4006 MW; D10FA237FAED61F3 CRC64;

Query Match	23.3%;	Score 516.5;	DB 4;	Length 356;
Best Local Similarity	30.7%;	Pred. No. 1.5e-36;		
Matches 111;	Conservative 78;	Mismatches 123;	Indels 49;	Gaps 10;

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QY 69 WM---DLEASLLFTGPNASNTSDGPDNLTSAGSPPRGTGTSYINIIMPSVEFTICLLGI 124
   1: 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 14 WLSIFEDLNGSVST--NTSMQTEPYD LTS-----NAVLTFTYFVVCII GL 58

QY 125 IGNSTVIFAVYKKS KLHWCNNVPDIFILNSVDLLFLIGMDF-----MIHQLMGNVW 178
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 59 CGNTLVIVYLLRYAKM--KTITNIIYLLNLAIADLFMLGPEFLAMQVALVH-----W 108

QY 179 HGEETMCLITAMDANSQFTSYILITAMADRYLATVHPITSTKFRKPSVATLVICLLMA 238
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 109 PFGKAICRVAVTVDGINQFTSIFCLTVMSIDRYLAVVHPITSAKAWRRPRTAKMITMAVWG 168
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QY      239 LSFISITPVMVLARLIIPFGAVGCGIRLPNEDTDLY-WFTLYQGFETFAALPEFVVITAAV 297
      : : : : : | : : : : :
Db      169 VSLVLVPIIMVIAGLRNSQWGRSSCTINWPGESGAWYTGFIITYTFLIGLPLVPLTIICLCY 228

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QY      298 VRLQRMSSVAPASQSRIRLRTKRVFTATAICLVEFVCWAPYYVLQTLQLSIS-RPTL 356
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      229 LFLIKVSSGIRVGSSKKRKKSEKVTBMSIYAVFIFCWLPEYIFENSVSMAISPTP 288

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QY      357 TFFVLYNMAISLGANSCLNPFIYIVLCETFRK---RLVLSVKPAAGGLRAVSNAQTAD 413
        :: : | |||| | : | : | : | : | : | : | : | : | : | : | : | : |
Db      289 ALKGMEFVVVLTYSANSCANPILYAFLSDNFKFSQNVLCLVK-----VDNSKSGE 339
```

QY	414	E	414
Db	340	E	340

RESULT 10
Q91Y73
ID Q91Y73 PRELIMINARY; PRT; 346 AA.

DT	01-DEC-2001 (TREMBlrel. 19, Created)
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE	Somatostatin receptor type 2.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RP SEQUENCE FROM N. A.
RC STRAIN=129; TISSUE=LIVER;
RX MEDLINE=21201198; PubMed=11278805;
RA Puente E., Saint-Laurent N., Torrisani J., Furet C., Schally A.V.,
RA Vaysse N., Buscail L., Susini C.;
RT "Transcriptional Activation of Mouse sst2 Somatostatin Receptor
RT Promoter by Transforming Growth Factor-beta. Involvement of Smad4.";
RL J. Biol. Chem. 276:13461-13468(2001).

DR MGD; MGI:98328; Smtstr2.
DR InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
DR PROSITE; PS02662; G_PROTEIN_RECIP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 346 AA; 38586 MW; D7A20AEFC1371C400 CRC64;

Query Match	23.3%;	Score 516;	DB 11;	Length 346;
Best Local Similarity	31.28;	Pred. No. 1.6e-36;		
Matches 115;	Conservative 77;	Mismatches 129;	Indels 48;	Gaps 11;

```
OY      62 EQATGTG-WM---DIEASLLPTGPNASNTSDGPNLTSAGSPRTGSISYINIIMPSVF 116
        || |::| | | | | | | | | | | | | | | | | | | | | | | | | |
```

QY 117 GTICLLGIGNSTVIAVVKSKSLHCNNVPDIFIINLSVDLLELLGMPF-----MIH 170

Db 51 FVVCVVGLCGNTLVIYVILRYAKM---KITITNIYLNLAIADLFLMGLPELMAQVALVH 107

QY 171 QLMGNGVWHFGEIMCTLITAMDANSQFTSTYILITAMADRYLATVHPISSTKFRKPSVAT 230

[illegible]

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Db      161 MINVAWCVSLVLPIMITYAGLRSNQWRSSCTINMPGESGAWYTGFIYAIFLGLVP 220
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Db      221 LTICLCYLFIIIKVSSGIRVGSSKKRKKSEKVTBMVSIVVAVFECWLPFIYNVSV 280
```

QY 350 SIS-RPTLFVYLYNAISLGYANSCINPFVYIVLCETFRKRL--VLSVKPAAGQLRAV 406

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QY      239 LSFISITPWWLVARLIIPFGAVGCGIRLPNEDTDLY-WFTLLYQETFLAALPEVVTAAAY 297
          :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      169 VSLVLVPLIMIYAGLRNSNQWRSSCTINWPGESGAWYTGFIIYTFILGLPLVPLTIICLCY 228
```

```

QY      298 VRLQRMSSVAPASQSRIRLRTKRVFTATAICLVEFVCWAPYYVLTQLTQLSIS-RPTL 356
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      229 LFLIKVSSGIRVSSSKRKKSEKVTBMSIYAVFIFCWLPEYIFENSSVMAISPPT 288

```

```
QY      357 TFFVLYNMAISLGANSCLNPFVIYLCEFERK---RLVLVKPAAOGGLEPAVSNAQTAD 413  
       :: : | ||||| | : | : | : |  
Db     289 ALKGMEFVVLLTYANSCLNPILYAFLSDNFKSQNVLCLK-----VDNSKSGE 339
```

QY	414	E	414
Db	340	E	340

RESULT 10
Q91Y73
ID Q91Y73 PRELIMINARY; PRT; 346 AA.

DT	01-DEC-2001 (TREMBlrel. 19, Created)
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE	Somatostatin receptor type 2.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RP SEQUENCE FROM N. A.
RC STRAIN=129; TISSUE=LIVER;
RX MEDLINE=21201198; PubMed=11278805;
RA Puente E., Saint-Laurent N., Torrisani J., Furet C., Schally A.V.,
RA Vaysse N., Buscail L., Susini C.,
RT "Transcriptional Activation of Mouse sst2 Somatostatin Receptor
RT Promoter by Transforming Growth Factor-beta. Involvement of Smad4.";
RL J. Biol. Chem. 276:13461-13468(2001).

DR MGD; MGI:98328; Smtstr2.
DR InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 346 AA; 38586 MW; D7A20AEFC1371C400 CRC64;

Query Match	23.3%;	Score 516;	DB 11;	Length 346;
Best Local Similarity	31.28;	Pred. No. 1.6e-36;		
Matches 115;	Conservative 77;	Mismatches 129;	Indels 48;	Gaps 11;

```
OY      62 EQATGTG-WM---DIEASLLPTGPNASNTSDGPNLTSAGSPRTGSISYINIIMPSVF 116
      || |::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

QY 117 GTICLLGIGNSTVIAVVKSKSLHCNNVPDIFIINLSVDLLELLGMPF-----MIH 170

Db 51 FVVCVVGLCGNTLVIYVILRYAKM---KITITNIYLNLAIADLFLMGLPELMAQVALVH 107

QY 171 QLMGNGVWHFGEIMCTLITAMDANSQFTSTYILITAMADRYLATVHPISSTKFRKPSVAT 230

[illegible]

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Db      161 MINVAWCVSLVLPIMITYAGLRSNQWRSSCTINMPGESGAWYTGFIYAIFLGLVP 220
```

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      :| | | | |
Db    221 LTTCLCYLFTIIKYKSSGIRVGSKKRKKSEKVTBMVSIVVAVFICWLPFIYFNSSV 280

```

QY 350 SIS-RPTLFVLYLNAISLGYANSCLNPFVYIVLCETFRKRL--VLSVKPAAGQLRAV 406

ID	Q9PVF9	PRELIMINARY;	PRT;	367 AA.
Db	281	SVAISPTPALKGMFEDFVILTYANSCANPILYAFUSDNEFKKSQYNVLCLVKA-----		332
QY	407	SNQOTADEE 415		
Db	333	DNSQSGAED 341		
RESULT 11				
Q9PVG0		PRELIMINARY;	PRT;	367 AA.
ID	Q9PVG0			
AC	Q9PVG0;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, last annotation update)			
DE	Somatostatin receptor type 1 subtype A.			
GN	SR1A.			
OC	Carassius auratus (Goldfish).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Carassius.			
OX	NCBI_Taxid=7957;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRAIN;			
RX	MEDLINE=20005543; PubMed=10537151;			
RA	Lin X., Janovick J.A., Brothers S., Conn P.M., Peter R.E.;			
RT	"Molecular cloning and expression of two type one somatostatin			
RT	receptors in goldfish brain."			
RL	Endocrinology 140:5211-5219(1999).			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR	EMBL: AF097726; AAF08613.1; "			
DR	InterPro: IPR000276; GPCR_Rhodpsn.			
DR	pfam: PF00001; 7tm_1; 1.			
DR	PRINTS: PR00237; GPCR_Rhodpsn.			
DR	PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.			
DR	G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.			
QW	SEQUENCE 367 AA; 41658 MW; BE85E6C26C103614 CRC64;			
Query Match	22.7%;	Score 502.5;	DB 13;	Length 367;
Best local Similarity	30.1%;	Pred. No. 2.5e-35;		
Matches 97;	Conservative 80;	Mismatches 120;	Indels 25;	Gaps 6;
QY	71	DLEASLIPTGPNASNTSDGPDNLTSAGSPRTGTSISYINIMPSVFGTICLLGIIGNSTV 130		
Db	9	NLEDGLYLINFSSNETHNGDSHGSSA-----IFISFIYSVCLVGLGNSMV 55		
QY	131	IFAAVVKSKLHWCNVDPDIFIINLSVVDLLFLGMPFMIHQLMGNGVWHFGETMCTLITA 190		
Db	56	IYVIFRYAKMKTATN--IYLNLTAIDELMLSVPLVTSSLLH-WPFGSLLCRLVLS 111		
QY	191	MDANSQETSTYIITAMAIIDRYLATVHPISSTKFRKPSVATLVICLMAISFITPVWLY 250		
Db	112	VDAINMETSICYCLTVLSIDRYISVHPKARRYRPTIAKMVNLGVWMSILVLPITIF 171		
QY	251	ARLIPFGGAVGCGIRLPNDTDLW--FTLYQFLAFALPFVVITAAVRIIQRTSS 307		
Db	172	STTAPNSDGSVACNMQMEPERQ-WMAVFIYAFLMGFLFPVIAICMCIILITVKRVV 229		
QY	308	VAPASQSRSTRLTRKVRTTAITACLVFVCWAPYVVLQTLQLSISRPTLFEVLYNAAIS 367		
Db	230	ALKAGWQQRKKSEKRTITLMVMVMVTVFVICMWFHIMQLVSVFVQGHAT---LSQLAVI 286		
QY	368	LGYANSCLPFYIVLCETFRK 389		
Db	287	LGYANSCANPILYGLSDNFR 308		
RESULT 12				
Q9PVF9		PRELIMINARY;	PRT;	367 AA.
ID	Q9PVF9			

AC	Q9PVE9;	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE	Somatostatin receptor type 1 subtype B.	
GN	STR1B.	
OS	Carassius auratus (Goldfish).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC	Cyprinidae; Carassius.	
OX	NCBI_TaxID=7957;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE-BRAIN;	
RX	MEDLINE=20005543; PubMed=10537151;	
RA	Lin X., Janovick J.A., Brothers S., Conn P.M., Peter R.E.;	
RT	"Molecular cloning and expression of two type one somatostatin	
RT	receptors in goldfish brain."	
RL	Endocrinology 140:5211-5219(1999).	
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
DR	EMBL: AF097727; AAF08614.1; -.	
DR	InterPro: IPR000276; GPCR_Rhodpsn.	
DR	Pfam: PF00001; 7tm_1; 1.	
DR	PRINTS: PR00237; GPCR_RHODPSN.	
DR	PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.	
DR	PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.	
KW	G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.	
SQ	SEQUENCE 367 AA; 41614 MW; A5BA0AE68D47C455 CRC64;	
Query Match 22.6%; Score 499.5; DB 13; Length 367;		
Best Local Similarity 30.1%; Pred. No. 4.5e-35;		
Matches 97; Conservative 80; Mismatches 120; Indels 25; Gaps 6;		
QY	71 DLEASLLPTGPNASNTSDGPDNLTSAGSPPTGTSISYINIMPSVFGTICLLIGTIGNSTY 130	
DB	9 NLEEDGLYLLNFSSNETHNGDSHGSSA-----IFISFIYSVCLVGLCGNSMV 55	
QY	131 IFAYVKKSKLHWCNNVDPDIFIINLSVDLLFLGMPFIHOLMGNGVWHGETMCTLITA 190	
DB	56 IYVIFRYAKMKTATN--IYLLNLAADLLMLSVPLVTSSLHH-WPFGSLCRLVLS 111	
QY	191 MDANSQFTSTYIILTAMADRYLATVHPISSTRKPKPSVATLVICLLMALSFISITPWLY 250	
DB	112 VDAINMFTSYICLTVLSIDRYISVHPIKARARRPTIAKMVNLGVWMSILVILPIIF 171	
QY	251 ARLIPPGGAVGCGIRLPNDTDLW--FTLYQFLAFALPFVVITNAYVRILQRMVTS 307	
DB	172 STTAPNSDGSVACNMQMPERQ--WMAVFVITYAFLMGLFPVIAICGCIILIIYKMRV 229	
QY	308 VAPASQSRILRTKRVTRTAIAICLVFVCWAPYVYLQTLQSLISRPILTFVLYNAIS 367	
DB	230 ALKAGWQQRKSEKRTILMVMVTVFVICMPEHIVQLVSVFVQGHNST--LSQLAVI 286	
QY	368 LGYANSCLNPEVYIVLCETFRK 389	
DB	287 LGYANSCANPILYGLSDNFR 308	
RESULT 13		
Q9GKP7		
ID	Q9GKP7	PRELIMINARY; PRT; 315 AA.
AC	Q9GKP7;	
DT	01-MAR-2001 (TREMBLrel. 16, Created)	
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE	Somatostatin receptor 1 (Fragment).	
GN	SSTR1.	
OS	Sus scrofa (Pig).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
OX	NCBI_TaxID=9823;	
RN	[1]	

RP SEQUENCE FROM N.A.
RL MEDLINE=20556840; Pubmed=11105212;
RA Marklund S., Tuggle C.K., Rothschild M.F.;
RT "Mapping of the CYP1A1, SSTR1 and TTF1 genes to pig chromosome 7q
RT refines the porcine-human comparative map.";
RL AnIm. Genet. 31:318-321(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF148990; AAG40780.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECCEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECCEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1 1
FT NON_TER 315 315
SQ SEQUENCE 315 AA; 34355 MW; 0B973038C472A882 CRC64;

Query Match 22.5%; Score 497; DB 6; Length 315;
Best Local Similarity 30.6%; Pred. No. 6.1e-35;
Matches 108; Conservative 67; Mismatches 134; Indels 44; Gaps 7;

QY 29 PLPDCGACAPGGGRRRLPQPAWVEGSSARLWEQATGTGMMDLEASLLPTGPNASNSD 88
Db 2 PSPCPGSGEGXSGSR-----GPGAGTAD---GMEEPGRNASQNGT 38
QY 89 GPDNLTSGSPRTGSISYINIMPSVEGTICLLGIGNSTVIFAVVKKSKLHWCNNVFD 148
Db 39 LSEGQSA-----ILISFIYSVCLVGLCGNSMWIYILRYAKMKTATN--- 82
QY 149 IFIINLSVVDLFLGMPFMIHQMGNGVHFGETMCTLTITAMDANSQFTSTYILTAMAI 208
Db 83 IYILNLAIADLMLSVPLVTSTLLRH-WFGALLCRLVLSVDAVNMTSICYCLTVLSV 141
QY 209 DRYLATVHPISSTKFRKPSVATLVICLLMAISFISTPVMLYARLIPPGAVGCGIRLP 268
Db 142 DRYVAVVHPKARVRRPTVAKVNVNLGVVLSLVLPPIVVESTRTANSDGTVACNMMLP 201
QY 269 NP-DTDLWFTLYQFFLAFALPFVITAAVYRILQRTSSVAPASQSRIRLRTKRYTRA 327
Db 202 EPAQRWLVGFLVTFMLGFLLPVGAICLCYVLIITAKRMVALKAGWQQRKRSEKITLMV 261
QY 328 IAICLVFVCWAFYVYLQTLQSLISRPITLTFVYLYNAAISLGYANSCINPFVY 380
Db 262 MMYVAVVICMMPFYVQLVNVFAEQDDATVSQL--SVILGYANSCANPILY 311

RESULT 14
Q95KS6 PRELIMINARY; PRT; 346 AA.
AC Q95KS6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Somatostatin receptor subtype 1 (Fragment).
GN SST1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PIUTITARY;
RA Debus N., Dutour A., Vuaroqueaux V., Oliver C., Ouafik L.;
RT "The ovine somatostatin receptor subtype 1 (osst1): Partial cloning
RT and tissue distribution.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PIUTITARY;
RA Debus N.;

RL Thesis (1999),
RL Department of Intercellular communications in Endocrinology,
RL University of Aix-Marselles II, Marselles, France.
DR EMBL; AJ314853; CAC69545.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECCEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECCEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 346 AA; 38479 MW; 65547713CF2CA5C6 CRC64;
SQ SEQUENCE 346 AA; 38479 MW; 65547713CF2CA5C6 CRC64;

Query Match 22.4%; Score 494.5; DB 6; Length 346;
Best Local Similarity 33.3%; Pred. No. 1.1e-34;
Matches 98; Conservative 69; Mismatches 116; Indels 11; Gaps 5;

QY 100 PRGGSISY--INIIMPSVEGTICLLGIGNSTVIFAVVKKSKLHWCNNVDFIINLSV 156
Db 1 PQNGTLESGQSAIILISFIYSVCLVGLCGNSMWIYILRYAKMKTATN---IYILNLAI 57
QY 157 VDLLELGMFPMIHQMGNGVHFGETMCTLTITAMDANSQFTSTYILTAMADRYLATVH 216
Db 58 ADELMLSVPLVTSTLLRH-WFGALLCRLVLSVDAVNMTSICYCLTVLSVDRYAVVH 116
QY 217 PISSTKFRKPSVATLVICLLMAISFISTPVMLYARLIPPGAVGCGIRLPN-DTDLX 275
Db 117 PIKAARYRRPTVAKVNVNLGVVLSLVLPPIVVESTRTANSDGTVACNMMLPEPAQRWL 176
QY 276 WFTLYQFFLAFALPFVITAAVYRILQRTSSVAPASQSRIRLRTKRYTRAIAICLVF 335
Db 177 GFVLYTFMLGFLLPVGAICLCYVLIITAKRMVALKAGWQQRNGSERKITLMVAVVVFV 236
QY 336 VCMAPYVYLQTLQSLISRPITLTFVYLYNAAISLGYANSCINPFYIVLCETFRK 389
Db 237 ICMPFYVQLVNVFAEQDDATVSQL--SVILGYANSCANPILYGLSDMFKR 287

RESULT 15
Q9DGQ6 PRELIMINARY; PRT; 380 AA.
ID Q9DGQ6
AC Q9DGQ6;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Somatostatin receptor type two.
GN SST2.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20453044; Pubmed=10996426;
RA Lin X., Janovick J.A., Cardenas R., Conn P.M., Peter R.E.;
RT "Molecular cloning and expression of a type-two somatostatin receptor
RT in goldfish brain and pituitary.";
RL Mol. Cell. Endocrinol. 166:75-87(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF139597; AAF98367.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECCEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECCEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 380 AA; 43146 MW; CE897FF7537CFA30 CRC64;

Query Match 22.0%; Score 487; DB 13; Length 380;
Best Local Similarity 32.4%; Pred. No. 5.6e-34;
Matches 112; Conservative 68; Mismatches 140; Indels 26; Gaps 8;

[illegible]

Search completed: February 13, 2003, 14:00:15
Job time : 31.2615 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:56:01 ; Search time 15.1596 Seconds
(without alignments)
2676.114 Million cell updates/sec

Title: US-09-885-478-2
Perfect score: 2212
Sequence: 1 MSVGAMKKGVGRAVLGGGS.....LRVSNAGTADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	2207	99.8	422	2 JC7080	melanin-concentrat
2	565.5	25.6	340	2 JC7695	G protein-coupled
3	533	24.1	369	2 D41795	somatostatin recep
4	531.5	24.0	369	2 B41795	somatostatin recep
5	527	23.8	369	2 A45291	somatostatin recep
6	525.5	23.8	369	2 JC2083	somatostatin recep
7	515	23.3	346	2 S29248	somatostatin recep
8	514	23.2	391	2 A41795	somatostatin recep
9	513.5	23.2	388	2 JN0605	somatostatin recep
10	508	23.0	391	2 C41795	somatostatin recep
11	504.5	22.8	418	2 A46226	somatostatin recep
12	497.5	22.5	391	2 A39297	somatostatin recep
13	494.5	22.4	384	2 JC4629	brain-specific som
14	483	21.8	384	2 JC4629	somatostatin recep
15	480.5	21.7	428	2 S30508	probable G protein
16	478.5	21.6	363	2 I57955	somatostatin recep
17	478.5	21.6	364	2 JN0763	somatostatin recep
18	472	21.3	428	2 A44021	somatostatin recep
19	470.5	21.3	363	2 I57940	somatostatin recep
20	453.5	20.5	398	2 A57510	mu opioid receptor
21	453	20.5	372	2 I38532	delta opioid recep
22	452.5	20.5	398	2 I56517	mu opioid receptor
23	448	20.3	400	2 I56553	mu opiate receptor
24	447	20.2	392	2 S65693	opioid receptor mu
25	446.5	20.2	372	2 S34592	delta opioid recep
26	445.5	20.1	398	2 I56504	mu opioid receptor
27	441	19.9	372	2 B48227	delta opioid recep
28	435.5	19.7	380	2 JC2338	kappa opioid recep
29	431.5	19.5	380	2 A55259	kappa opioid recep

30	421	19.0	328	2 I38973	G protein-coupled
31	420.5	19.0	380	2 A48227	kappa opioid recep
32	419	18.9	380	2 S36143	kappa opioid recep
33	413	18.7	370	2 S43087	orphan opioid rece
34	411.5	18.6	367	2 I49022	kappa opioid recep
35	411.5	18.6	367	2 JC2421	opioid receptor ho
36	410.5	18.6	367	2 I56520	G protein-coupled
37	409.5	18.5	333	2 I38974	G protein-coupled
38	409.5	18.5	380	2 JC2434	kappa opioid recep
39	407	18.4	373	2 JE0087	delta opioid recep
40	372.5	16.8	359	2 I51372	angiotensin II rec
41	368	16.6	362	2 JN0694	angiotensin II rec
42	361	16.3	423	2 JC7677	allatostatin recep
43	347	15.7	371	2 JC5796	probable chemotatr
44	341	15.4	350	2 A42009	N-formyl peptide r
45	341	15.4	359	2 A42656	angiotensin II rec

ALIGNMENTS

RESULT 1					
JC7080					
melanin-concentrating hormone receptor [validated] - human					
N;Alternate names: MCHR; orphan somatostatin-like receptor 1 (SLC-1)					
C;Species: Homo sapiens (man)					
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000					
C;Accession: JC7080					
R;Shimomura, Y.; Mori, M.; Sugo, T.; Ishibashi, Y.; Abe, M.; Kurokawa, T.; Onda, H.;					
Biochem. Biophys. Res. Commun. 261, 622-626, 1999					
A;Title: Isolation and identification of melanin-concentrating hormone as the endogen					
A;Reference number: JC7080; MUID:99373129; PMID:10441476					
A;Accession: JC7080					
A;Molecule type: mRNA					
A;Residues: 1-422 <SH1>					
A;Note: It is uncertain wheather Met-1, Met-6 or Met-70 is the initiation codon					
C;Superfamily: neurokinin 1 receptor					
C;Keywords: hormone receptor; transmembrane protein					
Query Match					
Best Local Similarity 99.8%; Score 2207; DB 2; length 422;					
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MSVGAMKKGVGRAVLGGSGCOATEDEPLDGCACAPGGGRWRLPQPAWEGSSARL	60		
DB	1	MSVGAMKKGVGRAVLGGSGCOATEDEPLDGCACAPGGGRWRLPQPAWEGSSARL	60		
QY	61	WEQATGTGWMDEASLLPTGPNASNTSDPDNLTASGSPRTGTSYINIIMPSVFGTTC	120		
DB	61	WEQATGTGWMDEASLLPTGPNASNTSDPDNLTASGSPRTGTSYINIIMPSVFGTTC	120		
QY	121	LLGIIGNSTVFPAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNVWHF	180		
DB	121	LLGIIGNSTVFPAVVKKSKLHWCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNVWHF	180		
QY	181	GETMCTLTAMDANSQFTSTYIILTAMADRYLATVHPISSTFRKPSVATLVICLMAIS	240		
DB	181	GETMCTLTAMDANSQFTSTYIILTAMADRYLATVHPISSTFRKPSVATLVICLMAIS	240		
QY	241	FISITPWLTYARLIPFGGAVGCGILPNPDTLWFTLYQFFLAFALPFVITAAYVRI	300		
DB	241	FISITPWLTYARLIPFGGAVGCGILPNPDTLWFTLYQFFLAFALPFVITAAYVRI	300		
QY	301	LQRMSSVAPASQSRIRLRTKRVFPAIAICLVFVWCAPYVVLQTLQSLSRPTLFVY	360		
DB	301	LQRMSSVAPASQSRIRLRTKRVFPAIAICLVFVWCAPYVVLQTLQSLSRPTLFVY	360		
QY	361	LYNAALISGYANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK	420		
DB	361	LYNAALISGYANSCLNPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK	420		
QY	421	GT 422			


```

Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
A>Title: Cloning and characterization of a fourth human somatostatin receptor.
A:Reference number: A47457; MUID:93248256; PMID:8483934
A:Accession: A47457
A:Molecule type: DNA
A:Residues: 1-82, 'T', 84-364, 'K', 366-388 <ROH>
A:Cross-references: GB:L07883; NID:g307429; PIDN:AAA60565.1; PID:g307430
A>Note: sequence extracted from NCBI backbone (NCBIN:130856, NCBIIP:130858)
C:Comment: This protein mediates the diverse actions of the tetradecapptide somatostatin.
C:Genetics:
A:Gene: GDB:SSTR4
A:Cross-references: GDB:202662; OMIM:182454
A:Map position: 20p11.2-20p11.2
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phospholipase;
F;47-73/Domain: transmembrane #status predicted <TM1>
F;84-109/Domain: transmembrane #status predicted <TM2>
F;121-142/Domain: transmembrane #status predicted <TM3>
F;162-184/Domain: transmembrane #status predicted <TM4>
F;208-238/Domain: transmembrane #status predicted <TM5>
F;257-284/Domain: transmembrane #status predicted <TM6>
F;291-314/Domain: transmembrane #status predicted <TM7>
F;24/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;119-198/Disulfide bonds: #status predicted
F;161,253/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted
F;327/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match          23.2%; Score 513.5; DB 2; Length 388;
Best Local Similarity 31.7%; Pred. No. 2,7e-35;
Matches 107; Conservative 74; Mismatches 118; Indels 39; Gaps 9;

QY 62 EQATGTGMDLEASLTGPNASNTSDGPDNLTSGSPRTGSISYINIMPSVEGTICL 121
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 12 EEGLGTAW-----PSAANASSAPAEAEAEVAGPGDARAAGM-VAIQCIYALVCL 59

QY 122 LGIIGNSTVIFAVVKKSKLHWCNPNPDIIFIINLSYVDLFLGLMPFMI-----HQLMGN 175
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 VGLVGNALVIFVILRYAKMKTATN---IYLLNLAVADELFMLSVFVASSALRH----- 111

QY 176 GWHFEGTMTLLTPAMDANSQFTSTYILLTAMADRYLATVHPISSTKFRKSVATLVICL 235
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 --WPEGSVLCRAVLSVDGLNMFSTVECLTVLSVDRYVAVVHPLRAATYRRPSVAKLINLG 169

QY 236 LMAISFISITPVMYLARLIPERPGG-AVCGGIRLPNPDIDLW---FTLYQFFLAFLPFV 291
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 170 VWLASLVLTLPALFADTRPARGGQAVACINQMPHP---AWSAVFVVYTFLLGLLPVL 225

QY 292 VITAAYVRILQRMSSVAPASQSRISRLRKRYTRTAIAICLVFVWCWAPYVVLQTLQSI 351
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 226 AIGLCYLLIVGKRAVALRAGWQRRRSEKIKTRVLVMVVVFVLCWMDYVYVQLNLVV 285

QY 352 SRPTLTFVLYLNAAISLGYANSCLNPFVYIVLCETFRK 389
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 286 TSLDAT--VNHVSLILSYANSKANPILYGFLLSDNERR 320

RESULT 10
C41795
somatostatin receptor 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
C:Accession: C41795
R:Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A>Title: Cloning and functional characterization of a family of human and mouse somatostatin receptors.
A:Reference number: A41795; MUID:92108031; PMID:1346068
A:Accession: C41795
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-391 <YAM>
A:Cross-references: GB:M81831; NID:g201058; PIDN:AAA58255.1; PID:g201059
C:Superfamily: vertebrate rhodopsin

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C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein	
Query Match	23.0%; Score 508; DB 2; Length 391;
Best Local Similarity	30.7%; Pred. No. 7.8e-35;
Matches 111; Conservative	73; Mismatches 134; Indels 44; Gaps 8;
QY	29 PLPDCGACAPGGGRRRLPQPAWEGSSARLWEQATGTGWMDEASLPTGPNASNTSD 88
Db	14 PSPSPGSCG-----EGACSR---GPGSGAAD---GMEEPGRNASQNGT 50
QY	89 GPDNLTSGASPPRTGSISYINIMPSVEGTICLLIGNSTVIFA VVKSKSLHWCNNVPD 148
Db	51 LSEGQSA-----LISFIYSVCLVGLCGNSMVIYILRYAKMKTA TN--- 94
QY	149 IFIINLSVVDLFLGLMPEMIHQLMGNGVWHFGETMCTLTITAMDANSQFTSTYITAMAI 208
Db	95 IYIINLAIADELLMSVPELVSTLRLH-WPFGALLCRLVLSVDVNMFTSIYCLTVLSV 153
QY	209 DRYLATVHPISSTFKRKPVSATLVLCILMALSFISITPVMLEVARLIPFGAGVGGRILP 268
Db	154 DRYVAVVHPKAKARYRRPTVAKVNVNLGWWLSDLVILPIVFSRTAANSDDGTACNMILMP 213
QY	269 NP-DTDLXWETLYQFLAFALPEVVITAAVVRILQRM TSSVAPASQRSIRLRTRKVRTA 327
Db	214 EPAQRWLVGVELTYELMGFLLPVGAIICLYVLLIAKRMVALKAGWQQRKRSEKITLMV 273
QY	328 IAICLVEFVCWAPYVVLQTLQSLISRPTLTFFVYLYNNAISLGYANSCLNPEFYIVLCETF 387
Db	274 MMVVMVEVICMPEFYVVLVNVFAEQDATVSQ L---SVILGYANSCANPILGLFLSDNF 330
QY	388 RK 389
Db	331 KR 332

RESULT 11
A46226
somatostatin receptor 3 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A46226; S32501
R:Yamada, Y.; Reisine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Seino, M.;
Mol. Endocrinol. 6, 2136-2142, 1992
A:Title: Somatostatin receptors, an expanding gene family: cloning and functional cha
A:Reference number: A46226; MUID:93149123; PMID:1337145
A:Accession: A46226
A:Molecule type: DNA
A:Residues: 1-418 <YAM>
A:Cross-references: GB:M96738; NID:g338498; PIDN:AAA60592.1; PID:g338499
A:Note: sequence extracted from NCBI backbone (NCBIN:123685, NCBI:P:123690)
R:Corneiss, J.D.; Demchyshyn, L.L.; Seeman, P.; van Tol, H.H.M.; Srikant, C.B.; Kent,
FEBS Lett. 321, 279-284, 1993
A:Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays pr
A:Reference number: S32501; MUID:93238970; PMID:8097479
A:Accession: S32501
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-418 <COR>
C:Genetics:
A:Gene: GDB:SSTR3
A:Cross-references: GDB:134187; OMIM:182453
A:Map position: 22q13.1-22q13.1
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F:44-70/Domain: transmembrane #status predicted <TM1>
F:81-106/Domain: transmembrane #status predicted <TM2>
F:118-139/Domain: transmembrane #status predicted <TM3>
F:159-181/Domain: transmembrane #status predicted <TM4>
F:203-233/Domain: transmembrane #status predicted <TM5>
F:255-282/Domain: transmembrane #status predicted <TM6>
F:289-316/Domain: transmembrane #status predicted <TM7>
F:17,30/Binding site: carbohydrate (Asn) (covalent) #status predicted

